Table 70: Comparative Sequences relating to SAG 1280

ATACCTTTATTGAGTTTGAAAACCTTGGAATTGATTTTCTTTTTGTGGATGAGGCTCATC
ACTTCAAGAATATCCGTCCAATCACTGGACTTGGGAATGTAGCTGGAATCACCAACACAA
CTTCTAAAAAGAACGTGGATATGGAGATGAAGGTGAGACAAGTACAGGCAGAGCATGGAG
ATAGAAATGTCGTTTTTGCGACAGGAACACCAGTTTCTAACTCTATTAGTGAACTTTTCA
CCATGATGGATTACATTCAACCTGATGTCTTGGAACGATACCTGGTATCAAATTTTGACT
CCTGGGTTGGGGCTTTTGGGAATATCGAAAACTCCATGGAACTAGCCCCGACAGGAGATA
AGTACCAACCCAAGAAACGGTTCAAGAAATTTGTCAACCTTCCTGAACTCATGCGAATCT
ACAAGGAAACTGCCGATATTCAGACCTCAGACATGCTTGATTTACCAGTACCGGAAGCTA
AGATTATTGCGGTGGAAAGCGAGTTAACGCAAGCTCAGAAATACTATTTGGAAGAGCTGG
TAAAGCGTTCAGACGCTATCAAGTCAGGTAGTGTTGATCCAAGTAGAGATAACATGCTTA
AAATCACAGGAGAAGCCAGAAAACTAGCTATTGATATGCGGTTGATTGACCCTACTTACT
CCTTATCGGATAATCAGAAAATCCTTCAAGTAGTCGATAATGTCGAGCGGATTTACCGTG
ATGGAGCTGGAGACAAAGCCACTCAGATGATTTTCTCAGATATTGGAACCCCTAAAAGTA
AGGAAGAAGGGTTTGATGTCTACAATGAACTTAAGGACTTGTTTGTCGATCGAGGGATAC
CAAAAGAAGAAATTGCCTTTGTCCATGATGCCAATACTGATGAGAAGAAAAACTCTCTGT
CACGCAAGGTCAATAGTGGAGAAGTACGGATTCTCATGGCTTCTACGGAAAAAGGGGGAA
CAGGATTAAACGTCCAATCTCGCATGAAAGCTGTCCACTATTTAGACGTTCCCTGGAGGC
CCTCAGACATTGTCCAGCGAAATGGACGACTAATTCGACAAGGAAACATGCACCAGGAGG
TAGATATTTATCACTATATTACTAAAGGGAGCTTTGACAATTACCTCTGGCAGACGCAGG
AGAATAAGCTAAAGTATATCACCCAGATAATGACCTCAAAAGATCCTGTGAGATCAGCTG
AAGACATTGATGAACAAACCATGACCGCCTCAGACTTTAAGGCATTGGCAACTGGGAACC
CTTATCTCAAACTCAAAATGGAGTTGGAAAATGAACTGACAGTTTTAGAGAATCAAAAAC
GAGCCTTTAATCGCTCCAAAGACGAGTATCGCCATACCATTTCCTATAGCGAGAAGCACC
TCCCTATTATGGAAAAACGGTTGAGTCAATATGATAAAGATATTGCCCAATCTTTGGCAA
CCAAGTCGCAAGATTTTGTCATGCGATTTGACAATCAAGCAATGGATAATCGTGCTGAAG
CTGGGGACTATCTGCGAAAACTCATTACCTATAACCGCTCAGAGACCAAGGAAGTCAGGA
CACTTGCCAGCTTTAGAGGATTTGATTTAAAAATGACTACACGAGGTGCTAGTGAGCCCT
TACCAGAAACCATTTCTTTAATGATTGTAGGTGATAACCAGTATACTGTCGCCCTTGATT
TGAAATCAGACGTGGGAACCATTCAACGGATTAGTAATGCCATTGACCATATTATAGATG
ACCAAGAAAAGACGCAAGAGCTGGTAAAGGATTTAAAAGATAAGCTACGAGTAGCCAAAG
TAGAAGTTGATAAAGTCTTTCCAAAGGAAGAGGACTATCAGCTTGTAAAGGCTAAGTATG
ATGTTTTAGCTCCCTTGGTTGAAAAAGAAGCAGAGATTGAAGAGATAGATGCAGCTTTGG
CCAAGTTTAGTGAAGATACAACACCCCAAAAGAAGCAACAAATAGCACTCGAGATA

SEQ ID. NO. 7002
STRAIN H36B
GGAGGGAAAATGAATCAAGAAGTCTTACTACAAATGAT
GAGAGCCACTATTCCTCGTGATAGAGCCTTGCTTGAGGCATTTTTATATT
ACCAAGCAGAGCATTTTGATGAGGAGTGGGATAGTCTTATTCATCAGTTT
ATGACCAATAGGCAAGAAATAAATAAGTCTGTTCAAGTACTTCACTTTGA
GACAGATGTTTCAGCTTTTGTCCAGGCTAGTCCTTATGATACTGCTCATG
ATCTATTGACCTATACACAAGTTTTCGGCCAAAGTGGTCTTCAAAAACTA
GATAAACTATCGCCGTCTGAAAAAAACTTGGTGATAGAAGTGGCCTTGTT
CAATCTGGCCACTCGTTTTCAATTATTGGATTCCAATGGACACTACCAAA
CCATATCGCCGGATTCACTCTTACAAAAGAGTAGGGGAGCTAATTTGGTC
AATGTGTATCGTGTGGCTAATAATTTAGCGGATCGTATTAGTCGAGATAT
TGAACAGTTTCTCTTAACTTACGAGCCTGAGCTTGAAACTAGAGCTGATG
AAACTGTTCTAGAAAATGAAGAAACTGTTGATGAGCACAAAACAAGTGTT
CATCAAGCAATATCTTTTCGAGAAGAGGGCTCTCTGGTTATTGCTAGTTT
GGATGTAGATTTGTCTCAACTAGATGTTCAAATAGGAAAAACCAGTCATC
TGCCAGCTTATGAAGAGTTATCCTTACGACGTAAATTTGAGATTCTAACA
TATTTTGACCAAATTCGAAATGAACGTTCCAAAGTCCCAAGTTTTAGACG
AGGTGATTTTGACACAGAGATGGAAATGACACCAGTCTTTGATGGCGAGG
AATTACTTACTTATCTCGAAGCTGATGGCAGTCCCTATGAGCTGAAACGA
ACGCTGACTACAGTCGAAGAAAAGGAATTAGAAAAAATTGGACAAGCCAT
TAGGATAGAAAATCAAGAAAAATTGACTCAGCTAsGkATTGrTTTATCTC
AGTTTGACCCAGACCGAGTCGGTATTTTATTGkATGCAGCAGGTCGTyyT
CGTTTAwAwAATGCAGACCTTGCTTCACTAGGTGGTTATCCCAAAGCCTC
GGTAACTCAACTAGCCCTTGCGACAGAACTACTCCAAATGGGACTAAGTC
ATGAAAAGGTTGAATTTTTCTTTGGTAGCCAGCTTTCCATTGAAGAGCTG
CGACAAGTTGCCTACGCCTTTTTACACCAAGAACTCAGCAGAGAAGATGC
GGAGCAATTTGAAAAAGATAAAGGTAATCAGCCAGATTTAACTCTCAGAG
ATTGGAAAAGCAAGCTAGAGAAAGCTGAGGGAAAAGAAGTAGTTGATGAA
GAATTCGCGGAAAATCCACTGGTTCAGAGAGTATTGGACACTTATCCTCT
GGGGTCATTGGTTTCCTATAAGGGACAGGACTTTGAGGTCATGTCGGTCA
GCGATGCTCGAtTGAACGGTTTGATTCGGATTGAGTTAGTCAATGACTTT
TCGGATATCATTGAACAAAATCCAGTTCTTTATGTGAGGACCTGGGAAGA
AGTCAGTCAGGCACTTCATCAGCCAAAGGCAGAACCACAAACAGAGTTAG
AAGAAGCGGACCAAGAATTAAACCTATTCTCATTTCTGGAAGAGGAGCTA
GTTCAGAGTATTGGACTATTGGAACCAGATGATTCAGAAAATGGTCATAA
CGATACTGATCTTGAAGAAACAGATAATCAAATTCCTGAAGAGGAAGTCG
TCGAAACAATTCCAGAGATTCCAGTAACGGACTTTTATTTTCCAGAAGAT
TTGACGGACTTTTATCCTAAGACTGCTAGAGATAAGGTTGAGACAAACAT
TGTGGCCATTCGTTTGGTAAAAAATCTAGAAGTAGAGCACCGCAATGCTT
CACCAAGTGAACAAGAACTCCTTGCCAAGTATGTAGGCTGGGGTGGACTA
GCCAATGAATTTTTTGATGACTATAATCCAAAATTTTCTAAGGAACGAGA
AGAACTGAAGAGCCTAGTCACAGATAAAGAGTATTCGGATATGAAACAGT
CCTCCCTGACAGCCTATTACACAGACCCATCCCTGATCCGTCAGATGTGG
GATAAGTTGGAAAGAGATGGCTTTACAGGTGGCAAAATCCTAGATCCTTC
CATGGGAACAGGGAATTTCTTTGCGGCTATGCCAAAACACTTAAGAGAAA
AGAGTGAGTTGTATGGCGTAGAGTTAGATACTATTACAGGAGCTATTGCC
AAACACCTTCATCCCAATAGTCATATTGAAATTAAGGGATTTGAGACGGT
GGCTTTTAACGACAATAGTTTTGATTTGGTGATTTCAAATGTGCCCTTTG

Table 70: Comparative Sequences relating to SAG 1280

CCAATATACGAATTGCGGATAATAGGTACGATAGGCCTTACATGATTCAT
GACTACTTTGTCAAAAAGTCACTTGATTTGCTTCATGATGGTGGACAAGT
AGCGATTATCTCTTCCACAGGAACTATGGATAAGCGAACAGAAAACATCT
TACAAGATATTCGTGAGACAACTGAATTTCTTGGTGGGGTTCGACTGCCT
GACTCTGCCTTTAAGGCCATTGCAGGAACGAGTGTCACAACGGATATGTT
ATTCTTCCAGAAACACTTAGACAAGGGATATGTGGCAGACGATTTAGCCT
TTTCAGGTTCCATTCGCTATGACAAGGATAGTCGCATTTGGCTCAATCCT
TATTTTGATGGAGAATACAATAGCCAGGTGCTAGGAACCTACGAGGTCAG
GAATTTTAACGGAGGAACACTTTCTGTTAAGGGGACTAGTGATGACTTGA
TTGCAAGTGTTGAAACAGCTCTAAATCACGTTAAGGCCCCAAGAGAGATT
GATAGAAATGAGGTCATCATTAACCCAGATGTGTTGACCAAACAAGTCAA
TGATACCTCCATTCCAGCTGAAATGAGGGAAAATCTAGGTCAGTACAGTT
TTGGTTATCAGGGGTCTACAGTTTACTATCGAGATAACAAAGGCATTCGA
GTCGGAACCAAGACGGAAGAAATCAGTTACTATGTCGATGAAGAG

SEQ ID. NO. 7003
STRAIN 18RS21
GnAGGGAAAATGAATCAAGAAGTCTTACTACAAATGATGAGA
GCCACTATTCCTCGTGATAGAGCCTTGCTTGAGGCATTTTTATATTACCA
AGCAGAGCATTTTGATGAGGAGTGGGATAGTCTTATTCATCAGTTTATGA
CCAATAGGCAAGAAATAAATAAGTCTGTTCAAGTACTTCACTTTGAGACA
GATGTTTCAGCTTTTGTCCAGGCTAGTCCTTATGATACTGCTCATGATCT
ATTGACCTATACACAAGTTTTCGGCCAAAGTGGTCTTCAAAAACTAGATA
AACTATCGCCGTCTGAAAAAAACTTGGTGATAGAAGTGGCCTTGTTCAAT
CTGGCCACTCGTTTTCAATTATTGGATTCCAATGGACACTACCAAACCAT
ATCGCCGGATTCACTCTTACaAAAGAGTAGGGGAGCTAATTTGGTCAATG
TGTATCGTGTGGCTAATAATTTAGCGGATCGTATTAGTCGAGATATTGAA
CAGTTTCTCTTAACTTACGAGCCTGAGCTTGAAACTAGAGCTGATGAAAC
TGTTCTAGAAAATGAAGAAACTGTTGATGAGCACAAAACAAGTGTTCATC
AAGCAATATCTTTTCGAGAAGAGGGCTCTCTGGTTATTGCTAGTTTGGAT
GTAGATTTGTCTCAACTAGATGTTCAAATAGGAAAAACCAGTCATCTGCC
AGCTTATGAAGAGTTATCCTTACGACGTAAATTTGAGATTCTAACATATT
TTGACCAAATTCGAAATGAACGTTCCAAAGTCCCAAGTTTTAGACGAGGT
GATTTTGACACAGAGATGGAAATGACACCAGTCTTTGATGGCGAGGAATT
ACTTACTTATCTCGAAGCTGATGGCAGTCCCTATGAGCTGAAACGAACGC
TGACTACAGTtcGAAGAAAAGGAATTAGAAAAAATTGGACAAGCCATTAGG
ATAGAAAATCAAGAAAAATTGACTCAGCTAGGGATTGATTTATCTCAGTT
TGACCCAGACCGAGTCGGTATTTTATTGGATGCAGCAGGTCGTTTTCGTT
TAAAAAATGCAGACCTTGCTTTACTAGGTGGTTATCCCAAAGCCTCGGTA
ACTCAACTAGCCCTTGCGACAGAACTACTCCAAATGGGACTAAGTCATGA
AAAGGTTGAATTTTTCTTTGGTAGCCAGCTTTCCATTGAAGAGCTGCGAC
AAGTTGCCTACGCCTTTTTACACCAAGAACTCAGCAGAGAAGATGCGGAG
CAATTTGAAAAAGATAAAGGTAATCAGCCAGATTTAACTCTCAGAGATTG
GAAAAGCAAGCTAGAGAAAGCTGAGGGAAAAGAAGTAGTTGATGAAGAAT
TCGCGGAAAATCCACTGGTTCAGAGAGTATTGGACACTTATCCTCTGGGG
TCATTGGTTTCCTATAAGGGACAGGACTTTGAGGTCATGTCGGTCAGCGA
TGCTCGATTGAACGGTTTGATTCGGATTGAGTTAGTCAATGACTTTTCGg
ATATCATTGAACAAAATCCAGTTCtTTAtGTGAGGACCTGGGAAGAAGTC
AGTCAGGCACTTCATCAGCCAAAGGCAGAACCACAAACAGAGTTAGAAGA
AGCGGACCAAGAATTAAACCTATTCTCATTTCTGGAAGAGGAGCCAGTTC
AGAGTATTGGACTATTGGAACCAGaTGATTCAGAAAATGGTCATAACGAT
ACTGATCTTGAAGAAACAGATAATCAAATTCCTGAAGAGGAAGTCGTCGA
AACAATTCCAGAGATTCCAGTAACGGACTTTTATTTTCCAGAAGATTTGA
CGGACTTTTATCCTAAGACTGCTAGAGATAAGGTTGAGACAAACATTGTG
GCCATTCGTTTGGTAAAAAATCTAGAAGTAGAGCACCGCAATGCTTCACC
AAGTGAACAAGAACTCCTTGCCAAGTATGTAGGCTGGGGTGGACTAGCCA
ATGAATTTTTTGATGACTATAATCCAAAATTTTCTAAGGaACGAGAAGAA
CTGAAGAGCCTAGTCACAGATAAAGAGTATTCGGATATGAAACAGTCCTC
CCTGACAGCCTATTACACAGACCCATCCCTGATCCGTCAGATGTGGGATA
AGTTGGAAAGAGATGGCTTTACAGGTGGCAAAATCCTAGATCCTTCCATG
GGAACAGGGAATTTCTTTGCGGCTATGCCAAAACACTTAAGAGAAAAGAG
TGAGTTGTATGGCGTAGAGTTAGATACTATTACAGGAGCTATTGCCAAAC
ACCTTCATCCCAATAGTCATATTGAAATTAAGGGATTTGAGACGGTGGCT
TTTAACGACAATAGTTTTGATTTGGTGATTTCAAATGTGCCCTTTGCCAA
TATACGAATTGCGGATAATAGGTACGATAGGCCTTACATGATTCATGACT
ACTTTGTCAAAAAGTCACTTGATTTGCTTCATGATGGTGGACAAGTAGCG
ATTATCTCTTCCACAGGAACTATGGATAAGCGAACAGAAAACATCTTACA
AGATATTCGTGAGACAACTGAATTTCTTGGTGGGGTTCGACTGCCTGACT
CTGCCTTTAAGGCCATTGCAGGAACGAGTGTCACAACGGATATGTTATTC
TTCCAGAAACACTTAGACAAGGGATATGTGGCAGACGATTTAGCCTTTTC
AGGTTCCATTCGCTATGACAAGGATAGTCGCATTTGGCTCAATCCTTATT
TTGATGGAGAATACAATAGCCAGGTGCTAGGAACCTACGAGGTCAGGAAT
TTTAACGGAGGAACACTTTCTGTTAAGGGGACTAGTGATGACTTGATTGC
AAGTGTTGAAACAGCTCTAAATCACGTTAAGGCCCCAAGAGAGATTGATA
GAAATGAGGTCATCATTAACCCAGATGTGTTGACCAAACAAGTCAATGAT
ACCTCCATTCCAGCTGAAATGAGGGAAAATCTAGGTCAGTACAGTTTTGG
TTATCAGGGGTCTACAGTTTACTATCGAGATAACAAAGGCATTCGAGTCG
GAACCAAGACGGAAGAAATCAGTTACTATGTCGATGAAGAG

MSA Alignment Results: Pretty output

```
PRETTY of: /biotmp/msa31161.2{*}   June 20, 2002 10:41  ..
```

Table 70: Comparative Sequences relating to SAG 1280

```
msa31161.2{327dNt_2603}   GgAGGGAAAA TGAATCAAGA AGTCTTACTA CAAATGATGA GAGCCACTAT
msa31161.2{327d_18RS21}   GnAGGGAAAA TGAATCAAGA AGTCTTACTA CAAATGATGA GAGCCACTAT
msa31161.2{327dNT_H36B}   GgAGGGAAAA TGAATCAAGA AGTCTTACTA CAAATGATGA GAGCCACTAT
              Consensus   *-******** ********** ********** ********** **********

                          51                                                100
msa31161.2{327dNt_2603}   TCCTCGTGAT AGAGCCTTGC TTGAGGCATT TTTATATTAC CAAGCAGAGC
msa31161.2{327d_18RS21}   TCCTCGTGAT AGAGCCTTGC TTGAGGCATT TTTATATTAC CAAGCAGAGC
msa31161.2{327dNT_H36B}   TCCTCGTGAT AGAGCCTTGC TTGAGGCATT TTTATATTAC CAAGCAGAGC
              Consensus   ********** ********** ********** ********** **********

                          101                                               150
msa31161.2{327dNt_2603}   ATTTTGATGA GGAGTGGGAT AGTCTTATTC ATCAGTTTAT GACCAATAGG
msa31161.2{327d_18RS21}   ATTTTGATGA GGAGTGGGAT AGTCTTATTC ATCAGTTTAT GACCAATAGG
msa31161.2{327dNT_H36B}   ATTTTGATGA GGAGTGGGAT AGTCTTATTC ATCAGTTTAT GACCAATAGG
              Consensus   ********** ********** ********** ********** **********

                          151                                               200
msa31161.2{327dNt_2603}   CAAGAAATAA ATAAGTCTGT TCAAGTACTT CACTTTGAGA CAGATGTTTC
msa31161.2{327d_18RS21}   CAAGAAATAA ATAAGTCTGT TCAAGTACTT CACTTTGAGA CAGATGTTTC
msa31161.2{327dNT_H36B}   CAAGAAATAA ATAAGTCTGT TCAAGTACTT CACTTTGAGA CAGATGTTTC
              Consensus   ********** ********** ********** ********** **********

                          201                                               250
msa31161.2{327dNt_2603}   AGCTTTTGTC CAGGCTAGTC CTTATGATAC TGCTCATGAT CTATTGACCT
msa31161.2{327d_18RS21}   AGCTTTTGTC CAGGCTAGTC CTTATGATAC TGCTCATGAT CTATTGACCT
msa31161.2{327dNT_H36B}   AGCTTTTGTC CAGGCTAGTC CTTATGATAC TGCTCATGAT CTATTGACCT
              Consensus   ********** ********** ********** ********** **********

                          251                                               300
msa31161.2{327dNt_2603}   ATACACAAGT TTTCGGCCAA AGTGGTCTTC AAAAACTAGA TAAACTATCG
msa31161.2{327d_18RS21}   ATACACAAGT TTTCGGCCAA AGTGGTCTTC AAAAACTAGA TAAACTATCG
msa31161.2{327dNT_H36B}   ATACACAAGT TTTCGGCCAA AGTGGTCTTC AAAAACTAGA TAAACTATCG
              Consensus   ********** ********** ********** ********** **********

                          301                                               350
msa31161.2{327dNt_2603}   CCGTCTGAAA AAAACTTGGT GATAGAAGTG GCCTTGTTCA ATCTGGCCAC
msa31161.2{327d_18RS21}   CCGTCTGAAA AAAACTTGGT GATAGAAGTG GCCTTGTTCA ATCTGGCCAC
msa31161.2{327dNT_H36B}   CCGTCTGAAA AAAACTTGGT GATAGAAGTG GCCTTGTTCA ATCTGGCCAC
              Consensus   ********** ********** ********** ********** **********

                          351                                               400
msa31161.2{327dNt_2603}   TCGTTTTCAA TTATTGGATT CCAATGGACA CTACCAAACC ATATCGCCGG
msa31161.2{327d_18RS21}   TCGTTTTCAA TTATTGGATT CCAATGGACA CTACCAAACC ATATCGCCGG
msa31161.2{327dNT_H36B}   TCGTTTTCAA TTATTGGATT CCAATGGACA CTACCAAACC ATATCGCCGG
              Consensus   ********** ********** ********** ********** **********

                          401                                               450
msa31161.2{327dNt_2603}   ATTCACTCTT ACAAAAGAGT AGGGGAGCTA ATTTGGTCAA TGTGTATCGT
msa31161.2{327d_18RS21}   ATTCACTCTT ACAAAAGAGT AGGGGAGCTA ATTTGGTCAA TGTGTATCGT
msa31161.2{327dNT_H36B}   ATTCACTCTT ACAAAAGAGT AGGGGAGCTA ATTTGGTCAA TGTGTATCGT
              Consensus   ********** ********** ********** ********** **********

                          451                                               500
msa31161.2{327dNt_2603}   GTGGCTAATA ATTTAGCGGA TCGTATTAGT CGAGATATTG AACAGTTTCT
msa31161.2{327d_18RS21}   GTGGCTAATA ATTTAGCGGA TCGTATTAGT CGAGATATTG AACAGTTTCT
msa31161.2{327dNT_H36B}   GTGGCTAATA ATTTAGCGGA TCGTATTAGT CGAGATATTG AACAGTTTCT
              Consensus   ********** ********** ********** ********** **********

                          501                                               550
msa31161.2{327dNt_2603}   CTTAACTTAC GAGCCTGAGC TTGAAACTAG AGCTGATGAA ACTGTTCTAG
msa31161.2{327d_18RS21}   CTTAACTTAC GAGCCTGAGC TTGAAACTAG AGCTGATGAA ACTGTTCTAG
msa31161.2{327dNT_H36B}   CTTAACTTAC GAGCCTGAGC TTGAAACTAG AGCTGATGAA ACTGTTCTAG
              Consensus   ********** ********** ********** ********** **********

                          551                                               600
msa31161.2{327dNt_2603}   AAAATGAAGA AACTGTTGAT GAGCACAAAA CAAGTGTTCA TCAAGCAATA
msa31161.2{327d_18RS21}   AAAATGAAGA AACTGTTGAT GAGCACAAAA CAAGTGTTCA TCAAGCAATA
msa31161.2{327dNT_H36B}   AAAATGAAGA AACTGTTGAT GAGCACAAAA CAAGTGTTCA TCAAGCAATA
              Consensus   ********** ********** ********** ********** **********

                          601                                               650
msa31161.2{327dNt_2603}   TCTTTTCGAG AAGAGGGCTC TCTGGTTATT GCTAGTTTGG ATGTAGATTT
msa31161.2{327d_18RS21}   TCTTTTCGAG AAGAGGGCTC TCTGGTTATT GCTAGTTTGG ATGTAGATTT
msa31161.2{327dNT_H36B}   TCTTTTCGAG AAGAGGGCTC TCTGGTTATT GCTAGTTTGG ATGTAGATTT
              Consensus   ********** ********** ********** ********** **********

                          651                                               700
msa31161.2{327dNt_2603}   GTCTCAACTA GATGTTCAAA TAGGAAAAAC CAGTCATCTG CCAGCTTATG
msa31161.2{327d_18RS21}   GTCTCAACTA GATGTTCAAA TAGGAAAAAC CAGTCATCTG CCAGCTTATG
msa31161.2{327dNT_H36B}   GTCTCAACTA GATGTTCAAA TAGGAAAAAC CAGTCATCTG CCAGCTTATG
              Consensus   ********** ********** ********** ********** **********
```

Table 70: Comparative Sequences relating to SAG 1280

```
                         701                                                750
msa31161.2{327dNt_2603}  AAGAGTTATC CTTACGACGT AAATTTGAGA TTCTAACATA TTTTGACCAA
msa31161.2{327d_18RS21}  AAGAGTTATC CTTACGACGT AAATTTGAGA TTCTAACATA TTTTGACCAA
msa31161.2{327dNT_H36B}  AAGAGTTATC CTTACGACGT AAATTTGAGA TTCTAACATA TTTTGACCAA
              Consensus  ********** ********** ********** ********** **********

                         751                                                800
msa31161.2{327dNt_2603}  ATTCGAAATG AACGTTCCAA AGTCCCAAGT TTTAGACGAG GTGATTTTGA
msa31161.2{327d_18RS21}  ATTCGAAATG AACGTTCCAA AGTCCCAAGT TTTAGACGAG GTGATTTTGA
msa31161.2{327dNT_H36B}  ATTCGAAATG AACGTTCCAA AGTCCCAAGT TTTAGACGAG GTGATTTTGA
              Consensus  ********** ********** ********** ********** **********

                         801                                                850
msa31161.2{327dNt_2603}  CACAGAGATG GAAATGACAC CAGTCTTTGA TGGCGAGGAA TTACTTACTT
msa31161.2{327d_18RS21}  CACAGAGATG GAAATGACAC CAGTCTTTGA TGGCGAGGAA TTACTTACTT
msa31161.2{327dNT_H36B}  CACAGAGATG GAAATGACAC CAGTCTTTGA TGGCGAGGAA TTACTTACTT
              Consensus  ********** ********** ********** ********** **********

                         851                                                900
msa31161.2{327dNt_2603}  ATCTCGAAGC TGATGGCAGT CCCTATGAGC TGAAACGAAC GCTGACTACA
msa31161.2{327d_18RS21}  ATCTCGAAGC TGATGGCAGT CCCTATGAGC TGAAACGAAC GCTGACTACA
msa31161.2{327dNT_H36B}  ATCTCGAAGC TGATGGCAGT CCCTATGAGC TGAAACGAAC GCTGACTACA
              Consensus  ********** ********** ********** ********** **********

                         901                                                950
msa31161.2{327dNt_2603}  GTCGAAGAAA AGGAATTAGA AAAAATTGGA CAAGCCATTA GGATAGAAAA
msa31161.2{327d_18RS21}  GTCGAAGAAA AGGAATTAGA AAAAATTGGA CAAGCCATTA GGATAGAAAA
msa31161.2{327dNT_H36B}  GTCGAAGAAA AGGAATTAGA AAAAATTGGA CAAGCCATTA GGATAGAAAA
              Consensus  ********** ********** ********** ********** **********

                         951                                               1000
msa31161.2{327dNt_2603}  TCAAGAAAAA TTGACTCAGC TAgGgATTGa TTTATCTCAG TTTGACCCAG
msa31161.2{327d_18RS21}  TCAAGAAAAA TTGACTCAGC TAgGgATTGa TTTATCTCAG TTTGACCCAG
msa31161.2{327dNT_H36B}  TCAAGAAAAA TTGACTCAGC TAsGkATTGr TTTATCTCAG TTTGACCCAG
              Consensus  ********** ********** **_*_****_ ********** **********

                         1001                                              1050
msa31161.2{327dNt_2603}  ACCGAGTCGG TATTTTATTG gATGCAGCAG GTCGTttTCG TTTAaAaAAT
msa31161.2{327d_18RS21}  ACCGAGTCGG TATTTTATTG gATGCAGCAG GTCGTttTCG TTTAaAaAAT
msa31161.2{327dNT_H36B}  ACCGAGTCGG TATTTTATTG kATGCAGCAG GTCGTyyTCG TTTAwAwAAT
              Consensus  ********** ********** _********* *****__*** ****_*_***

                         1051                                              1100
msa31161.2{327dNt_2603}  GCAGACCTTG CTTtACTAGG TGGTTATCCC AAAGCCTCGG TAACTCAACT
msa31161.2{327d_18RS21}  GCAGACCTTG CTTtACTAGG TGGTTATCCC AAAGCCTCGG TAACTCAACT
msa31161.2{327dNT_H36B}  GCAGACCTTG CTTcACTAGG TGGTTATCCC AAAGCCTCGG TAACTCAACT
              Consensus  ********** ***_****** ********** ********** **********

                         1101                                              1150
msa31161.2{327dNt_2603}  AGCCCTTGCG ACAGAACTAC TCCAAATGGG ACTAAGTCAT GAAAAGGTTG
msa31161.2{327d_18RS21}  AGCCCTTGCG ACAGAACTAC TCCAAATGGG ACTAAGTCAT GAAAAGGTTG
msa31161.2{327dNT_H36B}  AGCCCTTGCG ACAGAACTAC TCCAAATGGG ACTAAGTCAT GAAAAGGTTG
              Consensus  ********** ********** ********** ********** **********

                         1151                                              1200
msa31161.2{327dNt_2603}  AATTTTTCTT TGGTAGCCAG CTTTCCATTG AAGAGCTGCG ACAAGTTGCC
msa31161.2{327d_18RS21}  AATTTTTCTT TGGTAGCCAG CTTTCCATTG AAGAGCTGCG ACAAGTTGCC
msa31161.2{327dNT_H36B}  AATTTTTCTT TGGTAGCCAG CTTTCCATTG AAGAGCTGCG ACAAGTTGCC
              Consensus  ********** ********** ********** ********** **********

                         1201                                              1250
msa31161.2{327dNt_2603}  TACGCCTTTT TAtACCAAGA ACTCAGCAGA GAAGATGCGG AGCAATTTGA
msa31161.2{327d_18RS21}  TACGCCTTTT TAcACCAAGA ACTCAGCAGA GAAGATGCGG AGCAATTTGA
msa31161.2{327dNT_H36B}  TACGCCTTTT TAcACCAAGA ACTCAGCAGA GAAGATGCGG AGCAATTTGA
              Consensus  ********** **_******* ********** ********** **********

                         1251                                              1300
msa31161.2{327dNt_2603}  AAAAGATAAA GGTAATCAGC CAGATTTAAC TCTCAGAGAT TGGAAAAGCA
msa31161.2{327d_18RS21}  AAAAGATAAA GGTAATCAGC CAGATTTAAC TCTCAGAGAT TGGAAAAGCA
msa31161.2{327dNT_H36B}  AAAAGATAAA GGTAATCAGC CAGATTTAAC TCTCAGAGAT TGGAAAAGCA
              Consensus  ********** ********** ********** ********** **********

                         1301                                              1350
msa31161.2{327dNt_2603}  AGCTAGAGAA AGCTGAGGGA AAAGAAGTAG TTGATGAAGA ATTCGCGGAA
msa31161.2{327d_18RS21}  AGCTAGAGAA AGCTGAGGGA AAAGAAGTAG TTGATGAAGA ATTCGCGGAA
msa31161.2{327dNT_H36B}  AGCTAGAGAA AGCTGAGGGA AAAGAAGTAG TTGATGAAGA ATTCGCGGAA
              Consensus  ********** ********** ********** ********** **********

                         1351                                              1400
msa31161.2{327dNt_2603}  AATCCACTGG TTCAGAGAGT ATTGGACACT TATCCTCTGG GGTCATTGGT
msa31161.2{327d_18RS21}  AATCCACTGG TTCAGAGAGT ATTGGACACT TATCCTCTGG GGTCATTGGT
msa31161.2{327dNT_H36B}  AATCCACTGG TTCAGAGAGT ATTGGACACT TATCCTCTGG GGTCATTGGT
              Consensus  ********** ********** ********** ********** **********
```

Table 70: Comparative Sequences relating to SAG 1280

```
                           1401                                                   1450
msa31161.2{327dNt_2603}    TTCCTATAAG GGACAGGACT TTGAGGTCAT GTCGGTCAGC GATGCTCGAT
msa31161.2{327d_18RS21}    TTCCTATAAG GGACAGGACT TTGAGGTCAT GTCGGTCAGC GATGCTCGAT
msa31161.2{327dNT_H36B}    TTCCTATAAG GGACAGGACT TTGAGGTCAT GTCGGTCAGC GATGCTCGAT
             Consensus     ********** ********** ********** ********** **********

                           1451                                                   1500
msa31161.2{327dNt_2603}    TGAACGGTTT GATTCGGATT GAGTTAGTCA ATGACTTTTC GGATATCATT
msa31161.2{327d_18RS21}    TGAACGGTTT GATTCGGATT GAGTTAGTCA ATGACTTTTC GGATATCATT
msa31161.2{327dNT_H36B}    TGAACGGTTT GATTCGGATT GAGTTAGTCA ATGACTTTTC GGATATCATT
             Consensus     ********** ********** ********** ********** **********

                           1501                                                   1550
msa31161.2{327dNt_2603}    GAACAAAATC CAGTTCTTTA TGTGAGGACC TGGGAAGAAG TCAGTCAGGC
msa31161.2{327d_18RS21}    GAACAAAATC CAGTTCTTTA TGTGAGGACC TGGGAAGAAG TCAGTCAGGC
msa31161.2{327dNT_H36B}    GAACAAAATC CAGTTCTTTA TGTGAGGACC TGGGAAGAAG TCAGTCAGGC
             Consensus     ********** ********** ********** ********** **********

                           1551                                                   1600
msa31161.2{327dNt_2603}    ACTTCATCAG CCAAAGGCAG AACCACAAAC AGAGTTAGAA GAAGCGGACC
msa31161.2{327d_18RS21}    ACTTCATCAG CCAAAGGCAG AACCACAAAC AGAGTTAGAA GAAGCGGACC
msa31161.2{327dNT_H36B}    ACTTCATCAG CCAAAGGCAG AACCACAAAC AGAGTTAGAA GAAGCGGACC
             Consensus     ********** ********** ********** ********** **********

                           1601                                                   1650
msa31161.2{327dNt_2603}    AAGAATTAAA CCTATTCTCA TTTCTGGAAG AGGAGCcAGT TCAGAGTATT
msa31161.2{327d_18RS21}    AAGAATTAAA CCTATTCTCA TTTCTGGAAG AGGAGCcAGT TCAGAGTATT
msa31161.2{327dNT_H36B}    AAGAATTAAA CCTATTCTCA TTTCTGGAAG AGGAGCtAGT TCAGAGTATT
             Consensus     ********** ********** ********** ******_*** **********

                           1651                                                   1700
msa31161.2{327dNt_2603}    GGACTATTGG AACCAGATGA TTCAGAAAAT GGTCATAACG ATACTGATCT
msa31161.2{327d_18RS21}    GGACTATTGG AACCAGATGA TTCAGAAAAT GGTCATAACG ATACTGATCT
msa31161.2{327dNT_H36B}    GGACTATTGG AACCAGATGA TTCAGAAAAT GGTCATAACG ATACTGATCT
             Consensus     ********** ********** ********** ********** **********

                           1701                                                   1750
msa31161.2{327dNt_2603}    TGAAGAAACA GATAATCAAA TTCCTGAAGA GGAAGTCGTC GAAACAATTC
msa31161.2{327d_18RS21}    TGAAGAAACA GATAATCAAA TTCCTGAAGA GGAAGTCGTC GAAACAATTC
msa31161.2{327dNT_H36B}    TGAAGAAACA GATAATCAAA TTCCTGAAGA GGAAGTCGTC GAAACAATTC
             Consensus     ********** ********** ********** ********** **********

                           1751                                                   1800
msa31161.2{327dNt_2603}    CAGAGATTCC AGTAACGGAC TTTTATTTTC CAGAAGATTT GACGGACTTT
msa31161.2{327d_18RS21}    CAGAGATTCC AGTAACGGAC TTTTATTTTC CAGAAGATTT GACGGACTTT
msa31161.2{327dNT_H36B}    CAGAGATTCC AGTAACGGAC TTTTATTTTC CAGAAGATTT GACGGACTTT
             Consensus     ********** ********** ********** ********** **********

                           1801                                                   1850
msa31161.2{327dNt_2603}    TATCCTAAGA CTGCTAGAGA TAAGGTTGAG ACAAACATTG TGGCCATTCG
msa31161.2{327d_18RS21}    TATCCTAAGA CTGCTAGAGA TAAGGTTGAG ACAAACATTG TGGCCATTCG
msa31161.2{327dNT_H36B}    TATCCTAAGA CTGCTAGAGA TAAGGTTGAG ACAAACATTG TGGCCATTCG
             Consensus     ********** ********** ********** ********** **********

                           1851                                                   1900
msa31161.2{327dNt_2603}    TTTGGTAAAA AATCTAGAAG TAGAGCACCG CAATGCTTCA CCAAGTGAAC
msa31161.2{327d_18RS21}    TTTGGTAAAA AATCTAGAAG TAGAGCACCG CAATGCTTCA CCAAGTGAAC
msa31161.2{327dNT_H36B}    TTTGGTAAAA AATCTAGAAG TAGAGCACCG CAATGCTTCA CCAAGTGAAC
             Consensus     ********** ********** ********** ********** **********

                           1901                                                   1950
msa31161.2{327dNt_2603}    AAGAACTCCT TGCCAAGTAT GTAGGCTGGG GTGGACTAGC CAATGAATTT
msa31161.2{327d_18RS21}    AAGAACTCCT TGCCAAGTAT GTAGGCTGGG GTGGACTAGC CAATGAATTT
msa31161.2{327dNT_H36B}    AAGAACTCCT TGCCAAGTAT GTAGGCTGGG GTGGACTAGC CAATGAATTT
             Consensus     ********** ********** ********** ********** **********

                           1951                                                   2000
msa31161.2{327dNt_2603}    TTTGATGACT ATAATCCAAA ATTTTCTAAG GAACGAGAAG AACTGAAGAG
msa31161.2{327d_18RS21}    TTTGATGACT ATAATCCAAA ATTTTCTAAG GAACGAGAAG AACTGAAGAG
msa31161.2{327dNT_H36B}    TTTGATGACT ATAATCCAAA ATTTTCTAAG GAACGAGAAG AACTGAAGAG
             Consensus     ********** ********** ********** ********** **********

                           2001                                                   2050
msa31161.2{327dNt_2603}    CCTAGTCACA GATAAAGAGT ATTCGGATAT GAAACAGTCC TCCCTGACAG
msa31161.2{327d_18RS21}    CCTAGTCACA GATAAAGAGT ATTCGGATAT GAAACAGTCC TCCCTGACAG
msa31161.2{327dNT_H36B}    CCTAGTCACA GATAAAGAGT ATTCGGATAT GAAACAGTCC TCCCTGACAG
             Consensus     ********** ********** ********** ********** **********

                           2051                                                   2100
msa31161.2{327dNt_2603}    CCTATTACAC AGACCCATCC CTGATCCGTC AGATGTGGGA TAAGTTGGAA
msa31161.2{327d_18RS21}    CCTATTACAC AGACCCATCC CTGATCCGTC AGATGTGGGA TAAGTTGGAA
msa31161.2{327dNT_H36B}    CCTATTACAC AGACCCATCC CTGATCCGTC AGATGTGGGA TAAGTTGGAA
```

Table 70: Comparative Sequences relating to SAG 1280

```
                  Consensus  ********** ********** ********** ********** **********

                             2101                                              2150
msa31161.2{327dNt_2603}      AGAGATGGCT TTACAGGTGG CAAAATCCTA GATCCTTCCA TGGGAACAGG
msa31161.2{327d_18RS21}      AGAGATGGCT TTACAGGTGG CAAAATCCTA GATCCTTCCA TGGGAACAGG
msa31161.2{327dNT_H36B}      AGAGATGGCT TTACAGGTGG CAAAATCCTA GATCCTTCCA TGGGAACAGG
                  Consensus  ********** ********** ********** ********** **********

                             2151                                              2200
msa31161.2{327dNt_2603}      GAATTTCTTT GCGGCTATGC CAAAACACTT AAGAGAAAAG AGTGAGTTGT
msa31161.2{327d_18RS21}      GAATTTCTTT GCGGCTATGC CAAAACACTT AAGAGAAAAG AGTGAGTTGT
msa31161.2{327dNT_H36B}      GAATTTCTTT GCGGCTATGC CAAAACACTT AAGAGAAAAG AGTGAGTTGT
                  Consensus  ********** ********** ********** ********** **********

                             2201                                              2250
msa31161.2{327dNt_2603}      ATGGCGTAGA GTTAGATACT ATTACAGGAG CTATTGCCAA ACACCTTCAT
msa31161.2{327d_18RS21}      ATGGCGTAGA GTTAGATACT ATTACAGGAG CTATTGCCAA ACACCTTCAT
msa31161.2{327dNT_H36B}      ATGGCGTAGA GTTAGATACT ATTACAGGAG CTATTGCCAA ACACCTTCAT
                  Consensus  ********** ********** ********** ********** **********

                             2251                                              2300
msa31161.2{327dNt_2603}      CCCAATAGTC ATATTGAAAT TAAGGGATTT GAGACGGTGG CTTTTAACGA
msa31161.2{327d_18RS21}      CCCAATAGTC ATATTGAAAT TAAGGGATTT GAGACGGTGG CTTTTAACGA
msa31161.2{327dNT_H36B}      CCCAATAGTC ATATTGAAAT TAAGGGATTT GAGACGGTGG CTTTTAACGA
                  Consensus  ********** ********** ********** ********** **********

                             2301                                              2350
msa31161.2{327dNt_2603}      CAATAGTTTT GATTTGGTGA TTTCAAATGT GCCCTTTGCC AATATACGAA
msa31161.2{327d_18RS21}      CAATAGTTTT GATTTGGTGA TTTCAAATGT GCCCTTTGCC AATATACGAA
msa31161.2{327dNT_H36B}      CAATAGTTTT GATTTGGTGA TTTCAAATGT GCCCTTTGCC AATATACGAA
                  Consensus  ********** ********** ********** ********** **********

                             2351                                              2400
msa31161.2{327dNt_2603}      TTGCGGATAA TAGGTACGAT AGGCCTTACA TGATTCATGA CTACTTTGTC
msa31161.2{327d_18RS21}      TTGCGGATAA TAGGTACGAT AGGCCTTACA TGATTCATGA CTACTTTGTC
msa31161.2{327dNT_H36B}      TTGCGGATAA TAGGTACGAT AGGCCTTACA TGATTCATGA CTACTTTGTC
                  Consensus  ********** ********** ********** ********** **********

                             2401                                              2450
msa31161.2{327dNt_2603}      AAAAAGTCAC TTGATTTGCT TCATGATGGT GGACAAGTAG CGATTATCTC
msa31161.2{327d_18RS21}      AAAAAGTCAC TTGATTTGCT TCATGATGGT GGACAAGTAG CGATTATCTC
msa31161.2{327dNT_H36B}      AAAAAGTCAC TTGATTTGCT TCATGATGGT GGACAAGTAG CGATTATCTC
                  Consensus  ********** ********** ********** ********** **********

                             2451                                              2500
msa31161.2{327dNt_2603}      TTCCACAGGA ACTATGGATA AGCGAACAGA AAACATCTTA CAAGATATTC
msa31161.2{327d_18RS21}      TTCCACAGGA ACTATGGATA AGCGAACAGA AAACATCTTA CAAGATATTC
msa31161.2{327dNT_H36B}      TTCCACAGGA ACTATGGATA AGCGAACAGA AAACATCTTA CAAGATATTC
                  Consensus  ********** ********** ********** ********** **********

                             2501                                              2550
msa31161.2{327dNt_2603}      GTGAGACAAC TGAATTTCTT GGTGGGGTTC GACTGCCTGA CTCTGCCTTT
msa31161.2{327d_18RS21}      GTGAGACAAC TGAATTTCTT GGTGGGGTTC GACTGCCTGA CTCTGCCTTT
msa31161.2{327dNT_H36B}      GTGAGACAAC TGAATTTCTT GGTGGGGTTC GACTGCCTGA CTCTGCCTTT
                  Consensus  ********** ********** ********** ********** **********

                             2551                                              2600
msa31161.2{327dNt_2603}      AAGGCCATTG CAGGAACGAG TGTCACAACG GATATGTTAT TCTTCCAGAA
msa31161.2{327d_18RS21}      AAGGCCATTG CAGGAACGAG TGTCACAACG GATATGTTAT TCTTCCAGAA
msa31161.2{327dNT_H36B}      AAGGCCATTG CAGGAACGAG TGTCACAACG GATATGTTAT TCTTCCAGAA
                  Consensus  ********** ********** ********** ********** **********

                             2601                                              2650
msa31161.2{327dNt_2603}      ACACTTAGAC AAGGGATATG TGGCAGACGA TTTAGCCTTT TCAGGTTCCA
msa31161.2{327d_18RS21}      ACACTTAGAC AAGGGATATG TGGCAGACGA TTTAGCCTTT TCAGGTTCCA
msa31161.2{327dNT_H36B}      ACACTTAGAC AAGGGATATG TGGCAGACGA TTTAGCCTTT TCAGGTTCCA
                  Consensus  ********** ********** ********** ********** **********

                             2651                                              2700
msa31161.2{327dNt_2603}      TTCGCTATGA CAAGGATAGT CGCATTTGGC TCAATCCTTA TTTTGATGGA
msa31161.2{327d_18RS21}      TTCGCTATGA CAAGGATAGT CGCATTTGGC TCAATCCTTA TTTTGATGGA
msa31161.2{327dNT_H36B}      TTCGCTATGA CAAGGATAGT CGCATTTGGC TCAATCCTTA TTTTGATGGA
                  Consensus  ********** ********** ********** ********** **********

                             2701                                              2750
msa31161.2{327dNt_2603}      GAATACAATA GCCAGGTGCT AGGAACCTAC GAGGTCAGGA ATTTTAACGG
msa31161.2{327d_18RS21}      GAATACAATA GCCAGGTGCT AGGAACCTAC GAGGTCAGGA ATTTTAACGG
msa31161.2{327dNT_H36B}      GAATACAATA GCCAGGTGCT AGGAACCTAC GAGGTCAGGA ATTTTAACGG
                  Consensus  ********** ********** ********** ********** **********

                             2751                                              2800
msa31161.2{327dNt_2603}      AGGAACACTT TCTGTTAAGG GGACTAGTGA TGACTTGATT GCAAGTGTTG
msa31161.2{327d_18RS21}      AGGAACACTT TCTGTTAAGG GGACTAGTGA TGACTTGATT GCAAGTGTTG
```

Table 70: Comparative Sequences relating to SAG 1280

```
msa31161.2{327dNT_H36B}  AGGAACACTT TCTGTTAAGG GGACTAGTGA TGACTTGATT GCAAGTGTTG
              Consensus  ********** ********** ********** ********** **********

                         2801                                              2850
msa31161.2{327dNt_2603}  AAACAGCTCT AAATCACGTT AAGGCCCCAA GAGAGATTGA TAGAAATGAG
msa31161.2{327d_18RS21}  AAACAGCTCT AAATCACGTT AAGGCCCCAA GAGAGATTGA TAGAAATGAG
msa31161.2{327dNT_H36B}  AAACAGCTCT AAATCACGTT AAGGCCCCAA GAGAGATTGA TAGAAATGAG
              Consensus  ********** ********** ********** ********** **********

                         2851                                              2900
msa31161.2{327dNt_2603}  GTCATCATTA ACCCAGATGT GTTGACCAAA CAAGTCAATG ATACCTCCAT
msa31161.2{327d_18RS21}  GTCATCATTA ACCCAGATGT GTTGACCAAA CAAGTCAATG ATACCTCCAT
msa31161.2{327dNT_H36B}  GTCATCATTA ACCCAGATGT GTTGACCAAA CAAGTCAATG ATACCTCCAT
              Consensus  ********** ********** ********** ********** **********

                         2901                                              2950
msa31161.2{327dNt_2603}  TCCAGCTGAA ATGAGGGAAA ATCTAGGTCA GTACAGTTTT GGTTATCAGG
msa31161.2{327d_18RS21}  TCCAGCTGAA ATGAGGGAAA ATCTAGGTCA GTACAGTTTT GGTTATCAGG
msa31161.2{327dNT_H36B}  TCCAGCTGAA ATGAGGGAAA ATCTAGGTCA GTACAGTTTT GGTTATCAGG
              Consensus  ********** ********** ********** ********** **********

                         2951                                              3000
msa31161.2{327dNt_2603}  GGTCTACAGT TTACTATCGA GATAACAAAG GCATTCGAGT CGGAACCAAG
msa31161.2{327d_18RS21}  GGTCTACAGT TTACTATCGA GATAACAAAG GCATTCGAGT CGGAACCAAG
msa31161.2{327dNT_H36B}  GGTCTACAGT TTACTATCGA GATAACAAAG GCATTCGAGT CGGAACCAAG
              Consensus  ********** ********** ********** ********** **********

                         3001                           3033
msa31161.2{327dNt_2603}  ACGGAAGAAA TCAGTTACTA TGTCGATGAA GAG
msa31161.2{327d_18RS21}  ACGGAAGAAA TCAGTTACTA TGTCGATGAA GAG
msa31161.2{327dNT_H36B}  ACGGAAGAAA TCAGTTACTA TGTCGATGAA GAG
              Consensus  ********** ********** ********** ***
```

SEQ ID. NO. 7004
STRAIN H36B frame: 1
GGKMNQEVLLQMMRATIPRDRALLEAFLYYQAEHFDEEWDSLIHQFMTNRQEINKSVQVL
HFETDVSAFVQASPYDTAHDLLTYTQVFGQSGLQKLDKLSPSEKNLVIEVALFNLATRFQ
LLDSNGHYQTISPDSLLQKSRGANLVNVYRVANNLADRISRDIEQFLLTYEPELETRADE
TVLENEETVDEHKTSVHQAISFREEGSLVIASLDVDLSQLDVQIGKTSHLPAYEELSLRR
KFEILTYFDQIRNERSKVPSFRRGDFDTEMEMTPVFDGEELLTYLEADGSPYELKRTLTT
VEEKELEKIGQAIRIENQEKLTQLXIXLSQFDPDRVGILLXAAGRXRLXNADLASLGGYP
KASVTQLALATELLQMGLSHEKVEFFFGSQLSIEELRQVAYAFLHQELSREDAEQFEKDK
GNQPDLTLRDWKSKLEKAEGKEVVDEEFAENPLVQRVLDTYPLGSLVSYKGQDFEVMSVS
DARLNGLIRIELVNDFSDIIEQNPVLYVRTWEEVSQALHQPKAEPQTELEEADQELNLFS
FLEEELVQSIGLLEPDDSENGHNDTDLEETDNQIPEEEVVETIPEIPVTDFYFPEDLTDF
YPKTARDKVETNIVAIRLVKNLEVEHRNASPSEQELLAKYVGWGGLANEFFDDYNPKFSK
EREELKSLVTDKEYSDMKQSSLTAYYTDPSLIRQMWDKLERDGFTGGKILDPSMGTGNFF
AAMPKHLREKSELYGVELDTITGAIAKHLHPNSHIEIKGFETVAFNDNSFDLVISNVPFA
NIRIADNRYDRPYMIHDYFVKKSLDLLHDGGQVAIISSTGTMDKRTENILQDIRETTEFL
GGVRLPDSAFKAIAGTSVTTDMLFFQKHLDKGYVADDLAFSGSIRYDKDSRIWLNPYFDG
EYNSQVLGTYEVRNFNGGTLSVKGTSDDLIASVETALNHVKAPREIDRNEVIINPDVLTK
QVNDTSIPAEMRENLGQYSFGYQGSTVYYRDNKGIRVGTKTEEISYYVDEE

SEQ ID. NO. 7005
STRAIN 18RS21 frame: 1
XGKMNQEVLLQMMRATIPRDRALLEAFLYYQAEHFDEEWDSLIHQFMTNRQEINKSVQVL
HFETDVSAFVQASPYDTAHDLLTYTQVFGQSGLQKLDKLSPSEKNLVIEVALFNLATRFQ
LLDSNGHYQTISPDSLLQKSRGANLVNVYRVANNLADRISRDIEQFLLTYEPELETRADE
TVLENEETVDEHKTSVHQAISFREEGSLVIASLDVDLSQLDVQIGKTSHLPAYEELSLRR
KFEILTYFDQIRNERSKVPSFRRGDFDTEMEMTPVFDGEELLTYLEADGSPYELKRTLTT
VEEKELEKIGQAIRIENQEKLTQLGIDLSQFDPDRVGILLDAAGRFRLKNADLALLGGYP
KASVTQLALATELLQMGLSHEKVEFFFGSQLSIEELRQVAYAFLHQELSREDAEQFEKDK
GNQPDLTLRDWKSKLEKAEGKEVVDEEFAENPLVQRVLDTYPLGSLVSYKGQDFEVMSVS
DARLNGLIRIELVNDFSDIIEQNPVLYVRTWEEVSQALHQPKAEPQTELEEADQELNLFS
FLEEEPVQSIGLLEPDDSENGHNDTDLEETDNQIPEEEVVETIPEIPVTDFYFPEDLTDF
YPKTARDKVETNIVAIRLVKNLEVEHRNASPSEQELLAKYVGWGGLANEFFDDYNPKFSK
EREELKSLVTDKEYSDMKQSSLTAYYTDPSLIRQMWDKLERDGFTGGKILDPSMGTGNFF
AAMPKHLREKSELYGVELDTITGAIAKHLHPNSHIEIKGFETVAFNDNSFDLVISNVPFA
NIRIADNRYDRPYMIHDYFVKKSLDLLHDGGQVAIISSTGTMDKRTENILQDIRETTEFL
GGVRLPDSAFKAIAGTSVTTDMLFFQKHLDKGYVADDLAFSGSIRYDKDSRIWLNPYFDG
EYNSQVLGTYEVRNFNGGTLSVKGTSDDLIASVETALNHVKAPREIDRNEVIINPDVLTK
QVNDTSIPAEMRENLGQYSFGYQGSTVYYRDNKGIRVGTKTEEISYYVDEE

SEQ ID. NO. 7006
STRAIN 2603 frame: 1
GGKMNQEVLLQMMRATIPRDRALLEAFLYYQAEHFDEEWDSLIHQFMTNRQEINKSVQVL
HFETDVSAFVQASPYDTAHDLLTYTQVFGQSGLQKLDKLSPSEKNLVIEVALFNLATRFQ
LLDSNGHYQTISPDSLLQKSRGANLVNVYRVANNLADRISRDIEQFLLTYEPELETRADE
TVLENEETVDEHKTSVHQAISFREEGSLVIASLDVDLSQLDVQIGKTSHLPAYEELSLRR
KFEILTYFDQIRNERSKVPSFRRGDFDTEMEMTPVFDGEELLTYLEADGSPYELKRTLTT
VEEKELEKIGQAIRIENQEKLTQLGIDLSQFDPDRVGILLDAAGRFRLKNADLALLGGYP
KASVTQLALATELLQMGLSHEKVEFFFGSQLSIEELRQVAYAFLYQELSREDAEQFEKDK
GNQPDLTLRDWKSKLEKAEGKEVVDEEFAENPLVQRVLDTYPLGSLVSYKGQDFEVMSVS

Table 70: Comparative Sequences relating to SAG 1280

```
DARLNGLIRIELVNDFSDIIEQNPVLYVRTWEEVSQALHQPKAEPQTELEEADQELNLFS
FLEEEPVQSIGLLEPDDSENGHNDTDLEETDNQIPEEEVVETIPEIPVTDFYFPEDLTDF
YPKTARDKVETNIVAIRLVKNLEVEHRNASPSEQELLAKYVGWGGLANEFFDDYNPKFSK
EREELKSLVTDKEYSDMKQSSLTAYYTDPSLIRQMWDKLERDGFTGGKILDPSMGTGNFF
AAMPKHLREKSELYGVELDTITGAIAKHLHPNSHIEIKGFETVAFNDNSFDLVISNVPFA
NIRIADNRYDRPYMIHDYFVKKSLDLLHDGGQVAIISSTGTMDKRTENILQDIRETTEFL
GGVRLPDSAFKAIAGTSVTTDMLFFQKHLDKGYVADDLAFSGSIRYDKDSRIWLNPYFDG
EYNSQVLGTYEVRNFNGGTLSVKGTSDDLIASVETALNHVKAPREIDRNEVIINPDVLTK
QVNDTSIPAEMRENLGQYSFGYQGSTVYYRDNKGIRVGTKTEEISYYVDEE

PRETTY of: /biotmp/msa23816.2{*}   June 20, 2002 11:04  ..

                         1                                                   50
msa23816.2{327dNT_H36B}  gGKMNQEVLL QMMRATIPRD RALLEAFLYY QAEHFDEEWD SLIHQFMTNR
msa23816.2{327dNt_2603}  gGKMNQEVLL QMMRATIPRD RALLEAFLYY QAEHFDEEWD SLIHQFMTNR
msa23816.2{327d_18RS21}  xGKMNQEVLL QMMRATIPRD RALLEAFLYY QAEHFDEEWD SLIHQFMTNR
              Consensus  -********* ********** ********** ********** **********

                         51                                                 100
msa23816.2{327dNT_H36B}  QEINKSVQVL HFETDVSAFV QASPYDTAHD LLTYTQVFGQ SGLQKLDKLS
msa23816.2{327dNt_2603}  QEINKSVQVL HFETDVSAFV QASPYDTAHD LLTYTQVFGQ SGLQKLDKLS
msa23816.2{327d_18RS21}  QEINKSVQVL HFETDVSAFV QASPYDTAHD LLTYTQVFGQ SGLQKLDKLS
              Consensus  ********** ********** ********** ********** **********

                         101                                                150
msa23816.2{327dNT_H36B}  PSEKNLVIEV ALFNLATRFQ LLDSNGHYQT ISPDSLLQKS RGANLVNVYR
msa23816.2{327dNt_2603}  PSEKNLVIEV ALFNLATRFQ LLDSNGHYQT ISPDSLLQKS RGANLVNVYR
msa23816.2{327d_18RS21}  PSEKNLVIEV ALFNLATRFQ LLDSNGHYQT ISPDSLLQKS RGANLVNVYR
              Consensus  ********** ********** ********** ********** **********

                         151                                                200
msa23816.2{327dNT_H36B}  VANNLADRIS RDIEQFLLTY EPELETRADE TVLENEETVD EHKTSVHQAI
msa23816.2{327dNt_2603}  VANNLADRIS RDIEQFLLTY EPELETRADE TVLENEETVD EHKTSVHQAI
msa23816.2{327d_18RS21}  VANNLADRIS RDIEQFLLTY EPELETRADE TVLENEETVD EHKTSVHQAI
              Consensus  ********** ********** ********** ********** **********

                         201                                                250
msa23816.2{327dNT_H36B}  SFREEGSLVI ASLDVDLSQL DVQIGKTSHL PAYEELSLRR KFEILTYFDQ
msa23816.2{327dNt_2603}  SFREEGSLVI ASLDVDLSQL DVQIGKTSHL PAYEELSLRR KFEILTYFDQ
msa23816.2{327d_18RS21}  SFREEGSLVI ASLDVDLSQL DVQIGKTSHL PAYEELSLRR KFEILTYFDQ
              Consensus  ********** ********** ********** ********** **********

                         251                                                300
msa23816.2{327dNT_H36B}  IRNERSKVPS FRRGDFDTEM EMTPVFDGEE LLTYLEADGS PYELKRTLTT
msa23816.2{327dNt_2603}  IRNERSKVPS FRRGDFDTEM EMTPVFDGEE LLTYLEADGS PYELKRTLTT
msa23816.2{327d_18RS21}  IRNERSKVPS FRRGDFDTEM EMTPVFDGEE LLTYLEADGS PYELKRTLTT
              Consensus  ********** ********** ********** ********** **********

                         301                                                350
msa23816.2{327dNT_H36B}  VEEKELEKIG QAIRIENQEK LTQLxIxLSQ FDPDRVGILL xAAGRxRLxN
msa23816.2{327dNt_2603}  VEEKELEKIG QAIRIENQEK LTQLgIdLSQ FDPDRVGILL dAAGRfRLkN
msa23816.2{327d_18RS21}  VEEKELEKIG QAIRIENQEK LTQLgIdLSQ FDPDRVGILL dAAGRfRLkN
              Consensus  ********** ********** ****-*-*** ********** -****-**-*

                         351                                                400
msa23816.2{327dNT_H36B}  ADLAsLGGYP KASVTQLALA TELLQMGLSH EKVEFFFGSQ LSIEELRQVA
msa23816.2{327dNt_2603}  ADLAlLGGYP KASVTQLALA TELLQMGLSH EKVEFFFGSQ LSIEELRQVA
msa23816.2{327d_18RS21}  ADLAlLGGYP KASVTQLALA TELLQMGLSH EKVEFFFGSQ LSIEELRQVA
              Consensus  ****-***** ********** ********** ********** **********

                         401                                                450
msa23816.2{327dNT_H36B}  YAFLhQELSR EDAEQFEKDK GNQPDLTLRD WKSKLEKAEG KEVVDEEFAE
msa23816.2{327dNt_2603}  YAFLyQELSR EDAEQFEKDK GNQPDLTLRD WKSKLEKAEG KEVVDEEFAE
msa23816.2{327d_18RS21}  YAFLhQELSR EDAEQFEKDK GNQPDLTLRD WKSKLEKAEG KEVVDEEFAE
              Consensus  ****-***** ********** ********** ********** **********

                         451                                                500
msa23816.2{327dNT_H36B}  NPLVQRVLDT YPLGSLVSYK GQDFEVMSVS DARLNGLIRI ELVNDFSDII
msa23816.2{327dNt_2603}  NPLVQRVLDT YPLGSLVSYK GQDFEVMSVS DARLNGLIRI ELVNDFSDII
msa23816.2{327d_18RS21}  NPLVQRVLDT YPLGSLVSYK GQDFEVMSVS DARLNGLIRI ELVNDFSDII
              Consensus  ********** ********** ********** ********** **********

                         501                                                550
msa23816.2{327dNT_H36B}  EQNPVLYVRT WEEVSQALHQ PKAEPQTELE EADQELNLFS FLEEElVQSI
msa23816.2{327dNt_2603}  EQNPVLYVRT WEEVSQALHQ PKAEPQTELE EADQELNLFS FLEEEpVQSI
msa23816.2{327d_18RS21}  EQNPVLYVRT WEEVSQALHQ PKAEPQTELE EADQELNLFS FLEEEpVQSI
              Consensus  ********** ********** ********** ********** *****-****

                         551                                                600
msa23816.2{327dNT_H36B}  GLLEPDDSEN GHNDTDLEET DNQIPEEEVV ETIPEIPVTD FYFPEDLTDF
msa23816.2{327dNt_2603}  GLLEPDDSEN GHNDTDLEET DNQIPEEEVV ETIPEIPVTD FYFPEDLTDF
msa23816.2{327d_18RS21}  GLLEPDDSEN GHNDTDLEET DNQIPEEEVV ETIPEIPVTD FYFPEDLTDF
              Consensus  ********** ********** ********** ********** **********
```

Table 70: Comparative Sequences relating to SAG 1280

```
                        601                                                    650
msa23816.2{327dNT_H36B}  YPKTARDKVE TNIVAIRLVK NLEVEHRNAS PSEQELLAKY VGWGGLANEF
msa23816.2{327dNt_2603}  YPKTARDKVE TNIVAIRLVK NLEVEHRNAS PSEQELLAKY VGWGGLANEF
msa23816.2{327d_18RS21}  YPKTARDKVE TNIVAIRLVK NLEVEHRNAS PSEQELLAKY VGWGGLANEF
              Consensus  ********** ********** ********** ********** **********

                        651                                                    700
msa23816.2{327dNT_H36B}  FDDYNPKFSK EREELKSLVT DKEYSDMKQS SLTAYYTDPS LIRQMWDKLE
msa23816.2{327dNt_2603}  FDDYNPKFSK EREELKSLVT DKEYSDMKQS SLTAYYTDPS LIRQMWDKLE
msa23816.2{327d_18RS21}  FDDYNPKFSK EREELKSLVT DKEYSDMKQS SLTAYYTDPS LIRQMWDKLE
              Consensus  ********** ********** ********** ********** **********

                        701                                                    750
msa23816.2{327dNT_H36B}  RDGFTGGKIL DPSMGTGNFF AAMPKHLREK SELYGVELDT ITGAIAKHLH
msa23816.2{327dNt_2603}  RDGFTGGKIL DPSMGTGNFF AAMPKHLREK SELYGVELDT ITGAIAKHLH
msa23816.2{327d_18RS21}  RDGFTGGKIL DPSMGTGNFF AAMPKHLREK SELYGVELDT ITGAIAKHLH
              Consensus  ********** ********** ********** ********** **********

                        751                                                    800
msa23816.2{327dNT_H36B}  PNSHIEIKGF ETVAFNDNSF DLVISNVPFA NIRIADNRYD RPYMIHDYFV
msa23816.2{327dNt_2603}  PNSHIEIKGF ETVAFNDNSF DLVISNVPFA NIRIADNRYD RPYMIHDYFV
msa23816.2{327d_18RS21}  PNSHIEIKGF ETVAFNDNSF DLVISNVPFA NIRIADNRYD RPYMIHDYFV
              Consensus  ********** ********** ********** ********** **********

                        801                                                    850
msa23816.2{327dNT_H36B}  KKSLDLLHDG GQVAIISSTG TMDKRTENIL QDIRETTEFL GGVRLPDSAF
msa23816.2{327dNt_2603}  KKSLDLLHDG GQVAIISSTG TMDKRTENIL QDIRETTEFL GGVRLPDSAF
msa23816.2{327d_18RS21}  KKSLDLLHDG GQVAIISSTG TMDKRTENIL QDIRETTEFL GGVRLPDSAF
              Consensus  ********** ********** ********** ********** **********

                        851                                                    900
msa23816.2{327dNT_H36B}  KAIAGTSVTT DMLFFQKHLD KGYVADDLAF SGSIRYDKDS RIWLNPYFDG
msa23816.2{327dNt_2603}  KAIAGTSVTT DMLFFQKHLD KGYVADDLAF SGSIRYDKDS RIWLNPYFDG
msa23816.2{327d_18RS21}  KAIAGTSVTT DMLFFQKHLD KGYVADDLAF SGSIRYDKDS RIWLNPYFDG
              Consensus  ********** ********** ********** ********** **********

                        901                                                    950
msa23816.2{327dNT_H36B}  EYNSQVLGTY EVRNFNGGTL SVKGTSDDLI ASVETALNHV KAPREIDRNE
msa23816.2{327dNt_2603}  EYNSQVLGTY EVRNFNGGTL SVKGTSDDLI ASVETALNHV KAPREIDRNE
msa23816.2{327d_18RS21}  EYNSQVLGTY EVRNFNGGTL SVKGTSDDLI ASVETALNHV KAPREIDRNE
              Consensus  ********** ********** ********** ********** **********

                        951                                                   1000
msa23816.2{327dNT_H36B}  VIINPDVLTK QVNDTSIPAE MRENLGQYSF GYQGSTVYYR DNKGIRVGTK
msa23816.2{327dNt_2603}  VIINPDVLTK QVNDTSIPAE MRENLGQYSF GYQGSTVYYR DNKGIRVGTK
msa23816.2{327d_18RS21}  VIINPDVLTK QVNDTSIPAE MRENLGQYSF GYQGSTVYYR DNKGIRVGTK
              Consensus  ********** ********** ********** ********** **********

                        1001   1011
msa23816.2{327dNT_H36B}  TEEISYYVDE E
msa23816.2{327dNt_2603}  TEEISYYVDE E
msa23816.2{327d_18RS21}  TEEISYYVDE E
              Consensus  ********** *
```

Table 71: Comparative Sequences relating to SAG1333

SEQ ID NO. 7101
STRAIN 2603
ATGAAAAAGAAAATTATTTTGAAAAGTAGTGTTCTTGGTTTAGTCGCTGGGACTTCTATT
ATGTTCTCAAGCGTGTTCGCGGACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTT
CATGGTGCACTTGACAATACTGGAACAGCAAATATGCCTGATGGAAAAGTTGCTAATGCT
GGTACTGCTGCTCAATTAGATGCTTATATGGATGACGCTCAAAAAGATTTCAAACAAACT
AACCCTAATGGTGAAAGCATTAGGGTTCAAGCAGGCGATATGGTTGGAGCAAGTCCAGCC
AACTCTGGGCTTCTTCAAGATGAACCAACTGTCAAAAATTTTAATGCAATGAATGTTGAG
TATGGCACATTGGGTAACCATGAATTTGATGAAGGGTTGGCAGAATATAATCGTATCGTT
ACTGGTAAAGCCCCTGCTCCAGATTCTAATATTAATAATATTACGAAATCATACCCACAT
GAAGCTGCAAAACAAGAAATTGTAGTGGCAAATGTTATTGATAAAGTTAACAAACAAATT
CCTTACAATTGGAAGCCTTACGCTATTAAAAATATTCCTGTAAATAACAAAAGTGTGAAC
GTTGGCTTTATCGGGATTGTCACCAAAGACATCCCAAACCTTGTCTTACGTAAAAATTAT
GAACAATATGAATTTTTAGATGAAGCTGAAACAATCGTTAAATACGCCAAAGAATTACAA
GCTAAAAATGTCAAAGCTATTGTAGTTCTCGCACATGTACCTGCAACAAGTAAAAATGAT
ATTGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAAGTCAATCAACTCTTCCCTGAAAAT
AGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAATGGTCTTGTTGGTAAA
ACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAGCCTATGCTGATGTACGTGGTGTCTTA
GATACTGATACACAAGATTTCATTGAGACCCCTTCAGCTAAAGTAATTGCAGTTGCTCCT
GGTAAAAAAACAGGTAGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTT
AAACAAGTAACAGAAGCTAAAATTGGTACTGCCGAGGTAAGTGTCATGATTACGCGTTCT
GTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGAGGCTCAACTAGCAATT
GCTCGAAAAAGCTGGCCAGATATCGATTTTGCCATGACAAATAATGGTGGCATTCGTGCT
GACTTACTCATCAAACCAGATGGAACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCT
TTTGGTAATATCTTACAAGTCGTCGAAATTACTGGTAGAGATCTTTATAAAGCACTCAAC
GAACAATACGACCAAAAACAAAATTTCTTCCTTCAAATAGCTGGTCTGCGATACACTTAC
ACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTTGTAAAAGCTTATAAATCA
AATGGTGAGGAAATCAATCCTGATGCAAAATACAAATTAGTTATCAATGACTTTTTATTC
GGTGGTGGTGATGGCTTTGCAAGCTTCAGAAATGCCAAACTTCTAGGAGCCATTAACCCC
GATACAGAGGTATTTATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGC
GTTCCAAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTTAATGAAACTATTACA
CAAAATGATGGTACACATAGCATTATTAAGAAACTTTATTTAGATCGACAAGGAAATATT
GTAGCACAAGAGATTGTATCAGACACTTTAAACCAAACAAAATCAAAATCTACAAAAATC
AACCCTGTAACTACAATTCACAAAAAACAATTACACCAATTTACAGCTATTAACCCTATG
AGAAATTATGGCAAACCATCAAACTCCACTACTGTAAAATCAAAACAATTACCAAAAACA
AACTCTGAATATGGACAATCATTCCTTATGTCTGTCTTTGGTGTTGGACTTATAGGAATT
GCTTTAAATACAAAGAAAAAACATATGAAA

SEQ ID NO. 7102
STRAIN 090
AAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTCATGGTGCACTTGAC
AATACTGGAACAGCAAATATGCCTGACGGAAAAGTTACTAATGCTGGCAC
TGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAAAC
AAACTAACCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATGGTT
GGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTTAA
AACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATGAAT
TTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCCCCT
GCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGAAGC
TGCAAAACAAGAAATTGTAGTGGCAAACGTTATTGATAAAGTTAACAAAC
AAATCCCTTACAATTGGAAACCTTACGCTATTAAAAATATTCCTGTAAAT
AACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAGACATCCC
AAACCTTGTCTTACGTAAAAATTATGAACAATATGAATTTTTAGATGAAG
CTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTCAAG
GCTATTGTAGTCCTTGCTCATGTACCTGCAACAAGCAAGGATGATATTGC
TGAAGGTGAAGCAGCAGAAATGATGAAAAAAGTCAATCAACTCTTCCCTG
AAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAAT
GGTCTTGTTGGTAAAACTCGCATTGTACAAGCGCTCTCTCAAGGAAAAGC
CTATGCTGACGTACGTGGTGTCCTAGATACTGATACACAAGATTTCATTG
AAACCCCTTCAGCTAAAGTAGTTGCAGTTGCTCCTGGTAAAAAAACAGGT
AGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAACA
AGTAACAGAAGCTAAAATTGGTACTGCCGAGGTAAGTGGCATGATTACGC
GTTCTGTTGATCAAGATAATGTTAGTCCAGTAGGCAGCCTCATCACAGAG
GCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGCCAT
GACAAATAATGGTGGCATTCGTGCTGACTTACTCATCAAACCAGATGGAA
CAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTTA
CAAGTCGTCGAAATTACTGGTAGAGATCTTTATAAAGCACTCAACGAACA
ATACGACCAAAAACAAAATTTCTTCCTTCAAATAGCTGGTCTGCGATACA
CTTACACAGATAATAAAGAGGGCGGAGAAGAAACACCATTTAAAGTTGTA
AAAGCTTATAAATCAAATGGTGAAGAAATCAATCCTGATGCAAAATACAA
ATTAGTTATCAATGACTTTTTATTCGGTGGTGGTGATGGCTTTGCAAGCT
TCAGAAATGCCAAACTTCTAGGAGCCATTAATCCCGATACAGAGGTATTT
ATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGCGTTCC
AAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTTAATGAAACTA
TTACACAAAATGATGGTACACATAGCATTATTAAGAAACTTTATTTAGAT
CGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAACCA
AACAAAATCAAAATCTACAAAAATCAACCCTGTAACTACAATTCACAAAA
AACAATTACACCAATTTACAGCTATTAACCCTATGAGAAATTATGGCAAA
CCATCAAACTCCACTACTGTAAAATCAAAACAA

SEQ ID NO. 7103
STRAIN A909
GCGTCAATGACTTTCATGGTGCaCTTGACAATACTGGAACAGCAAATATG
CCTGACGGAAAAGTTACTAATGCTGGCACTGCTGCTCAATTAGATGCTTA

Table 71: Comparative Sequences relating to SAG1333

TATGGATGATGCTCAAAAAGATTTCAAACAAACTAACCCTAATGGTGAAA
GCATTAGAGTTCAAGCTGGTGATATGGTTGGAGCAAGTCCAGCTAACTCA
GGGCTTCTTCAAGATGAACCAACCGTTAAAACATTTAATGCAATGAATGT
TGAGTATGGCACATTAGGTAACCATGAATTTGATGAAGGTTTGGCAGAAT
ACAATCGTATCGTTACTGGAAAGGCCCCTGCTCCaGaTTCTAATATAAAT
AATATTACGAAATCATACCCACACGAAGCTGCAAAACAAGAAATTGTAGT
GGCAAACGTTATTGATAAAGTTAACAAACAAATCCCTTACAATTGGAAAC
CTTACACTATTAAAAATATTCCTGTAAATAACAAAAGTGTGAACGTTGGC
TTTATCGGAATCGTTACCAAAGACATCCCAAACCTTGTCTTACGTAAAAA
TTATGAACAATATGAATTTTTAGATGAAGCTGAAACAATCGTTAAATACG
CCAAAGAATTACAAGCTAAAAATGTCAAGGCTATTGTAGTCCTTGCTCAT
GTACCTGCAACAAGCAAGGATGATATTGCTGAAGGTGAAGCAGCAGAAAT
GATGAAAAAAGTCAATCAACTCTTCCCTGAAAATAGCGTAGATATTGTCT
TTGCTGGACACAATCATCAATATACAAATGGTCTTGTTGGTAAAACTCGT
ATTGTACAAGCGCTCTCTCAAGGAAAAGCCTATGCTGATGTACGTGGTGT
CCTAGATACTGATACACAAGATTTCATTGAAACCCCTTCAGCTAAAGTAA
TTGCAGTTGCTCCTGGTAAAAAAACAGGTAGTGCCGATATTCAAGCCATT
GTTGACCAAGCTAATACTATCGTTAAACAAGTAACAGAAGCTAAAATTGG
TACTGCCGAGGTAAGTGGCATGATTACGCGTTCTGTTGATCAAGATAATG
TTAGTCCGGTAGGCAGCCTCATCACAGAGGCTCAACTAGCAATTGCTCGA
AAAAGCTGGCCAGATATCGATTTTGCCATGACAAATAATGGTGGCATTCG
TGCTGACTTACTCATCAAACCAGATGGAACAATCACCTGGGGAGCTGCAC
AAGCAGTTCAACCTTTTGGTAATATCTTACAAGTCGTCGAAATTACTGGT
AGAGATCTTTATAAAGCACTCAACGAACAATACGACCAAAAACAAAATTT
CTTCCTTCAAATAGCTGGTCTGCGATACACTTACACAGATAATAAAGAGG
GCGGGGAAGAAACACCATTTAAAGTTGTAAAAGCTTATAAATCAAATGGT
GAGGAAATCAATCCTGATGCAAAATACAAATTAGTTATCAATGACTTTTT
ATTCGGTGGTGGTGATGGCTTTGCAAGCTTCAGAAATGCCAAACTTCTAG
GAGCCATTAATCCCGATACAGAGGTATTTATGGCCTATATCACTGATTTA
GAAAAAGCTGGTAAAAAAGTGAGCGTTCCAAATAATAAACCTAAAATCTA
TGTCACTATGAAGATGGTTAATGAAACTATTACACAAAATGATGGTACAT
ATAGCATTATTAAGAAACTTTATTTAGATCGACAAGGAAATATTGTAGCA
CAAGAGATTGTATCAGACACTTTAAACCAAACAAAATCAAAATCTACAAA
AATCAACCCTGTAACTACAATTCACAAAAAACAATTACACCAATTTACAG
CTATTAACCCTATGAGAAATTATGGCAAACCATCAAACTCCACTACTGTA
AAATCAAAACAA

SEQ ID NO. 7104
STRAIN H36B
CCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTCATGGTGCACTTG
ACAATACTGGAACAGCAAATATGCCTGACGGAAAAGTTACTAATGCTGGC
ACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAA
ACAAACTAACCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATGG
TTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTT
AAAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATGA
ATTTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCCC
CTGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGAA
GCTGCAAAACAAGAAATTGTAGTGGCAAACGTTATTGATAAAGTTAACAA
ACAAATCCCTTACAATTGGAAACCTTACACTATTAAAAATATTCCTGTAA
ATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAGACATC
CCAAACCTTGTCTTACGTAAAAATTATGAACAATATGAATTTTTAGATGA
AGCTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTCA
AGGCTATTGTAGTCCTTGCTCATGTACCTGCAACAAGCAAGGATGATATT
GCTGAAGGTGAAGCAGCAGAAATGATGAAAAAAGTCAATCAACTCTTCCC
TGAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAA
ATGGTCTTGTTGGTAAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAAA
GCCTATGCTGATGTACGTGGTGTCCTAGATACTGATACACAAGATTTCAT
TGAAACCCCTTCAGCTAAAGTAATTGCAGTTGCTCCTGGTAAAAAAACAG
GTAGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAA
CAAGTAACAGAAGCTAAAATTGGTACTGCCGAGGTAAGTGGCATGATTAC
GCGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAG
AGGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGCC
ATGACAAATAATGGTGGCATTCGTGCTGACTTACTCATCAAACCAGATGG
AACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCT
TACAAGTCGTCGAAATTACTGGTAGAGATCTTTATAAAGCACTCAACGAA
CAATACGACCAAAAACAAAATTTCTTCCTTCAAATAGCTGGTCTGCGATA
CACTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTTG
TAAAAGCTTATAAATCAAATGGTGAGGAAATCAATCCTGATGCAAAATAC
AAATTAGTTATCAATGACTTTTTATTCGGTGGTGGTGATGGCTTTGCAAG
CTTCAGAAATGCCAAACTTCTAGGAGCCATTAATCCCGATACAGAGGTAT
TTATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGCGTT
CCAAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTTAATGAAAC
TATTACACAAAATGATGGTACATATAGCATTATTAAGAAACTTTATTTAG
ATCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAAC
CAAACAAAATCAAAATCTACAAAAATCAACCCTGTAACTACAATTCACAA
AAAACAATTACACCAATTTACAGCTATTAACCCTATGAGAAATTATGGCA
AACCATCAAACTCCACTACTGTAAAATCAAA

SEQ ID NO. 7105
STRAIN 18RS21
GACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTC
ATGGTGCACTTGACAATACTGGAACAGCAAATATGCCTGACGGAAAAGTT
AnTAATGCTGGCACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCA

Table 71: Comparative Sequences relating to SAG1333

AAAAGATTTCAAACAAACTAACCCTAATGGTGAAAGCATTAGAGTTCAAG
CTGGTGATATGGTTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGAT
GAACCAACCGTTAAAACATTTAATGCAATGAATGTTGAGTATGGCACATT
AGGTAACCATGAATTTGATGAAGGTTTGGCAGAATACAATCGTATCGTTA
CTGGAAAGGCCCCTGCTCCAGATTCTAATATAAATAATATTACGAAATCA
TACCCACACGAAGCTGCAAAACAAGAAATTGTAGTGGCAAACGTTATTGA
TAAAGTTAACAAACAAATCCCTTACAATTGGAAACCTTACACTATTAAAA
ATATTCCTGTAAATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTT
ACCAAAGACATCCCAAACCTTGTCTTACGTAAAAATTATGAACAATATGA
ATTTTTAGATGAAGCTGAAACAATCGTTAAATACGCCAAAGAATTACAAG
CTAAAAATGTCAAGGCTATTGTAGTCCTTGCTCATGTACCTGCAACAAGC
AAGGATGATATTGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAAGTCAA
TCAACTCTTCCCTGAAAATAGCGTAGATATTGTCTTTGCTGGACACAATC
ATCAATATACAAATGGTCTTGTTGGTAAAACTCGTATTGTACAAGCGCTC
TCTCAAGGAAAAGCCTATGCTGATGTACGTGGTGTCCTAGATACTGATAC
ACAAGATTTCATTGAAACCCCTTCAGCTAAAGTAATTGCAGTTGCTCCTG
GTAAAAAAACAGGTAGTGCCGATATTCAAGCCATTGTTGACCAAGCTAAT
ACTATCGTTAAACAAGTAACAGAAGCTAAAATTGGTACTGCCGAGGTAAG
TGGCATGATTACGCGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCA
GCCTCATCACAGAGGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGAT
ATCGATTTTGCCATGACAAATAATGGTGGCATTCGTGCTGACTTACTCAT
CAAACCAGATGGAACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTT
TTGGTAATATCTTACAAGTCGTCGAAATTACTGGTAGAGATCTTTATAAA
GCACTCAACGAACAATACGACCAAAAACAAAATTTCTTCCTTCAAATAGC
TGGTCTGCGATACACTTACACAGATAATAAAGAGGGCGGGGAAGAAACAC
CATTTAAAGTTGTAAAAGCTTATAAATCAAATGGTGAGGAAATCAATCCT
GATGCAAAATACAAATTAGTTATCAATGACTTTTTATTCGGTGGTGGTGA
TGGCTTTGCAAGCTTCAGAAATGCCAAACTTCTAGGAGCCATTAATCCCG
ATACAGAGGTATTTATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAA
AAAGTGAGCGTTCCAAATAATAAACCTAAAATCTATGTCACTATGAAGAT
GGTTAATGAAACTATTACACAAAATGATGGTACATATAGCATTATTAAGA
AACTTTATTTAGATCGACAAGGAAATATTGTAGCACAAGAGATTGTATCA
GACACTTTAAACCAAACAAAATCAAAATCTACAAAAATCAACCCTGTAAC
TACAATTCACAAAAAACAATTACACCAATTTACAGCTATTAACCCTATGA
GAAATTATGGCAAACCATCAAACTCCACTACTGTAAAATCAAAA

SEQ ID NO. 7106
STRAIN M732
ACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTCATGGTGCACTT
GACAATACTGGAACAGCAAATATGCCTGACGGAAAAGTTACTAATGCTGG
CACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCA
AACAAACTAACCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATG
GTTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGT
TAAAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATG
AATTTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCC
CCTGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGA
AGCTGCAAAACAAGAAATTGTAGTGGCAAACGTTATTGATAAAGTTAACA
AACAAATCCCTTACAATTGGAAACCTTACACTATTAAAAATATTCCTGTA
AATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAGACAT
CCCAAACCTTGTCTTACGTAAAAATTATGAACAATATGAATTTTTAGATG
AAGCTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTC
AAGGCTATTGTAGTCCTTGCTCATGTACCTGCAACAAGCAAGGATGATAT
TGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAAGTCAATCAACTCTTCC
CTGAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACA
AATGGTCTTGTTGGTAAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAA
AGCCTATGCTGATGTACGTGGTGTCCTAGATACTGATACACAAGATTTCA
TTGAAACCCCTTCAGCTAAAGTAATTGCAGTTGCTCCTGGTAAAAAAACA
GGTAGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAA
ACAAGTAACAGAAGCTAAAATTGGTACTGCCGAGGTAAGTGGCATGATTA
CGCGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACA
GAGGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGC
CATGACAAATAATGGTGGCATTCGTGCTGACTTACTCATCAAACCAGATG
GAACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATC
TTACAAGTCGTCGAAATTACTGGTAGAGATCTTTATAAAGCACTCAACGA
ACAATACGACCAAAAACAAAATTTCTTCCTTCAAATAGCTGGTCTGCGAT
ACACTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTT
GTAAAAGCTTATAAATCAAATGGTGAGGAAATCAATCCTGATGCAAAATA
CAAATTAGTTATCAATGACTTTTTATTCGGTGGTGGTGATGGCTTTGCAA
GCTTCAGAAATGCCAAACTTCTAGGAGCCATTAATCCCGATACAGAGGTA
TTTATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGCAT
TCCAAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTTAATGAAA
CTATTACACAAAATGATGGTACATATAGCATTATTAAGAAACTTTATTTA
GATCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAA
CCAAACAAAATCAAAATCTACAAAAATCAACCCTGTAACTACAATTCACA
AAAAACAATTACACCAATTTACAGCTATTAACCCTATGAGAAATTATGGC
AAACCATCAAACTCCACTACTGTAAAATCAAAACAA

SEQ ID NO. 7107
STRAIN COH1
ACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTCATGGTGCACTT
GACAATACTGGAACAGCAAATATGCCTGACGGAAAAGTTACTAATGCTGG
CACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCA
AACAAACTAACCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATG

Table 71: Comparative Sequences relating to SAG1333

GTTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGT
TAAAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATG
AATTTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCC
CCTGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGA
AGCTGCAAAACAAGAAATTGTAGTGGCAAACGTTATTGATAAAGTTAACA
AACAAATCCCTTACAATTGGAAACCTTACACTATTAAAAATATTCCTGTA
AATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAGACAT
CCCAAACCTTGtCTTACGTAAAAATTATGAACAATATGAATTTTTAGATG
AAGCTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTC
AAGGCTATTGTAGTCCTTGCTCATGTACCTGCAACAAGCAAGGATGATAT
TGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAAGTCAATCAACTCTTCC
CTGAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACA
AATGGTCTTGTTGGTAAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAA
AGCCTATGCTGATGTACGTGGTGTCCTAGATACTGATACACAAGATTTCA
TTGAAACCCCTTCAGCTAAAGTAATTGCAGTTGCTCCTGGTAAAAAAACA
GGTAGTGCCGATATTCAAGCCATTGtTGACCAAGCTAATACTATCGTTAA
ACAAGTAACAGAAGCTAAAATTGGTACTGCCGAGGTAAGTGGCATGATTA
CGCGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACA
GAGGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGC
CATGACAAATAATGGTGGCATTCGTGCTGACTTACTCATCAAACCAGATG
GAACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATC
TTACAAGTCGTCGAAATTACTGGTAGAGATCTTTATAAAGCACTCAACGA
ACAATACGACCAAAAACAAAATTTCTTCCTTCAAATAGCTGGTCTGCGAT
ACACTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTT
GTAAAAGCTTATAAATCAAATGGTGAGGAAATCAATCCTGATGCAAAATA
CAAATTAGTTATCAATGACTTTTTATTCGGTGGTGGTGATGGCTTTGCAA
GCTTCAGAAATGCCAAACTTCTAGGAGCCATTAATCCCGATACAGAGGTA
TTTATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGCAT
TCCAAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTTAATGAAA
CTATTACACAAAATGATGGTACATATAGCATTATTAAGAAACTTTATTTA
GATCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAA
CCAAACAAAATCAAAATCTACAAAAATCAACCCTGTAACTACAATTCACA
AAAAACAATTACACCAATTTACAGCTATTAACCCTATGAGAAATTATGGC
AAACCATCAAACTCCACTACTGTAAAATCAAA

SEQ ID NO. 7108
STRAIN M781
CAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTCATGGTGCACTTGA
CAATACTGGAACAGCAAATATGCCTGACGGAAAAGTTACTAATGCTGGCA
CTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAAA
CAAACTAACCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATGGT
TGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTTA
AAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATGAA
TTTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCCCC
TGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGAAG
CTGCAAAACAAGAAATTGTAGTGGCAAACGTTATTGATAAAGTTAACAAA
CAAATCCCTTACAATTGGAAACCTTACACTATTAAAAATATTCCTGTAAA
TAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAGACATCC
CAAACCTTGTCTTACGTAAAAATTATGAACAATATGAATTTTTAGATGAA
GCTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTCAA
GGCTATTGTAGTCCTTGCTCATGTACCTGCAACAAGCAAGGATGATATTG
CTGAAGGTGAAGCAGCAGAAATGATGAAAAAAGTCAAtCAACTCTTCCCT
GAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAA
TGGTCTTGTTGGTAAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAG
CCTATGCTGATGTACGTGGTGTCCTAGATACTGATACACAAGATTTCATT
GAAACCCCTTCAGCTAAAGTAATTGCAGTTGCTCCTGGTAAAAAAACAGG
TAGTGCCGATATTCAAGCCATTGtTGACCAAGCTAATACTATCGTTAAAC
AAGTAACAGAAGCTAAAATTGGTACTGCCGAGGTAAGTGGCATGATTACG
CGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGA
GGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGCCA
TGACAAATAATGGTGGCATTCGTGCTGACTTACTCATCAAACCAGATGGA
ACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTT
ACAAGTCGTCGAAATTACTGGTAGAGATCTTTATAAAGCACTCAACGAAC
AATACGACCAAAAACAAAATTTCTTCCTTCAAATAGCTGGTCTGCGATAC
ACTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTTGT
AAAAGCTTATAAATCAAATGGTGAGGAAATCAATCCTGATGCAAAATACA
AATTAGTTATCAATGACTTTTTATTCGGTGGTGGTGATGGCTTTGCAAGC
TTCAGAAATGCCAAACTTCTAGGAGCCATTAATCCCGATACAGAgGTATT
TATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGCATTC
CAAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTTAATGAAACT
ATTACACAAAATGATGGTACATATAGCATTATTAAGAAACTTTATTTAGA
TCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAACC
AAACAAAATCAAAATCTACAAAAATCAACCCTGTAACTACAATTCACAAA
AAACAATTACACCAATTTACAGCTATTAACCCTATGAGAAATTATGGCAA
ACCATCAAACTCCACTACTGTAAAATCAAA

SEQ ID NO. 7109
STRAIN CJB110
GACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTCATGGTGC
ACTTGACAATACTGGAACAGCAAATATGCCTGACGGAAAAGTTACTAATG
CTGGCACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGAT
TTCAAACAAACTAACCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGA
TATGGTTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAA

Table 71: Comparative Sequences relating to SAG1333

CCGTTAAAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAAC
CATGAATTTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAA
GGCCCCTGCTCCAGATTcTAATATAAATAATATTACGAAATCATACCCAC
ACGAAGCTGCAAAACAAGAAATTGTAGTGGCAAACGTTATTGATAAAGTT
AACAAACAAATCCCTTACAATTGGAAACCTTACGCTATTAAAAATATTCC
TGTAAATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAG
ACATCCCAAACCTTGTCTTACGTAAAAATTATGAACAATATGAATTTTTA
GATGAAGCTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAA
TGTCAAGGCTATTGTAGTCCTTGCTCATGTACCTGCAACAAGCAAGGATG
ATATTGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAAGTCAATCAACTC
TTCCCTGAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATA
TACAAATGGTCTTGTTGGTAAAACTCGCATTGTACAAGCGCTCTCTCAAG
GAAAAGCCTATGCTGACGTACGTGGTGTCCTAGATACTGATACACAAGAT
TTCATTGAAACCCCTTCAGCTAAAGTAGTTGCAGTTGCTCCTGGTAAAAA
AACAGGTAGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCG
TTAAACAAGTAACAGAAGCTAAAATTGGTACTGCCGAGGTAAGTGGCATG
ATTACGCGTTCTGTTGATCAAGATAATGTTAGTCCAGTAGGCAGCCTCAT
CACAGAGGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATT
TTGCCATGACAAATAATGGTGGCATTCGTGCTGACTTACTCATCAAACCA
GATGGAACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAA
TATCTTACAAGTCGTCGAAATTACTGGTAGAGATCTTTATAAAGCACTCA
ACGAACAATACGACCAAAAACAAAATTTCTTCCTTCAAATAGCTGGTCTG
CGATACACTTACACAGATAATAAAGAGGGCGGAGAAGAAACACCATTTAA
AGTTGTAAAAGCTTATAAATCAAATGGTGAAGAAATCAATCCTGATGCAA
AATACAAATTAGTTATCAATGACTTTTTATTCGGTGGTGGTGATGGCTTT
GCAAGCTTCAGAAATGCCAAACTTCTAGGAGCCATTAATCCCGATACAGA
GGTATTTATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGA
GCGTTCCAAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTTAAT
GAAACTATTACACAAAATGATGGTACACATAGCATTATTAAGAAACTTTA
TTTAGATCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTT
TAAACCAAACAAAATCAAAATCTACAAAAATCAACCCTGTAACTACAATT
CACAAAAAACAATTACACCAATTTACAGCTATTAACCCTATGAGAAATTA
TGGCAAACCATCAAACTCCACTACTGTAAAATCA

SEQ ID NO. 7110
STRAIN 1169NT
CAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTCATGGTGCACTTGA
CAATACTGGAACAGCAAATATGCCTGATGGAAAAGTTGCTAATGCTGGTA
CTGCTGCTCAATTAGATGCTTATATGGATGACGCTCAAAAAGATTTCAAA
CAAACTAACCCTAATGGTGAAAGCATTAGGGTTCAAGCAGGCGATATGGT
TGGAGCAAGTCCAGCCAACTCTGGGCTTCTTCAAGATGAACCAACTGTCA
AAAATTTTAATGCAATGAATGTTGAGTATGGCACATTGGGTAACCATGAA
TTTGATGAAGGGTTGGCAGAATATAATCGTATCGTTACTGGTAAAGCCCC
TGCTCCAGATTCTAATATTAATAATATTACGAAATCATACCCACATGAAG
CTGCAAAACAAGAAATTGTAGTGGCAAATGTTATTGATAAAGTTAACAAA
CAAATTCCTTACAATTGGAAGCCTTACGCTATTAAAAATATTCCTGTAAA
TAACAAAAGTGTGAACGTTGGCTTTATCGGGATTGTCACCAAAGACATCC
CAAACCTTGTCTTACGTAAAAATTATGAACAATATGAATTTTTAGATGAA
GCTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTCAA
AGCTATTGTAGtTCTCGCACATGTACCTGCAACAAGTAAAAATGATATTG
CTGAAGGTGAAGCAGCAGAAATGATGAAAAAAGTCAATCAACTCTTCCCT
GAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAA
TGGTCTTGTTGGTAAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAG
CCTATGCTGATGTACGTGGTGTCTTAGATACTGATACACAAGATTTCATT
GAGACCCCTTCAGCTAAAGTAATTGCAGTTGCTCCTGGTAAAAAAACAGG
TAGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAAC
AAGTAACAGAAGCTAAAATTGGTACTGCCGAGGTAAGTGTCATGATTACG
CGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGA
GGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGCCA
TGACAAATAATGGTGGCATTCGTGCTGACTTACTCATCAAACCAGATGGA
ACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTT
ACAAGTCGTCGAAATTACTGGTAGAGATCTTTATAAAGCACTCAACGAAC
AATACGACCAAAAACAAAATTTCTTCCTTCAAATAGCTGGTCTGCGATAC
ACTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTTGT
AAAAGCTTATAAATCAAATGGTGAGGAAATCAATCCTGATGCAAAATACA
AATTAGTTATCAATGACTTTTTATTCGGTGGTGGTGATGGCTTTGCAAGC
TTCAGAAATGCCAAACTTCTAGGAGCCATTAACCCCGATACAGAGGTATT
TATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGCGTTC
CAAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTTAATGAAACT
ATTACACAAAATGATGGTACACATAGCATTATTAAGAAACTTTATTTAGA
TCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAACC
AAACAAAATCAAAATCTACAAAAATCAACCCTGTAACTACAATTCACAAA
AAACAATTACACCAATTTACAGCTATTAACCCTATGAGAAATTATGGCAA
ACCATCAAACTCCACTACTGTAAAATCAAA

SEQ ID NO. 7111
STRAIN JM9130013
CGGTGTCCAAGTTATAGGCGTCAATGACTTTCATGGTGCACTTGACAATA
CTGGAACAGCAAATATGCCTGACGGAAAAGTTACTAATGCTGGCACTGCT
GCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAAACAAAC
TAACCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATGGTTGGAG
CAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTTAAAACA
TTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATGAATTTGA

Table 71: Comparative Sequences relating to SAG1333

```
TGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCCCCTGCTC
CAGATTcTAATATAAATAATATTACGAAATCATACCCACACGAAGCTGCA
AAACAAGAAATTGTAGTGGCAAACGTTATTGATAAAGTTAACAAACAAAT
CCCTTACAATTGGAAACCTTACACTATTAAAAATATTCCTGTAAATAACA
AAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAGACATCCCAAAC
CTTGTCTTACGTAAAAATTATGAACAATATGAATTTTTAGATGAAGCTGA
AACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTCAAGGCTA
TTGTAGTCCTTGCTCATGTACCTGCAACAAGCAAGGATGATATTGCTGAA
GGTGAAGCAGCAGAAATGATGAAAAAAGTCAATCAACTCTTCCCTGAAAA
TAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAATGGTC
TTGTTGGTAAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAGCCTAT
GCTGATGTACGTGGTGTCCTAGATACTGATACACAAGATTTCATTGAAAC
CCCTTCAGCTAAAGTAATTGCAGTTGCTCCTGGTAAAAAAACAGGTAGTG
CCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAACAAGTA
ACAGAAGCTAAAATTGGTACTGCCGAGGTAAGTGGCATGATTACGCGTTC
TGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGAGGCTC
AACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGCCATGACA
AATAATGGTGGCATTCGTGCTGACTTACTCATCAAACCAGATGGAACAAT
CACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTTACAAG
TCGTCGAAATTACTGGTAGAGATCTTTATAAAGCACTCAACGAACAATAC
GACCAAAAACAAAATTTCTTCCTTCAAATAGCTGGTCTGCGATACACTTA
CACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTTGTAAAAG
CTTATAAATCAAATGGTGAGGAAATCAATCCTGATGCAAAATACAAATTA
GTTATCAATGACTTTTTATTCGGTGGTGGTGATGGCTTTGCAAGCTTCAG
AAATGCCAAACTTCTAGGAGCCATTAATCCCGATACAGAGGTATTTATGG
CCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGCGTTCCAAAT
AATAAACCTAAAATCTATGTCACTATGAAGATGGTTAATGAAACTATTAC
ACAAAATGATGGTACATATAGCATTATTGAGAAACTTTATTTAGATCGAC
AAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAACCAAACA
AAATCAAAATCTACAAAAATCAACCCTGTAACTACAATTCACAAAAAACA
ATTACACCAATTTACAGCTATTAACCCTATGAGAAATTATGGCAAACCAT
CAAACTCCACTACTGTAAAATCAAAA
```

```
PRETTY of: /biotmp/msa237456.2{*}   May 14, 2003 03:20  ..

                           1                                                50
  msa237456.2{328_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa237456.2{328_2603}  atgaaaaaga aaattatttt gaaaagtagt gttcttggtt tagtcgctgg
  msa237456.2{328_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa237456.2{328_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa237456.2{328_COH1}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa237456.2{328_M732}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa237456.2{328_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa237456.2{328_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa237456.2{328_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa237456.2{328_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa237456.2{328_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                Consensus  ********** ********** ********** ********** **********

                           51                                              100
  msa237456.2{328_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~caagtc ggtgtccaag
    msa237456.2{328_2603}  gacttctatt atgttctcaa gcgtgttcgc gGACcaagtc ggtgtccaag
  msa237456.2{328_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~GACcaagtc ggtgtccaag
    msa237456.2{328_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~Ccaagtc ggtgtccaag
    msa237456.2{328_COH1}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~ACcaagtc ggtgtccaag
    msa237456.2{328_M732}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~ACcaagtc ggtgtccaag
    msa237456.2{328_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~caagtc ggtgtccaag
msa237456.2{328_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~c ggtgtccaag
    msa237456.2{328_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa237456.2{328_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~aagtc ggtgtccaag
  msa237456.2{328_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~GACcaagtc ggtgtccaag
                Consensus  ********** ********** ********** ****------ ----------

                           101                                             150
  msa237456.2{328_1169NT}  ttatagGCGT CAATGACTTT CATGGTGCAC TTGACAATAC TGGAACAGCA
    msa237456.2{328_2603}  ttatagGCGT CAATGACTTT CATGGTGCAC TTGACAATAC TGGAACAGCA
  msa237456.2{328_18RS21}  ttatagGCGT CAATGACTTT CATGGTGCAC TTGACAATAC TGGAACAGCA
    msa237456.2{328_H36B}  ttatagGCGT CAATGACTTT CATGGTGCAC TTGACAATAC TGGAACAGCA
    msa237456.2{328_COH1}  ttatagGCGT CAATGACTTT CATGGTGCAC TTGACAATAC TGGAACAGCA
    msa237456.2{328_M732}  ttatagGCGT CAATGACTTT CATGGTGCAC TTGACAATAC TGGAACAGCA
    msa237456.2{328_M781}  ttatagGCGT CAATGACTTT CATGGTGCAC TTGACAATAC TGGAACAGCA
msa237456.2{328_JM9130013}  ttatagGCGT CAATGACTTT CATGGTGCAC TTGACAATAC TGGAACAGCA
    msa237456.2{328_A909}  ~~~~~~GCGT CAATGACTTT CATGGTGCAC TTGACAATAC TGGAACAGCA
     msa237456.2{328_090}  ttatagGCGT CAATGACTTT CATGGTGCAC TTGACAATAC TGGAACAGCA
  msa237456.2{328_CJB110}  ttatagGCGT CAATGACTTT CATGGTGCAC TTGACAATAC TGGAACAGCA
                Consensus  ------**** ********** ********** ********** **********

                           151                                             200
  msa237456.2{328_1169NT}  AATATGCCTG AtGGAAAAGT TgcTAATGCT GGtACTGCTG CTCAATTAGA
    msa237456.2{328_2603}  AATATGCCTG AtGGAAAAGT TgcTAATGCT GGtACTGCTG CTCAATTAGA
  msa237456.2{328_18RS21}  AATATGCCTG AcGGAAAAGT TanTAATGCT GGcACTGCTG CTCAATTAGA
    msa237456.2{328_H36B}  AATATGCCTG AcGGAAAAGT TacTAATGCT GGcACTGCTG CTCAATTAGA
    msa237456.2{328_COH1}  AATATGCCTG AcGGAAAAGT TacTAATGCT GGcACTGCTG CTCAATTAGA
```

Table 71: Comparative Sequences relating to SAG1333

```
      msa237456.2{328_M732}  AATATGCCTG AcGGAAAAGT TacTAATGCT GGcACTGCTG CTCAATTAGA
      msa237456.2{328_M781}  AATATGCCTG AcGGAAAAGT TacTAATGCT GGcACTGCTG CTCAATTAGA
 msa237456.2{328_JM9130013}  AATATGCCTG AcGGAAAAGT TacTAATGCT GGcACTGCTG CTCAATTAGA
      msa237456.2{328_A909}  AATATGCCTG AcGGAAAAGT TacTAATGCT GGcACTGCTG CTCAATTAGA
       msa237456.2{328_090}  AATATGCCTG AcGGAAAAGT TacTAATGCT GGcACTGCTG CTCAATTAGA
    msa237456.2{328_CJB110}  AATATGCCTG AcGGAAAAGT TacTAATGCT GGcACTGCTG CTCAATTAGA
                  Consensus  ********** *-******** *--******* **-******* **********

                             201                                              250
   msa237456.2{328_1169NT}  TGCTTATATG GATGAcGCTC AAAAAGATTT CAAACAAACT AACCCTAATG
      msa237456.2{328_2603}  TGCTTATATG GATGAcGCTC AAAAAGATTT CAAACAAACT AACCCTAATG
    msa237456.2{328_18RS21}  TGCTTATATG GATGAtGCTC AAAAAGATTT CAAACAAACT AACCCTAATG
      msa237456.2{328_H36B}  TGCTTATATG GATGAtGCTC AAAAAGATTT CAAACAAACT AACCCTAATG
      msa237456.2{328_COH1}  TGCTTATATG GATGAtGCTC AAAAAGATTT CAAACAAACT AACCCTAATG
      msa237456.2{328_M732}  TGCTTATATG GATGAtGCTC AAAAAGATTT CAAACAAACT AACCCTAATG
      msa237456.2{328_M781}  TGCTTATATG GATGAtGCTC AAAAAGATTT CAAACAAACT AACCCTAATG
 msa237456.2{328_JM9130013}  TGCTTATATG GATGAtGCTC AAAAAGATTT CAAACAAACT AACCCTAATG
      msa237456.2{328_A909}  TGCTTATATG GATGAtGCTC AAAAAGATTT CAAACAAACT AACCCTAATG
       msa237456.2{328_090}  TGCTTATATG GATGAtGCTC AAAAAGATTT CAAACAAACT AACCCTAATG
    msa237456.2{328_CJB110}  TGCTTATATG GATGAtGCTC AAAAAGATTT CAAACAAACT AACCCTAATG
                  Consensus  ********** *****-**** ********** ********** **********

                             251                                              300
   msa237456.2{328_1169NT}  GTGAAAGCAT TAGgGTTCAA GCaGGcGATA TGGTTGGAGC AAGTCCAGCc
      msa237456.2{328_2603}  GTGAAAGCAT TAGgGTTCAA GCaGGcGATA TGGTTGGAGC AAGTCCAGCc
    msa237456.2{328_18RS21}  GTGAAAGCAT TAGaGTTCAA GCtGGtGATA TGGTTGGAGC AAGTCCAGCt
      msa237456.2{328_H36B}  GTGAAAGCAT TAGaGTTCAA GCtGGtGATA TGGTTGGAGC AAGTCCAGCt
      msa237456.2{328_COH1}  GTGAAAGCAT TAGaGTTCAA GCtGGtGATA TGGTTGGAGC AAGTCCAGCt
      msa237456.2{328_M732}  GTGAAAGCAT TAGaGTTCAA GCtGGtGATA TGGTTGGAGC AAGTCCAGCt
      msa237456.2{328_M781}  GTGAAAGCAT TAGaGTTCAA GCtGGtGATA TGGTTGGAGC AAGTCCAGCt
 msa237456.2{328_JM9130013}  GTGAAAGCAT TAGaGTTCAA GCtGGtGATA TGGTTGGAGC AAGTCCAGCt
      msa237456.2{328_A909}  GTGAAAGCAT TAGaGTTCAA GCtGGtGATA TGGTTGGAGC AAGTCCAGCt
       msa237456.2{328_090}  GTGAAAGCAT TAGaGTTCAA GCtGGtGATA TGGTTGGAGC AAGTCCAGCt
    msa237456.2{328_CJB110}  GTGAAAGCAT TAGaGTTCAA GCtGGtGATA TGGTTGGAGC AAGTCCAGCt
                  Consensus  ********** ***-****** **-**-**** ********** *********-

                             301                                              350
   msa237456.2{328_1169NT}  AACTCtGGGC TTCTTCAAGA TGAACCAACt GTcAAAAatT TTAATGCAAT
      msa237456.2{328_2603}  AACTCtGGGC TTCTTCAAGA TGAACCAACt GTcAAAAatT TTAATGCAAT
    msa237456.2{328_18RS21}  AACTCaGGGC TTCTTCAAGA TGAACCAACc GTtAAAAcaT TTAATGCAAT
      msa237456.2{328_H36B}  AACTCaGGGC TTCTTCAAGA TGAACCAACc GTtAAAAcaT TTAATGCAAT
      msa237456.2{328_COH1}  AACTCaGGGC TTCTTCAAGA TGAACCAACc GTtAAAAcaT TTAATGCAAT
      msa237456.2{328_M732}  AACTCaGGGC TTCTTCAAGA TGAACCAACc GTtAAAAcaT TTAATGCAAT
      msa237456.2{328_M781}  AACTCaGGGC TTCTTCAAGA TGAACCAACc GTtAAAAcaT TTAATGCAAT
 msa237456.2{328_JM9130013}  AACTCaGGGC TTCTTCAAGA TGAACCAACc GTtAAAAcaT TTAATGCAAT
      msa237456.2{328_A909}  AACTCaGGGC TTCTTCAAGA TGAACCAACc GTtAAAAcaT TTAATGCAAT
       msa237456.2{328_090}  AACTCaGGGC TTCTTCAAGA TGAACCAACc GTtAAAAcaT TTAATGCAAT
    msa237456.2{328_CJB110}  AACTCaGGGC TTCTTCAAGA TGAACCAACc GTtAAAAcaT TTAATGCAAT
                  Consensus  *****-**** ********** *********- **-****--* **********

                             351                                              400
   msa237456.2{328_1169NT}  GAATGTTGAG TATGGCACAT TgGGTAACCA TGAATTTGAT GAAGGgTTGG
      msa237456.2{328_2603}  GAATGTTGAG TATGGCACAT TgGGTAACCA TGAATTTGAT GAAGGgTTGG
    msa237456.2{328_18RS21}  GAATGTTGAG TATGGCACAT TaGGTAACCA TGAATTTGAT GAAGGtTTGG
      msa237456.2{328_H36B}  GAATGTTGAG TATGGCACAT TaGGTAACCA TGAATTTGAT GAAGGtTTGG
      msa237456.2{328_COH1}  GAATGTTGAG TATGGCACAT TaGGTAACCA TGAATTTGAT GAAGGtTTGG
      msa237456.2{328_M732}  GAATGTTGAG TATGGCACAT TaGGTAACCA TGAATTTGAT GAAGGtTTGG
      msa237456.2{328_M781}  GAATGTTGAG TATGGCACAT TaGGTAACCA TGAATTTGAT GAAGGtTTGG
 msa237456.2{328_JM9130013}  GAATGTTGAG TATGGCACAT TaGGTAACCA TGAATTTGAT GAAGGtTTGG
      msa237456.2{328_A909}  GAATGTTGAG TATGGCACAT TaGGTAACCA TGAATTTGAT GAAGGtTTGG
       msa237456.2{328_090}  GAATGTTGAG TATGGCACAT TaGGTAACCA TGAATTTGAT GAAGGtTTGG
    msa237456.2{328_CJB110}  GAATGTTGAG TATGGCACAT TaGGTAACCA TGAATTTGAT GAAGGtTTGG
                  Consensus  ********** ********** *-******** ********** *****-****

                             401                                              450
   msa237456.2{328_1169NT}  CAGAATAtAA TCGTATCGTT ACTGGtAAaG CCCCTGCTCC AGATTCTAAT
      msa237456.2{328_2603}  CAGAATAtAA TCGTATCGTT ACTGGtAAaG CCCCTGCTCC AGATTCTAAT
    msa237456.2{328_18RS21}  CAGAATAcAA TCGTATCGTT ACTGGaAAgG CCCCTGCTCC AGATTCTAAT
      msa237456.2{328_H36B}  CAGAATAcAA TCGTATCGTT ACTGGaAAgG CCCCTGCTCC AGATTCTAAT
      msa237456.2{328_COH1}  CAGAATAcAA TCGTATCGTT ACTGGaAAgG CCCCTGCTCC AGATTCTAAT
      msa237456.2{328_M732}  CAGAATAcAA TCGTATCGTT ACTGGaAAgG CCCCTGCTCC AGATTCTAAT
      msa237456.2{328_M781}  CAGAATAcAA TCGTATCGTT ACTGGaAAgG CCCCTGCTCC AGATTCTAAT
 msa237456.2{328_JM9130013}  CAGAATAcAA TCGTATCGTT ACTGGaAAgG CCCCTGCTCC AGATTCTAAT
      msa237456.2{328_A909}  CAGAATAcAA TCGTATCGTT ACTGGaAAgG CCCCTGCTCC AGATTCTAAT
       msa237456.2{328_090}  CAGAATAcAA TCGTATCGTT ACTGGaAAgG CCCCTGCTCC AGATTCTAAT
    msa237456.2{328_CJB110}  CAGAATAcAA TCGTATCGTT ACTGGaAAgG CCCCTGCTCC AGATTCTAAT
                  Consensus  *******-** ********** *****-**-* ********** **********

                             451                                              500
   msa237456.2{328_1169NT}  ATtAATAATA TTACGAAATC ATACCCACAt GAAGCTGCAA AACAAGAAAT
      msa237456.2{328_2603}  ATtAATAATA TTACGAAATC ATACCCACAt GAAGCTGCAA AACAAGAAAT
    msa237456.2{328_18RS21}  ATaAATAATA TTACGAAATC ATACCCACAc GAAGCTGCAA AACAAGAAAT
      msa237456.2{328_H36B}  ATaAATAATA TTACGAAATC ATACCCACAc GAAGCTGCAA AACAAGAAAT
```

Table 71: Comparative Sequences relating to SAG1333

```
      msa237456.2{328_COH1}  ATaAATAATA TTACGAAATC ATACCCACAc GAAGCTGCAA AACAAGAAAT
      msa237456.2{328_M732}  ATaAATAATA TTACGAAATC ATACCCACAc GAAGCTGCAA AACAAGAAAT
      msa237456.2{328_M781}  ATaAATAATA TTACGAAATC ATACCCACAc GAAGCTGCAA AACAAGAAAT
 msa237456.2{328_JM9130013}  ATaAATAATA TTACGAAATC ATACCCACAc GAAGCTGCAA AACAAGAAAT
      msa237456.2{328_A909}  ATaAATAATA TTACGAAATC ATACCCACAc GAAGCTGCAA AACAAGAAAT
       msa237456.2{328_090}  ATaAATAATA TTACGAAATC ATACCCACAc GAAGCTGCAA AACAAGAAAT
    msa237456.2{328_CJB110}  ATaAATAATA TTACGAAATC ATACCCACAc GAAGCTGCAA AACAAGAAAT
                  Consensus  **-******* ********** *********- ********** **********

                             501                                               550
    msa237456.2{328_1169NT}  TGTAGTGGCA AAtGTTATTG ATAAAGTTAA CAAACAAATt CCTTACAATT
      msa237456.2{328_2603}  TGTAGTGGCA AAtGTTATTG ATAAAGTTAA CAAACAAATt CCTTACAATT
     msa237456.2{328_18RS21}  TGTAGTGGCA AAcGTTATTG ATAAAGTTAA CAAACAAATc CCTTACAATT
      msa237456.2{328_H36B}  TGTAGTGGCA AAcGTTATTG ATAAAGTTAA CAAACAAATc CCTTACAATT
      msa237456.2{328_COH1}  TGTAGTGGCA AAcGTTATTG ATAAAGTTAA CAAACAAATc CCTTACAATT
      msa237456.2{328_M732}  TGTAGTGGCA AAcGTTATTG ATAAAGTTAA CAAACAAATc CCTTACAATT
      msa237456.2{328_M781}  TGTAGTGGCA AAcGTTATTG ATAAAGTTAA CAAACAAATc CCTTACAATT
 msa237456.2{328_JM9130013}  TGTAGTGGCA AAcGTTATTG ATAAAGTTAA CAAACAAATc CCTTACAATT
      msa237456.2{328_A909}  TGTAGTGGCA AAcGTTATTG ATAAAGTTAA CAAACAAATc CCTTACAATT
       msa237456.2{328_090}  TGTAGTGGCA AAcGTTATTG ATAAAGTTAA CAAACAAATc CCTTACAATT
    msa237456.2{328_CJB110}  TGTAGTGGCA AAcGTTATTG ATAAAGTTAA CAAACAAATc CCTTACAATT
                  Consensus  ********** **-******* ********** *********- **********

                             551                                               600
    msa237456.2{328_1169NT}  GGAAgCCTTA CgCTATTAAA AATATTCCTG TAAATAACAA AAGTGTGAAC
      msa237456.2{328_2603}  GGAAgCCTTA CgCTATTAAA AATATTCCTG TAAATAACAA AAGTGTGAAC
    msa237456.2{328_18RS21}  GGAAaCCTTA CaCTATTAAA AATATTCCTG TAAATAACAA AAGTGTGAAC
      msa237456.2{328_H36B}  GGAAaCCTTA CaCTATTAAA AATATTCCTG TAAATAACAA AAGTGTGAAC
      msa237456.2{328_COH1}  GGAAaCCTTA CaCTATTAAA AATATTCCTG TAAATAACAA AAGTGTGAAC
      msa237456.2{328_M732}  GGAAaCCTTA CaCTATTAAA AATATTCCTG TAAATAACAA AAGTGTGAAC
      msa237456.2{328_M781}  GGAAaCCTTA CaCTATTAAA AATATTCCTG TAAATAACAA AAGTGTGAAC
 msa237456.2{328_JM9130013}  GGAAaCCTTA CaCTATTAAA AATATTCCTG TAAATAACAA AAGTGTGAAC
      msa237456.2{328_A909}  GGAAaCCTTA CaCTATTAAA AATATTCCTG TAAATAACAA AAGTGTGAAC
       msa237456.2{328_090}  GGAAaCCTTA CgCTATTAAA AATATTCCTG TAAATAACAA AAGTGTGAAC
    msa237456.2{328_CJB110}  GGAAaCCTTA CgCTATTAAA AATATTCCTG TAAATAACAA AAGTGTGAAC
                  Consensus  ****-***** *-******** ********** ********** **********

                             601                                               650
    msa237456.2{328_1169NT}  GTTGGCTTTA TCGGgATtGT cACCAAAGAC ATCCCAAACC TTGTCTTACG
      msa237456.2{328_2603}  GTTGGCTTTA TCGGgATtGT cACCAAAGAC ATCCCAAACC TTGTCTTACG
    msa237456.2{328_18RS21}  GTTGGCTTTA TCGGaATcGT tACCAAAGAC ATCCCAAACC TTGTCTTACG
      msa237456.2{328_H36B}  GTTGGCTTTA TCGGaATcGT tACCAAAGAC ATCCCAAACC TTGTCTTACG
      msa237456.2{328_COH1}  GTTGGCTTTA TCGGaATcGT tACCAAAGAC ATCCCAAACC TTGTCTTACG
      msa237456.2{328_M732}  GTTGGCTTTA TCGGaATcGT tACCAAAGAC ATCCCAAACC TTGTCTTACG
      msa237456.2{328_M781}  GTTGGCTTTA TCGGaATcGT tACCAAAGAC ATCCCAAACC TTGTCTTACG
 msa237456.2{328_JM9130013}  GTTGGCTTTA TCGGaATcGT tACCAAAGAC ATCCCAAACC TTGTCTTACG
      msa237456.2{328_A909}  GTTGGCTTTA TCGGaATcGT tACCAAAGAC ATCCCAAACC TTGTCTTACG
       msa237456.2{328_090}  GTTGGCTTTA TCGGaATcGT tACCAAAGAC ATCCCAAACC TTGTCTTACG
    msa237456.2{328_CJB110}  GTTGGCTTTA TCGGaATcGT tACCAAAGAC ATCCCAAACC TTGTCTTACG
                  Consensus  ********** ****-**-** -********* ********** **********

                             651                                               700
    msa237456.2{328_1169NT}  TAAAAATTAT GAACAATATG AATTTTTAGA TGAAGCTGAA ACAATCGTTA
      msa237456.2{328_2603}  TAAAAATTAT GAACAATATG AATTTTTAGA TGAAGCTGAA ACAATCGTTA
    msa237456.2{328_18RS21}  TAAAAATTAT GAACAATATG AATTTTTAGA TGAAGCTGAA ACAATCGTTA
      msa237456.2{328_H36B}  TAAAAATTAT GAACAATATG AATTTTTAGA TGAAGCTGAA ACAATCGTTA
      msa237456.2{328_COH1}  TAAAAATTAT GAACAATATG AATTTTTAGA TGAAGCTGAA ACAATCGTTA
      msa237456.2{328_M732}  TAAAAATTAT GAACAATATG AATTTTTAGA TGAAGCTGAA ACAATCGTTA
      msa237456.2{328_M781}  TAAAAATTAT GAACAATATG AATTTTTAGA TGAAGCTGAA ACAATCGTTA
 msa237456.2{328_JM9130013}  TAAAAATTAT GAACAATATG AATTTTTAGA TGAAGCTGAA ACAATCGTTA
      msa237456.2{328_A909}  TAAAAATTAT GAACAATATG AATTTTTAGA TGAAGCTGAA ACAATCGTTA
       msa237456.2{328_090}  TAAAAATTAT GAACAATATG AATTTTTAGA TGAAGCTGAA ACAATCGTTA
    msa237456.2{328_CJB110}  TAAAAATTAT GAACAATATG AATTTTTAGA TGAAGCTGAA ACAATCGTTA
                  Consensus  ********** ********** ********** ********** **********

                             701                                               750
    msa237456.2{328_1169NT}  AATACGCCAA AGAATTACAA GCTAAAAATG TCAAaGCTAT TGTAGTtCTc
      msa237456.2{328_2603}  AATACGCCAA AGAATTACAA GCTAAAAATG TCAAaGCTAT TGTAGTtCTc
    msa237456.2{328_18RS21}  AATACGCCAA AGAATTACAA GCTAAAAATG TCAAgGCTAT TGTAGTcCTt
      msa237456.2{328_H36B}  AATACGCCAA AGAATTACAA GCTAAAAATG TCAAgGCTAT TGTAGTcCTt
      msa237456.2{328_COH1}  AATACGCCAA AGAATTACAA GCTAAAAATG TCAAgGCTAT TGTAGTcCTt
      msa237456.2{328_M732}  AATACGCCAA AGAATTACAA GCTAAAAATG TCAAgGCTAT TGTAGTcCTt
      msa237456.2{328_M781}  AATACGCCAA AGAATTACAA GCTAAAAATG TCAAgGCTAT TGTAGTcCTt
 msa237456.2{328_JM9130013}  AATACGCCAA AGAATTACAA GCTAAAAATG TCAAgGCTAT TGTAGTcCTt
      msa237456.2{328_A909}  AATACGCCAA AGAATTACAA GCTAAAAATG TCAAgGCTAT TGTAGTcCTt
       msa237456.2{328_090}  AATACGCCAA AGAATTACAA GCTAAAAATG TCAAgGCTAT TGTAGTcCTt
    msa237456.2{328_CJB110}  AATACGCCAA AGAATTACAA GCTAAAAATG TCAAgGCTAT TGTAGTcCTt
                  Consensus  ********** ********** ********** ****-***** ******-**-

                             751                                               800
    msa237456.2{328_1169NT}  GCaCATGTAC CTGCAACAAG tAAaaATGAT ATTGCTGAAG GTGAAGCAGC
      msa237456.2{328_2603}  GCaCATGTAC CTGCAACAAG tAAaaATGAT ATTGCTGAAG GTGAAGCAGC
    msa237456.2{328_18RS21}  GCtCATGTAC CTGCAACAAG cAAggATGAT ATTGCTGAAG GTGAAGCAGC
```

Table 71: Comparative Sequences relating to SAG1333

```
     msa237456.2{328_H36B}  GCtCATGTAC CTGCAACAAG cAAggATGAT ATTGCTGAAG GTGAAGCAGC
     msa237456.2{328_COH1}  GCtCATGTAC CTGCAACAAG cAAggATGAT ATTGCTGAAG GTGAAGCAGC
     msa237456.2{328_M732}  GCtCATGTAC CTGCAACAAG cAAggATGAT ATTGCTGAAG GTGAAGCAGC
     msa237456.2{328_M781}  GCtCATGTAC CTGCAACAAG cAAggATGAT ATTGCTGAAG GTGAAGCAGC
msa237456.2{328_JM9130013}  GCtCATGTAC CTGCAACAAG cAAggATGAT ATTGCTGAAG GTGAAGCAGC
     msa237456.2{328_A909}  GCtCATGTAC CTGCAACAAG cAAggATGAT ATTGCTGAAG GTGAAGCAGC
      msa237456.2{328_090}  GCtCATGTAC CTGCAACAAG cAAggATGAT ATTGCTGAAG GTGAAGCAGC
   msa237456.2{328_CJB110}  GCtCATGTAC CTGCAACAAG cAAggATGAT ATTGCTGAAG GTGAAGCAGC
                 Consensus  **-******* ********** -**--***** ********** **********

                            801                                                850
  msa237456.2{328_1169NT}   AGAAATGATG AAAAAAGTCA ATCAACTCTT CCCTGAAAAT AGCGTAGATA
     msa237456.2{328_2603}  AGAAATGATG AAAAAAGTCA ATCAACTCTT CCCTGAAAAT AGCGTAGATA
   msa237456.2{328_18RS21}  AGAAATGATG AAAAAAGTCA ATCAACTCTT CCCTGAAAAT AGCGTAGATA
     msa237456.2{328_H36B}  AGAAATGATG AAAAAAGTCA ATCAACTCTT CCCTGAAAAT AGCGTAGATA
     msa237456.2{328_COH1}  AGAAATGATG AAAAAAGTCA ATCAACTCTT CCCTGAAAAT AGCGTAGATA
     msa237456.2{328_M732}  AGAAATGATG AAAAAAGTCA ATCAACTCTT CCCTGAAAAT AGCGTAGATA
     msa237456.2{328_M781}  AGAAATGATG AAAAAAGTCA ATCAACTCTT CCCTGAAAAT AGCGTAGATA
msa237456.2{328_JM9130013}  AGAAATGATG AAAAAAGTCA ATCAACTCTT CCCTGAAAAT AGCGTAGATA
     msa237456.2{328_A909}  AGAAATGATG AAAAAAGTCA ATCAACTCTT CCCTGAAAAT AGCGTAGATA
      msa237456.2{328_090}  AGAAATGATG AAAAAAGTCA ATCAACTCTT CCCTGAAAAT AGCGTAGATA
   msa237456.2{328_CJB110}  AGAAATGATG AAAAAAGTCA ATCAACTCTT CCCTGAAAAT AGCGTAGATA
                 Consensus  ********** ********** ********** ********** **********

                            851                                                900
  msa237456.2{328_1169NT}   TTGTCTTTGC TGGACACAAT CATCAATATA CAAATGGTCT TGTTGGTAAA
     msa237456.2{328_2603}  TTGTCTTTGC TGGACACAAT CATCAATATA CAAATGGTCT TGTTGGTAAA
   msa237456.2{328_18RS21}  TTGTCTTTGC TGGACACAAT CATCAATATA CAAATGGTCT TGTTGGTAAA
     msa237456.2{328_H36B}  TTGTCTTTGC TGGACACAAT CATCAATATA CAAATGGTCT TGTTGGTAAA
     msa237456.2{328_COH1}  TTGTCTTTGC TGGACACAAT CATCAATATA CAAATGGTCT TGTTGGTAAA
     msa237456.2{328_M732}  TTGTCTTTGC TGGACACAAT CATCAATATA CAAATGGTCT TGTTGGTAAA
     msa237456.2{328_M781}  TTGTCTTTGC TGGACACAAT CATCAATATA CAAATGGTCT TGTTGGTAAA
msa237456.2{328_JM9130013}  TTGTCTTTGC TGGACACAAT CATCAATATA CAAATGGTCT TGTTGGTAAA
     msa237456.2{328_A909}  TTGTCTTTGC TGGACACAAT CATCAATATA CAAATGGTCT TGTTGGTAAA
      msa237456.2{328_090}  TTGTCTTTGC TGGACACAAT CATCAATATA CAAATGGTCT TGTTGGTAAA
   msa237456.2{328_CJB110}  TTGTCTTTGC TGGACACAAT CATCAATATA CAAATGGTCT TGTTGGTAAA
                 Consensus  ********** ********** ********** ********** **********

                            901                                                950
  msa237456.2{328_1169NT}   ACTCGtATTG TACAAGCGCT CTCTCAAGGA AAAGCCTATG CTGAtGTACG
     msa237456.2{328_2603}  ACTCGtATTG TACAAGCGCT CTCTCAAGGA AAAGCCTATG CTGAtGTACG
   msa237456.2{328_18RS21}  ACTCGtATTG TACAAGCGCT CTCTCAAGGA AAAGCCTATG CTGAtGTACG
     msa237456.2{328_H36B}  ACTCGtATTG TACAAGCGCT CTCTCAAGGA AAAGCCTATG CTGAtGTACG
     msa237456.2{328_COH1}  ACTCGtATTG TACAAGCGCT CTCTCAAGGA AAAGCCTATG CTGAtGTACG
     msa237456.2{328_M732}  ACTCGtATTG TACAAGCGCT CTCTCAAGGA AAAGCCTATG CTGAtGTACG
     msa237456.2{328_M781}  ACTCGtATTG TACAAGCGCT CTCTCAAGGA AAAGCCTATG CTGAtGTACG
msa237456.2{328_JM9130013}  ACTCGtATTG TACAAGCGCT CTCTCAAGGA AAAGCCTATG CTGAtGTACG
     msa237456.2{328_A909}  ACTCGtATTG TACAAGCGCT CTCTCAAGGA AAAGCCTATG CTGAtGTACG
      msa237456.2{328_090}  ACTCGcATTG TACAAGCGCT CTCTCAAGGA AAAGCCTATG CTGAcGTACG
   msa237456.2{328_CJB110}  ACTCGcATTG TACAAGCGCT CTCTCAAGGA AAAGCCTATG CTGAcGTACG
                 Consensus  *****-**** ********** ********** ********** ****-*****

                            951                                               1000
  msa237456.2{328_1169NT}   TGGTGTCtTA GATACTGATA CACAAGATTT CATTGAgACC CCTTCAGCTA
     msa237456.2{328_2603}  TGGTGTCtTA GATACTGATA CACAAGATTT CATTGAgACC CCTTCAGCTA
   msa237456.2{328_18RS21}  TGGTGTCcTA GATACTGATA CACAAGATTT CATTGAaACC CCTTCAGCTA
     msa237456.2{328_H36B}  TGGTGTCcTA GATACTGATA CACAAGATTT CATTGAaACC CCTTCAGCTA
     msa237456.2{328_COH1}  TGGTGTCcTA GATACTGATA CACAAGATTT CATTGAaACC CCTTCAGCTA
     msa237456.2{328_M732}  TGGTGTCcTA GATACTGATA CACAAGATTT CATTGAaACC CCTTCAGCTA
     msa237456.2{328_M781}  TGGTGTCcTA GATACTGATA CACAAGATTT CATTGAaACC CCTTCAGCTA
msa237456.2{328_JM9130013}  TGGTGTCcTA GATACTGATA CACAAGATTT CATTGAaACC CCTTCAGCTA
     msa237456.2{328_A909}  TGGTGTCcTA GATACTGATA CACAAGATTT CATTGAaACC CCTTCAGCTA
      msa237456.2{328_090}  TGGTGTCcTA GATACTGATA CACAAGATTT CATTGAaACC CCTTCAGCTA
   msa237456.2{328_CJB110}  TGGTGTCcTA GATACTGATA CACAAGATTT CATTGAaACC CCTTCAGCTA
                 Consensus  *******-** ********** ********** ******-*** **********

                            1001                                              1050
  msa237456.2{328_1169NT}   AAGTAaTTGC AGTTGCTCCT GGTAAAAAAA CAGGTAGTGC CGATATTCAA
     msa237456.2{328_2603}  AAGTAaTTGC AGTTGCTCCT GGTAAAAAAA CAGGTAGTGC CGATATTCAA
   msa237456.2{328_18RS21}  AAGTAaTTGC AGTTGCTCCT GGTAAAAAAA CAGGTAGTGC CGATATTCAA
     msa237456.2{328_H36B}  AAGTAaTTGC AGTTGCTCCT GGTAAAAAAA CAGGTAGTGC CGATATTCAA
     msa237456.2{328_COH1}  AAGTAaTTGC AGTTGCTCCT GGTAAAAAAA CAGGTAGTGC CGATATTCAA
     msa237456.2{328_M732}  AAGTAaTTGC AGTTGCTCCT GGTAAAAAAA CAGGTAGTGC CGATATTCAA
     msa237456.2{328_M781}  AAGTAaTTGC AGTTGCTCCT GGTAAAAAAA CAGGTAGTGC CGATATTCAA
msa237456.2{328_JM9130013}  AAGTAaTTGC AGTTGCTCCT GGTAAAAAAA CAGGTAGTGC CGATATTCAA
     msa237456.2{328_A909}  AAGTAaTTGC AGTTGCTCCT GGTAAAAAAA CAGGTAGTGC CGATATTCAA
      msa237456.2{328_090}  AAGTAgTTGC AGTTGCTCCT GGTAAAAAAA CAGGTAGTGC CGATATTCAA
   msa237456.2{328_CJB110}  AAGTAgTTGC AGTTGCTCCT GGTAAAAAAA CAGGTAGTGC CGATATTCAA
                 Consensus  *****-**** ********** ********** ********** **********

                            1051                                              1100
  msa237456.2{328_1169NT}   GCCATTGTTG ACCAAGCTAA TACTATCGTT AAACAAGTAA CAGAAGCTAA
     msa237456.2{328_2603}  GCCATTGTTG ACCAAGCTAA TACTATCGTT AAACAAGTAA CAGAAGCTAA
```

Table 71: Comparative Sequences relating to SAG1333

```
   msa237456.2{328_18RS21}  GCCATTGTTG ACCAAGCTAA TACTATCGTT AAACAAGTAA CAGAAGCTAA
     msa237456.2{328_H36B}  GCCATTGTTG ACCAAGCTAA TACTATCGTT AAACAAGTAA CAGAAGCTAA
     msa237456.2{328_COH1}  GCCATTGTTG ACCAAGCTAA TACTATCGTT AAACAAGTAA CAGAAGCTAA
     msa237456.2{328_M732}  GCCATTGTTG ACCAAGCTAA TACTATCGTT AAACAAGTAA CAGAAGCTAA
     msa237456.2{328_M781}  GCCATTGTTG ACCAAGCTAA TACTATCGTT AAACAAGTAA CAGAAGCTAA
msa237456.2{328_JM9130013}  GCCATTGTTG ACCAAGCTAA TACTATCGTT AAACAAGTAA CAGAAGCTAA
     msa237456.2{328_A909}  GCCATTGTTG ACCAAGCTAA TACTATCGTT AAACAAGTAA CAGAAGCTAA
      msa237456.2{328_090}  GCCATTGTTG ACCAAGCTAA TACTATCGTT AAACAAGTAA CAGAAGCTAA
   msa237456.2{328_CJB110}  GCCATTGTTG ACCAAGCTAA TACTATCGTT AAACAAGTAA CAGAAGCTAA
                 Consensus  ********** ********** ********** ********** **********

                            1101                                             1150
   msa237456.2{328_1169NT}  AATTGGTACT GCCGAGGTAA GTGtCATGAT TACGCGTTCT GTTGATCAAG
     msa237456.2{328_2603}  AATTGGTACT GCCGAGGTAA GTGtCATGAT TACGCGTTCT GTTGATCAAG
   msa237456.2{328_18RS21}  AATTGGTACT GCCGAGGTAA GTGgCATGAT TACGCGTTCT GTTGATCAAG
     msa237456.2{328_H36B}  AATTGGTACT GCCGAGGTAA GTGgCATGAT TACGCGTTCT GTTGATCAAG
     msa237456.2{328_COH1}  AATTGGTACT GCCGAGGTAA GTGgCATGAT TACGCGTTCT GTTGATCAAG
     msa237456.2{328_M732}  AATTGGTACT GCCGAGGTAA GTGgCATGAT TACGCGTTCT GTTGATCAAG
     msa237456.2{328_M781}  AATTGGTACT GCCGAGGTAA GTGgCATGAT TACGCGTTCT GTTGATCAAG
msa237456.2{328_JM9130013}  AATTGGTACT GCCGAGGTAA GTGgCATGAT TACGCGTTCT GTTGATCAAG
     msa237456.2{328_A909}  AATTGGTACT GCCGAGGTAA GTGgCATGAT TACGCGTTCT GTTGATCAAG
      msa237456.2{328_090}  AATTGGTACT GCCGAGGTAA GTGgCATGAT TACGCGTTCT GTTGATCAAG
   msa237456.2{328_CJB110}  AATTGGTACT GCCGAGGTAA GTGgCATGAT TACGCGTTCT GTTGATCAAG
                 Consensus  ********** ********** ***.****** ********** **********

                            1151                                             1200
   msa237456.2{328_1169NT}  ATAATGTTAG TCCgGTAGGC AGCCTCATCA CAGAGGCTCA ACTAGCAATT
     msa237456.2{328_2603}  ATAATGTTAG TCCgGTAGGC AGCCTCATCA CAGAGGCTCA ACTAGCAATT
   msa237456.2{328_18RS21}  ATAATGTTAG TCCgGTAGGC AGCCTCATCA CAGAGGCTCA ACTAGCAATT
     msa237456.2{328_H36B}  ATAATGTTAG TCCgGTAGGC AGCCTCATCA CAGAGGCTCA ACTAGCAATT
     msa237456.2{328_COH1}  ATAATGTTAG TCCgGTAGGC AGCCTCATCA CAGAGGCTCA ACTAGCAATT
     msa237456.2{328_M732}  ATAATGTTAG TCCgGTAGGC AGCCTCATCA CAGAGGCTCA ACTAGCAATT
     msa237456.2{328_M781}  ATAATGTTAG TCCgGTAGGC AGCCTCATCA CAGAGGCTCA ACTAGCAATT
msa237456.2{328_JM9130013}  ATAATGTTAG TCCgGTAGGC AGCCTCATCA CAGAGGCTCA ACTAGCAATT
     msa237456.2{328_A909}  ATAATGTTAG TCCgGTAGGC AGCCTCATCA CAGAGGCTCA ACTAGCAATT
      msa237456.2{328_090}  ATAATGTTAG TCCaGTAGGC AGCCTCATCA CAGAGGCTCA ACTAGCAATT
   msa237456.2{328_CJB110}  ATAATGTTAG TCCaGTAGGC AGCCTCATCA CAGAGGCTCA ACTAGCAATT
                 Consensus  ********** ***.****** ********** ********** **********

                            1201                                             1250
   msa237456.2{328_1169NT}  GCTCGAAAAA GCTGGCCAGA TATCGATTTT GCCATGACAA ATAATGGTGG
     msa237456.2{328_2603}  GCTCGAAAAA GCTGGCCAGA TATCGATTTT GCCATGACAA ATAATGGTGG
   msa237456.2{328_18RS21}  GCTCGAAAAA GCTGGCCAGA TATCGATTTT GCCATGACAA ATAATGGTGG
     msa237456.2{328_H36B}  GCTCGAAAAA GCTGGCCAGA TATCGATTTT GCCATGACAA ATAATGGTGG
     msa237456.2{328_COH1}  GCTCGAAAAA GCTGGCCAGA TATCGATTTT GCCATGACAA ATAATGGTGG
     msa237456.2{328_M732}  GCTCGAAAAA GCTGGCCAGA TATCGATTTT GCCATGACAA ATAATGGTGG
     msa237456.2{328_M781}  GCTCGAAAAA GCTGGCCAGA TATCGATTTT GCCATGACAA ATAATGGTGG
msa237456.2{328_JM9130013}  GCTCGAAAAA GCTGGCCAGA TATCGATTTT GCCATGACAA ATAATGGTGG
     msa237456.2{328_A909}  GCTCGAAAAA GCTGGCCAGA TATCGATTTT GCCATGACAA ATAATGGTGG
      msa237456.2{328_090}  GCTCGAAAAA GCTGGCCAGA TATCGATTTT GCCATGACAA ATAATGGTGG
   msa237456.2{328_CJB110}  GCTCGAAAAA GCTGGCCAGA TATCGATTTT GCCATGACAA ATAATGGTGG
                 Consensus  ********** ********** ********** ********** **********

                            1251                                             1300
   msa237456.2{328_1169NT}  CATTCGTGCT GACTTACTCA TCAAACCAGA TGGAACAATC ACCTGGGGAG
     msa237456.2{328_2603}  CATTCGTGCT GACTTACTCA TCAAACCAGA TGGAACAATC ACCTGGGGAG
   msa237456.2{328_18RS21}  CATTCGTGCT GACTTACTCA TCAAACCAGA TGGAACAATC ACCTGGGGAG
     msa237456.2{328_H36B}  CATTCGTGCT GACTTACTCA TCAAACCAGA TGGAACAATC ACCTGGGGAG
     msa237456.2{328_COH1}  CATTCGTGCT GACTTACTCA TCAAACCAGA TGGAACAATC ACCTGGGGAG
     msa237456.2{328_M732}  CATTCGTGCT GACTTACTCA TCAAACCAGA TGGAACAATC ACCTGGGGAG
     msa237456.2{328_M781}  CATTCGTGCT GACTTACTCA TCAAACCAGA TGGAACAATC ACCTGGGGAG
msa237456.2{328_JM9130013}  CATTCGTGCT GACTTACTCA TCAAACCAGA TGGAACAATC ACCTGGGGAG
     msa237456.2{328_A909}  CATTCGTGCT GACTTACTCA TCAAACCAGA TGGAACAATC ACCTGGGGAG
      msa237456.2{328_090}  CATTCGTGCT GACTTACTCA TCAAACCAGA TGGAACAATC ACCTGGGGAG
   msa237456.2{328_CJB110}  CATTCGTGCT GACTTACTCA TCAAACCAGA TGGAACAATC ACCTGGGGAG
                 Consensus  ********** ********** ********** ********** **********

                            1301                                             1350
   msa237456.2{328_1169NT}  CTGCACAAGC AGTTCAACCT TTTGGTAATA TCTTACAAGT CGTCGAAATT
     msa237456.2{328_2603}  CTGCACAAGC AGTTCAACCT TTTGGTAATA TCTTACAAGT CGTCGAAATT
   msa237456.2{328_18RS21}  CTGCACAAGC AGTTCAACCT TTTGGTAATA TCTTACAAGT CGTCGAAATT
     msa237456.2{328_H36B}  CTGCACAAGC AGTTCAACCT TTTGGTAATA TCTTACAAGT CGTCGAAATT
     msa237456.2{328_COH1}  CTGCACAAGC AGTTCAACCT TTTGGTAATA TCTTACAAGT CGTCGAAATT
     msa237456.2{328_M732}  CTGCACAAGC AGTTCAACCT TTTGGTAATA TCTTACAAGT CGTCGAAATT
     msa237456.2{328_M781}  CTGCACAAGC AGTTCAACCT TTTGGTAATA TCTTACAAGT CGTCGAAATT
msa237456.2{328_JM9130013}  CTGCACAAGC AGTTCAACCT TTTGGTAATA TCTTACAAGT CGTCGAAATT
     msa237456.2{328_A909}  CTGCACAAGC AGTTCAACCT TTTGGTAATA TCTTACAAGT CGTCGAAATT
      msa237456.2{328_090}  CTGCACAAGC AGTTCAACCT TTTGGTAATA TCTTACAAGT CGTCGAAATT
   msa237456.2{328_CJB110}  CTGCACAAGC AGTTCAACCT TTTGGTAATA TCTTACAAGT CGTCGAAATT
                 Consensus  ********** ********** ********** ********** **********

                            1351                                             1400
   msa237456.2{328_1169NT}  ACTGGTAGAG ATCTTTATAA AGCACTCAAC GAACAATACG ACCAAAAACA
```

Table 71: Comparative Sequences relating to SAG1333

```
     msa237456.2{328_2603}  ACTGGTAGAG ATCTTTATAA AGCACTCAAC GAACAATACG ACCAAAAACA
   msa237456.2{328_18RS21}  ACTGGTAGAG ATCTTTATAA AGCACTCAAC GAACAATACG ACCAAAAACA
     msa237456.2{328_H36B}  ACTGGTAGAG ATCTTTATAA AGCACTCAAC GAACAATACG ACCAAAAACA
     msa237456.2{328_COH1}  ACTGGTAGAG ATCTTTATAA AGCACTCAAC GAACAATACG ACCAAAAACA
     msa237456.2{328_M732}  ACTGGTAGAG ATCTTTATAA AGCACTCAAC GAACAATACG ACCAAAAACA
     msa237456.2{328_M781}  ACTGGTAGAG ATCTTTATAA AGCACTCAAC GAACAATACG ACCAAAAACA
msa237456.2{328_JM9130013}  ACTGGTAGAG ATCTTTATAA AGCACTCAAC GAACAATACG ACCAAAAACA
     msa237456.2{328_A909}  ACTGGTAGAG ATCTTTATAA AGCACTCAAC GAACAATACG ACCAAAAACA
      msa237456.2{328_090}  ACTGGTAGAG ATCTTTATAA AGCACTCAAC GAACAATACG ACCAAAAACA
   msa237456.2{328_CJB110}  ACTGGTAGAG ATCTTTATAA AGCACTCAAC GAACAATACG ACCAAAAACA
                 Consensus  ********** ********** ********** ********** **********

                            1401                                              1450
   msa237456.2{328_1169NT}  AAATTTCTTC CTTCAAATAG CTGGTCTGCG ATACACTTAC ACAGATAATA
     msa237456.2{328_2603}  AAATTTCTTC CTTCAAATAG CTGGTCTGCG ATACACTTAC ACAGATAATA
   msa237456.2{328_18RS21}  AAATTTCTTC CTTCAAATAG CTGGTCTGCG ATACACTTAC ACAGATAATA
     msa237456.2{328_H36B}  AAATTTCTTC CTTCAAATAG CTGGTCTGCG ATACACTTAC ACAGATAATA
     msa237456.2{328_COH1}  AAATTTCTTC CTTCAAATAG CTGGTCTGCG ATACACTTAC ACAGATAATA
     msa237456.2{328_M732}  AAATTTCTTC CTTCAAATAG CTGGTCTGCG ATACACTTAC ACAGATAATA
     msa237456.2{328_M781}  AAATTTCTTC CTTCAAATAG CTGGTCTGCG ATACACTTAC ACAGATAATA
msa237456.2{328_JM9130013}  AAATTTCTTC CTTCAAATAG CTGGTCTGCG ATACACTTAC ACAGATAATA
     msa237456.2{328_A909}  AAATTTCTTC CTTCAAATAG CTGGTCTGCG ATACACTTAC ACAGATAATA
      msa237456.2{328_090}  AAATTTCTTC CTTCAAATAG CTGGTCTGCG ATACACTTAC ACAGATAATA
   msa237456.2{328_CJB110}  AAATTTCTTC CTTCAAATAG CTGGTCTGCG ATACACTTAC ACAGATAATA
                 Consensus  ********** ********** ********** ********** **********

                            1451                                              1500
   msa237456.2{328_1169NT}  AAGAGGGCGG gGAAGAAACA CCATTTAAAG TTGTAAAAGC TTATAAATCA
     msa237456.2{328_2603}  AAGAGGGCGG gGAAGAAACA CCATTTAAAG TTGTAAAAGC TTATAAATCA
   msa237456.2{328_18RS21}  AAGAGGGCGG gGAAGAAACA CCATTTAAAG TTGTAAAAGC TTATAAATCA
     msa237456.2{328_H36B}  AAGAGGGCGG gGAAGAAACA CCATTTAAAG TTGTAAAAGC TTATAAATCA
     msa237456.2{328_COH1}  AAGAGGGCGG gGAAGAAACA CCATTTAAAG TTGTAAAAGC TTATAAATCA
     msa237456.2{328_M732}  AAGAGGGCGG gGAAGAAACA CCATTTAAAG TTGTAAAAGC TTATAAATCA
     msa237456.2{328_M781}  AAGAGGGCGG gGAAGAAACA CCATTTAAAG TTGTAAAAGC TTATAAATCA
msa237456.2{328_JM9130013}  AAGAGGGCGG gGAAGAAACA CCATTTAAAG TTGTAAAAGC TTATAAATCA
     msa237456.2{328_A909}  AAGAGGGCGG gGAAGAAACA CCATTTAAAG TTGTAAAAGC TTATAAATCA
      msa237456.2{328_090}  AAGAGGGCGG aGAAGAAACA CCATTTAAAG TTGTAAAAGC TTATAAATCA
   msa237456.2{328_CJB110}  AAGAGGGCGG aGAAGAAACA CCATTTAAAG TTGTAAAAGC TTATAAATCA
                 Consensus  ********** -********* ********** ********** **********

                            1501                                              1550
   msa237456.2{328_1169NT}  AATGGTGAgG AAATCAATCC TGATGCAAAA TACAAATTAG TTATCAATGA
     msa237456.2{328_2603}  AATGGTGAgG AAATCAATCC TGATGCAAAA TACAAATTAG TTATCAATGA
   msa237456.2{328_18RS21}  AATGGTGAgG AAATCAATCC TGATGCAAAA TACAAATTAG TTATCAATGA
     msa237456.2{328_H36B}  AATGGTGAgG AAATCAATCC TGATGCAAAA TACAAATTAG TTATCAATGA
     msa237456.2{328_COH1}  AATGGTGAgG AAATCAATCC TGATGCAAAA TACAAATTAG TTATCAATGA
     msa237456.2{328_M732}  AATGGTGAgG AAATCAATCC TGATGCAAAA TACAAATTAG TTATCAATGA
     msa237456.2{328_M781}  AATGGTGAgG AAATCAATCC TGATGCAAAA TACAAATTAG TTATCAATGA
msa237456.2{328_JM9130013}  AATGGTGAgG AAATCAATCC TGATGCAAAA TACAAATTAG TTATCAATGA
     msa237456.2{328_A909}  AATGGTGAgG AAATCAATCC TGATGCAAAA TACAAATTAG TTATCAATGA
      msa237456.2{328_090}  AATGGTGAaG AAATCAATCC TGATGCAAAA TACAAATTAG TTATCAATGA
   msa237456.2{328_CJB110}  AATGGTGAaG AAATCAATCC TGATGCAAAA TACAAATTAG TTATCAATGA
                 Consensus  ********-* ********** ********** ********** **********

                            1551                                              1600
   msa237456.2{328_1169NT}  CTTTTTATTC GGTGGTGGTG ATGGCTTTGC AAGCTTCAGA AATGCCAAAC
     msa237456.2{328_2603}  CTTTTTATTC GGTGGTGGTG ATGGCTTTGC AAGCTTCAGA AATGCCAAAC
   msa237456.2{328_18RS21}  CTTTTTATTC GGTGGTGGTG ATGGCTTTGC AAGCTTCAGA AATGCCAAAC
     msa237456.2{328_H36B}  CTTTTTATTC GGTGGTGGTG ATGGCTTTGC AAGCTTCAGA AATGCCAAAC
     msa237456.2{328_COH1}  CTTTTTATTC GGTGGTGGTG ATGGCTTTGC AAGCTTCAGA AATGCCAAAC
     msa237456.2{328_M732}  CTTTTTATTC GGTGGTGGTG ATGGCTTTGC AAGCTTCAGA AATGCCAAAC
     msa237456.2{328_M781}  CTTTTTATTC GGTGGTGGTG ATGGCTTTGC AAGCTTCAGA AATGCCAAAC
msa237456.2{328_JM9130013}  CTTTTTATTC GGTGGTGGTG ATGGCTTTGC AAGCTTCAGA AATGCCAAAC
     msa237456.2{328_A909}  CTTTTTATTC GGTGGTGGTG ATGGCTTTGC AAGCTTCAGA AATGCCAAAC
      msa237456.2{328_090}  CTTTTTATTC GGTGGTGGTG ATGGCTTTGC AAGCTTCAGA AATGCCAAAC
   msa237456.2{328_CJB110}  CTTTTTATTC GGTGGTGGTG ATGGCTTTGC AAGCTTCAGA AATGCCAAAC
                 Consensus  ********** ********** ********** ********** **********

                            1601                                              1650
   msa237456.2{328_1169NT}  TTCTAGGAGC CATTAAcCCC GATACAGAGG TATTTATGGC CTATATCACT
     msa237456.2{328_2603}  TTCTAGGAGC CATTAAcCCC GATACAGAGG TATTTATGGC CTATATCACT
   msa237456.2{328_18RS21}  TTCTAGGAGC CATTAAtCCC GATACAGAGG TATTTATGGC CTATATCACT
     msa237456.2{328_H36B}  TTCTAGGAGC CATTAAtCCC GATACAGAGG TATTTATGGC CTATATCACT
     msa237456.2{328_COH1}  TTCTAGGAGC CATTAAtCCC GATACAGAGG TATTTATGGC CTATATCACT
     msa237456.2{328_M732}  TTCTAGGAGC CATTAAtCCC GATACAGAGG TATTTATGGC CTATATCACT
     msa237456.2{328_M781}  TTCTAGGAGC CATTAAtCCC GATACAGAGG TATTTATGGC CTATATCACT
msa237456.2{328_JM9130013}  TTCTAGGAGC CATTAAtCCC GATACAGAGG TATTTATGGC CTATATCACT
     msa237456.2{328_A909}  TTCTAGGAGC CATTAAtCCC GATACAGAGG TATTTATGGC CTATATCACT
      msa237456.2{328_090}  TTCTAGGAGC CATTAAtCCC GATACAGAGG TATTTATGGC CTATATCACT
   msa237456.2{328_CJB110}  TTCTAGGAGC CATTAAtCCC GATACAGAGG TATTTATGGC CTATATCACT
                 Consensus  ********** ******-*** ********** ********** **********

                            1651                                              1700
```

Table 71: Comparative Sequences relating to SAG1333

```
   msa237456.2{328_1169NT}  GATTTAGAAA AAGCTGGTAA AAAAGTGAGC gTTCCAAATA ATAAACCTAA
     msa237456.2{328_2603}  GATTTAGAAA AAGCTGGTAA AAAAGTGAGC gTTCCAAATA ATAAACCTAA
   msa237456.2{328_18RS21}  GATTTAGAAA AAGCTGGTAA AAAAGTGAGC gTTCCAAATA ATAAACCTAA
     msa237456.2{328_H36B}  GATTTAGAAA AAGCTGGTAA AAAAGTGAGC gTTCCAAATA ATAAACCTAA
     msa237456.2{328_COH1}  GATTTAGAAA AAGCTGGTAA AAAAGTGAGC aTTCCAAATA ATAAACCTAA
     msa237456.2{328_M732}  GATTTAGAAA AAGCTGGTAA AAAAGTGAGC aTTCCAAATA ATAAACCTAA
     msa237456.2{328_M781}  GATTTAGAAA AAGCTGGTAA AAAAGTGAGC aTTCCAAATA ATAAACCTAA
msa237456.2{328_JM9130013}  GATTTAGAAA AAGCTGGTAA AAAAGTGAGC gTTCCAAATA ATAAACCTAA
     msa237456.2{328_A909}  GATTTAGAAA AAGCTGGTAA AAAAGTGAGC gTTCCAAATA ATAAACCTAA
      msa237456.2{328_090}  GATTTAGAAA AAGCTGGTAA AAAAGTGAGC gTTCCAAATA ATAAACCTAA
    msa237456.2{328_CJB110}  GATTTAGAAA AAGCTGGTAA AAAAGTGAGC gTTCCAAATA ATAAACCTAA
                 Consensus  ********** ********** ********** -********* **********

                            1701                                              1750
   msa237456.2{328_1169NT}  AATCTATGTC ACTATGAAGA TGGTTAATGA AACTATTACA CAAAATGATG
     msa237456.2{328_2603}  AATCTATGTC ACTATGAAGA TGGTTAATGA AACTATTACA CAAAATGATG
   msa237456.2{328_18RS21}  AATCTATGTC ACTATGAAGA TGGTTAATGA AACTATTACA CAAAATGATG
     msa237456.2{328_H36B}  AATCTATGTC ACTATGAAGA TGGTTAATGA AACTATTACA CAAAATGATG
     msa237456.2{328_COH1}  AATCTATGTC ACTATGAAGA TGGTTAATGA AACTATTACA CAAAATGATG
     msa237456.2{328_M732}  AATCTATGTC ACTATGAAGA TGGTTAATGA AACTATTACA CAAAATGATG
     msa237456.2{328_M781}  AATCTATGTC ACTATGAAGA TGGTTAATGA AACTATTACA CAAAATGATG
msa237456.2{328_JM9130013}  AATCTATGTC ACTATGAAGA TGGTTAATGA AACTATTACA CAAAATGATG
     msa237456.2{328_A909}  AATCTATGTC ACTATGAAGA TGGTTAATGA AACTATTACA CAAAATGATG
      msa237456.2{328_090}  AATCTATGTC ACTATGAAGA TGGTTAATGA AACTATTACA CAAAATGATG
    msa237456.2{328_CJB110}  AATCTATGTC ACTATGAAGA TGGTTAATGA AACTATTACA CAAAATGATG
                 Consensus  ********** ********** ********** ********** **********

                            1751                                              1800
   msa237456.2{328_1169NT}  GTACAcATAG CATTATTaAG AAACTTTATT TAGATCGACA AGGAAATATT
     msa237456.2{328_2603}  GTACAcATAG CATTATTaAG AAACTTTATT TAGATCGACA AGGAAATATT
   msa237456.2{328_18RS21}  GTACAtATAG CATTATTaAG AAACTTTATT TAGATCGACA AGGAAATATT
     msa237456.2{328_H36B}  GTACAtATAG CATTATTaAG AAACTTTATT TAGATCGACA AGGAAATATT
     msa237456.2{328_COH1}  GTACAtATAG CATTATTaAG AAACTTTATT TAGATCGACA AGGAAATATT
     msa237456.2{328_M732}  GTACAtATAG CATTATTaAG AAACTTTATT TAGATCGACA AGGAAATATT
     msa237456.2{328_M781}  GTACAtATAG CATTATTaAG AAACTTTATT TAGATCGACA AGGAAATATT
msa237456.2{328_JM9130013}  GTACAtATAG CATTATTgAG AAACTTTATT TAGATCGACA AGGAAATATT
     msa237456.2{328_A909}  GTACAtATAG CATTATTaAG AAACTTTATT TAGATCGACA AGGAAATATT
      msa237456.2{328_090}  GTACAcATAG CATTATTaAG AAACTTTATT TAGATCGACA AGGAAATATT
    msa237456.2{328_CJB110}  GTACAcATAG CATTATTaAG AAACTTTATT TAGATCGACA AGGAAATATT
                 Consensus  *****-**** *******-** ********** ********** **********

                            1801                                              1850
   msa237456.2{328_1169NT}  GTAGCACAAG AGATTGTATC AGACACTTTA AACCAAACAA AATCAAAATC
     msa237456.2{328_2603}  GTAGCACAAG AGATTGTATC AGACACTTTA AACCAAACAA AATCAAAATC
   msa237456.2{328_18RS21}  GTAGCACAAG AGATTGTATC AGACACTTTA AACCAAACAA AATCAAAATC
     msa237456.2{328_H36B}  GTAGCACAAG AGATTGTATC AGACACTTTA AACCAAACAA AATCAAAATC
     msa237456.2{328_COH1}  GTAGCACAAG AGATTGTATC AGACACTTTA AACCAAACAA AATCAAAATC
     msa237456.2{328_M732}  GTAGCACAAG AGATTGTATC AGACACTTTA AACCAAACAA AATCAAAATC
     msa237456.2{328_M781}  GTAGCACAAG AGATTGTATC AGACACTTTA AACCAAACAA AATCAAAATC
msa237456.2{328_JM9130013}  GTAGCACAAG AGATTGTATC AGACACTTTA AACCAAACAA AATCAAAATC
     msa237456.2{328_A909}  GTAGCACAAG AGATTGTATC AGACACTTTA AACCAAACAA AATCAAAATC
      msa237456.2{328_090}  GTAGCACAAG AGATTGTATC AGACACTTTA AACCAAACAA AATCAAAATC
    msa237456.2{328_CJB110}  GTAGCACAAG AGATTGTATC AGACACTTTA AACCAAACAA AATCAAAATC
                 Consensus  ********** ********** ********** ********** **********

                            1851                                              1900
   msa237456.2{328_1169NT}  TACAAAAATC AACCCTGTAA CTACAATTCA CAAAAAACAA TTACACCAAT
     msa237456.2{328_2603}  TACAAAAATC AACCCTGTAA CTACAATTCA CAAAAAACAA TTACACCAAT
   msa237456.2{328_18RS21}  TACAAAAATC AACCCTGTAA CTACAATTCA CAAAAAACAA TTACACCAAT
     msa237456.2{328_H36B}  TACAAAAATC AACCCTGTAA CTACAATTCA CAAAAAACAA TTACACCAAT
     msa237456.2{328_COH1}  TACAAAAATC AACCCTGTAA CTACAATTCA CAAAAAACAA TTACACCAAT
     msa237456.2{328_M732}  TACAAAAATC AACCCTGTAA CTACAATTCA CAAAAAACAA TTACACCAAT
     msa237456.2{328_M781}  TACAAAAATC AACCCTGTAA CTACAATTCA CAAAAAACAA TTACACCAAT
msa237456.2{328_JM9130013}  TACAAAAATC AACCCTGTAA CTACAATTCA CAAAAAACAA TTACACCAAT
     msa237456.2{328_A909}  TACAAAAATC AACCCTGTAA CTACAATTCA CAAAAAACAA TTACACCAAT
      msa237456.2{328_090}  TACAAAAATC AACCCTGTAA CTACAATTCA CAAAAAACAA TTACACCAAT
    msa237456.2{328_CJB110}  TACAAAAATC AACCCTGTAA CTACAATTCA CAAAAAACAA TTACACCAAT
                 Consensus  ********** ********** ********** ********** **********

                            1901                                              1950
   msa237456.2{328_1169NT}  TTACAGCTAT TAACCCTATG AGAAATTATG GCAAACCATC AAACTCCACT
     msa237456.2{328_2603}  TTACAGCTAT TAACCCTATG AGAAATTATG GCAAACCATC AAACTCCACT
   msa237456.2{328_18RS21}  TTACAGCTAT TAACCCTATG AGAAATTATG GCAAACCATC AAACTCCACT
     msa237456.2{328_H36B}  TTACAGCTAT TAACCCTATG AGAAATTATG GCAAACCATC AAACTCCACT
     msa237456.2{328_COH1}  TTACAGCTAT TAACCCTATG AGAAATTATG GCAAACCATC AAACTCCACT
     msa237456.2{328_M732}  TTACAGCTAT TAACCCTATG AGAAATTATG GCAAACCATC AAACTCCACT
     msa237456.2{328_M781}  TTACAGCTAT TAACCCTATG AGAAATTATG GCAAACCATC AAACTCCACT
msa237456.2{328_JM9130013}  TTACAGCTAT TAACCCTATG AGAAATTATG GCAAACCATC AAACTCCACT
     msa237456.2{328_A909}  TTACAGCTAT TAACCCTATG AGAAATTATG GCAAACCATC AAACTCCACT
      msa237456.2{328_090}  TTACAGCTAT TAACCCTATG AGAAATTATG GCAAACCATC AAACTCCACT
    msa237456.2{328_CJB110}  TTACAGCTAT TAACCCTATG AGAAATTATG GCAAACCATC AAACTCCACT
                 Consensus  ********** ********** ********** ********** **********
```

Table 71: Comparative Sequences relating to SAG1333

```
                                  1951                                                2000
      msa237456.2{328_1169NT}   ACTGTAAAAT CAaa~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
        msa237456.2{328_2603}   ACTGTAAAAT CAaaACAAtt accaaaaaca aactctgaat atggacaatc
      msa237456.2{328_18RS21}   ACTGTAAAAT CAaaA~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
        msa237456.2{328_H36B}   ACTGTAAAAT CAaa~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
        msa237456.2{328_COH1}   ACTGTAAAAT CAaa~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
        msa237456.2{328_M732}   ACTGTAAAAT CAaaACAA~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
        msa237456.2{328_M781}   ACTGTAAAAT CAaa~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa237456.2{328_JM9130013}   ACTGTAAAAT CAaaA~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
        msa237456.2{328_A909}   ACTGTAAAAT CAaaACAA~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
         msa237456.2{328_090}   ACTGTAAAAT CAaaACAA~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa237456.2{328_CJB110}   ACTGTAAAAT CA~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                    Consensus   ********** **--****** ********** ********** **********

                                  2001                                                2050
      msa237456.2{328_1169NT}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
        msa237456.2{328_2603}   attccttatg tctgtctttg gtgttggact tataggaatt gctttaaata
      msa237456.2{328_18RS21}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
        msa237456.2{328_H36B}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
        msa237456.2{328_COH1}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
        msa237456.2{328_M732}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
        msa237456.2{328_M781}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa237456.2{328_JM9130013}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
        msa237456.2{328_A909}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
         msa237456.2{328_090}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa237456.2{328_CJB110}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                    Consensus   ********** ********** ********** ********** **********

                                  2051               2070
      msa237456.2{328_1169NT}   ~~~~~~~~~~ ~~~~~~~~~~
        msa237456.2{328_2603}   caaagaaaaa acatatgaaa
      msa237456.2{328_18RS21}   ~~~~~~~~~~ ~~~~~~~~~~
        msa237456.2{328_H36B}   ~~~~~~~~~~ ~~~~~~~~~~
        msa237456.2{328_COH1}   ~~~~~~~~~~ ~~~~~~~~~~
        msa237456.2{328_M732}   ~~~~~~~~~~ ~~~~~~~~~~
        msa237456.2{328_M781}   ~~~~~~~~~~ ~~~~~~~~~~
   msa237456.2{328_JM9130013}   ~~~~~~~~~~ ~~~~~~~~~~
        msa237456.2{328_A909}   ~~~~~~~~~~ ~~~~~~~~~~
         msa237456.2{328_090}   ~~~~~~~~~~ ~~~~~~~~~~
      msa237456.2{328_CJB110}   ~~~~~~~~~~ ~~~~~~~~~~
                    Consensus   ********** **********
```

SEQ ID NO. 7112

STRAIN 2603 frame: 1

```
MKKKIILKSSVLGLVAGTSIMFSSVFADQVGVQVIGVNDFHGALDNTGTANMPDGKVANA
GTAAQLDAYMDDAQKDFKQTNPNGESIRVQAGDMVGASPANSGLLQDEPTVKNFNAMNVE
YGTLGNHEFDEGLAEYNRIVTGKAPAPDSNINNITKSYPHEAAKQEIVVANVIDKVNKQI
PYNWKPYAIKNIPVNNKSVNVGFIGIVTKDIPNLVLRKNYEQYEFLDEAETIVKYAKELQ
AKNVKAIVVLAHVPATSKNDIAEGEAAEMMKKVNQLFPENSVDIVFAGHNHQYTNGLVGK
TRIVQALSQGKAYADVRGVLDTDTQDFIETPSAKVIAVAPGKKTGSADIQAIVDQANTIV
KQVTEAKIGTAEVSVMITRSVDQDNVSPVGSLITEAQLAIARKSWPDIDFAMTNNGGIRA
DLLIKPDGTITWGAAQAVQPFGNILQVVEITGRDLYKALNEQYDQKQNFFLQIAGLRYTY
TDNKEGGEETPFKVVKAYKSNGEEINPDAKYKLVINDFLFGGGDGFASFRNAKLLGAINP
DTEVFMAYITDLEKAGKKVSVPNNKPKIYVTMKMVNETITQNDGTHSIIKKLYLDRQGNI
VAQEIVSDTLNQTKSKSTKINPVTTIHKKQLHQFTAINPMRNYGKPSNSTTVKSKQLPKT
NSEYGQSFLMSVFGVGLIGIALNTKKKHMK
```

SEQ ID NO. 7113

STRAIN 090 frame: 3

```
VGVQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRV
QAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTLGNHEFDEGLAEYNRIVTGKAPAPDS
NINNITKSYPHEAAKQEIVVANVIDKVNKQIPYNWKPYAIKNIPVNNKSVNVGFIGIVTK
DIPNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIVVLAHVPATSKDDIAEGEAAEM
MKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDTQDFIE
TPSAKVVAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSPV
GSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVVE
ITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPDA
KYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAYITDLEKAGKKVSVPNNKPKIY
VTMKMVNETITQNDGTHSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHKK
QLHQFTAINPMRNYGKPSNSTTVKSKQ
```

SEQ ID NO. 7114

STRAIN A909 frame: 3

```
VNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRVQAGDMVG
ASPANSGLLQDEPTVKTFNAMNVEYGTLGNHEFDEGLAEYNRIVTGKAPAPDSNINNITK
SYPHEAAKQEIVVANVIDKVNKQIPYNWKPYTIKNIPVNNKSVNVGFIGIVTKDIPNLVL
RKNYEQYEFLDEAETIVKYAKELQAKNVKAIVVLAHVPATSKDDIAEGEAAEMMKKVNQL
FPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDTQDFIETPSAKVI
AVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSPVGSLITEA
QLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVVEITGRDLY
KALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPDAKYKLVIN
DFLFGGGDGFASFRNAKLLGAINPDTEVFMAYITDLEKAGKKVSVPNNKPKIYVTMKMVN
ETITQNDGTYSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHKKQLHQFTA
```

Table 71: Comparative Sequences relating to SAG1333

INPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7115
STRAIN H36B frame: 2
QVGVQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTLGNHEFDEGLAEYNRIVTGKAPAPD
SNINNITKSYPHEAAKQEIVVANVIDKVNKQIPYNWKPYTIKNIPVNNKSVNVGFIGIVT
KDIPNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIVVLAHVPATSKDDIAEGEAAE
MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDTQDFI
ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
VGSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVV
EITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPD
AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAYITDLEKAGKKVSVPNNKPKI
YVTMKMVNETITQNDGTYSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHK
KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7116
STRAIN 18RS21 frame: 1
DQVGVQVIGVNDFHGALDNTGTANMPDGKVXNAGTAAQLDAYMDDAQKDFKQTNPNGESI
RVQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTLGNHEFDEGLAEYNRIVTGKAPAP
DSNINNITKSYPHEAAKQEIVVANVIDKVNKQIPYNWKPYTIKNIPVNNKSVNVGFIGIV
TKDIPNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIVVLAHVPATSKDDIAEGEAA
EMMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDTQDF
IETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVS
PVGSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQV
VEITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINP
DAKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAYITDLEKAGKKVSVPNNKPK
IYVTMKMVNETITQNDGTYSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIH
KKQLHQFTAINPMRNYGKPSNSTTVKSK

SEQ ID NO. 7117
STRAIN M732 frame: 3
QVGVQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTLGNHEFDEGLAEYNRIVTGKAPAPD
SNINNITKSYPHEAAKQEIVVANVIDKVNKQIPYNWKPYTIKNIPVNNKSVNVGFIGIVT
KDIPNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIVVLAHVPATSKDDIAEGEAAE
MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDTQDFI
ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
VGSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVV
EITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPD
AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAYITDLEKAGKKVSIPNNKPKI
YVTMKMVNETITQNDGTYSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHK
KQLHQFTAINPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7118
STRAIN COH1 frame: 3
QVGVQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTLGNHEFDEGLAEYNRIVTGKAPAPD
SNINNITKSYPHEAAKQEIVVANVIDKVNKQIPYNWKPYTIKNIPVNNKSVNVGFIGIVT
KDIPNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIVVLAHVPATSKDDIAEGEAAE
MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDTQDFI
ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
VGSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVV
EITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPD
AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAYITDLEKAGKKVSIPNNKPKI
YVTMKMVNETITQNDGTYSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHK
KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7119
STRAIN M781 frame: 1
QVGVQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTLGNHEFDEGLAEYNRIVTGKAPAPD
SNINNITKSYPHEAAKQEIVVANVIDKVNKQIPYNWKPYTIKNIPVNNKSVNVGFIGIVT
KDIPNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIVVLAHVPATSKDDIAEGEAAE
MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDTQDFI
ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
VGSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVV
EITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPD
AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAYITDLEKAGKKVSIPNNKPKI
YVTMKMVNETITQNDGTYSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHK
KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7120
STRAIN CJB110 frame: 1
DQVGVQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESI
RVQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTLGNHEFDEGLAEYNRIVTGKAPAP
DSNINNITKSYPHEAAKQEIVVANVIDKVNKQIPYNWKPYAIKNIPVNNKSVNVGFIGIV
TKDIPNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIVVLAHVPATSKDDIAEGEAA
EMMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDTQDF
IETPSAKVVAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVS
PVGSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQV
VEITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINP

Table 71: Comparative Sequences relating to SAG1333

DAKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAYITDLEKAGKKVSVPNNKPK
IYVTMKMVNETITQNDGTHSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIH
KKQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7121
STRAIN 1169NT frame: 1
QVGVQVIGVNDFHGALDNTGTANMPDGKVANAGTAAQLDAYMDDAQKDFKQTNPNGESIR
VQAGDMVGASPANSGLLQDEPTVKNFNAMNVEYGTLGNHEFDEGLAEYNRIVTGKAPAPD
SNINNITKSYPHEAAKQEIVVANVIDKVNKQIPYNWKPYAIKNIPVNNKSVNVGFIGIVT
KDIPNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIVVLAHVPATSKNDIAEGEAAE
MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDTQDFI
ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSVMITRSVDQDNVSP
VGSLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVV
EITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPD
AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAYITDLEKAGKKVSVPNNKPKI
YVTMKMVNETITQNDGTHSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHK
KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7122
STRAIN JM9130013 frame: 2
GVQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRVQ
AGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTLGNHEFDEGLAEYNRIVTGKAPAPDSN
INNITKSYPHEAAKQEIVVANVIDKVNKQIPYNWKPYTIKNIPVNNKSVNVGFIGIVTKD
IPNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIVVLAHVPATSKDDIAEGEAAEMM
KKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDTDTQDFIET
PSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSPVG
SLITEAQLAIARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVVEI
TGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPDAK
YKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAYITDLEKAGKKVSVPNNKPKIYV
TMKMVNETITQNDGTYSIIEKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHKKQ
LHQFTAINPMRNYGKPSNSTTVKSK

```
PRETTY of: /biotmp/msa237615.2{*}   May 14, 2003 03:22  ..

                                 1                                                  50
   msa237615.2{328_1169NT}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~qv gvqvigVNDF HGALDNTGTA
     msa237615.2{328_2603}   mkkkiilkss vlglvagtsi mfssvfaDqv gvqvigVNDF HGALDNTGTA
     msa237615.2{328_A909}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~VNDF HGALDNTGTA
     msa237615.2{328_M732}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~qv gvqvigVNDF HGALDNTGTA
     msa237615.2{328_COH1}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~qv gvqvigVNDF HGALDNTGTA
     msa237615.2{328_M781}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~qv gvqvigVNDF HGALDNTGTA
     msa237615.2{328_H36B}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~qv gvqvigVNDF HGALDNTGTA
msa237615.2{328_JM9130013}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ gvqvigVNDF HGALDNTGTA
   msa237615.2{328_18RS21}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~Dqv gvqvigVNDF HGALDNTGTA
      msa237615.2{328_090}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~v gvqvigVNDF HGALDNTGTA
   msa237615.2{328_CJB110}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~Dqv gvqvigVNDF HGALDNTGTA
                 Consensus   ********** ********** ********-- ------**** **********

                             51                                                100
   msa237615.2{328_1169NT}   NMPDGKVaNA GTAAQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
     msa237615.2{328_2603}   NMPDGKVaNA GTAAQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
     msa237615.2{328_A909}   NMPDGKVtNA GTAAQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
     msa237615.2{328_M732}   NMPDGKVtNA GTAAQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
     msa237615.2{328_COH1}   NMPDGKVtNA GTAAQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
     msa237615.2{328_M781}   NMPDGKVtNA GTAAQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
     msa237615.2{328_H36B}   NMPDGKVtNA GTAAQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
msa237615.2{328_JM9130013}   NMPDGKVtNA GTAAQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
   msa237615.2{328_18RS21}   NMPDGKVxNA GTAAQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
      msa237615.2{328_090}   NMPDGKVtNA GTAAQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
   msa237615.2{328_CJB110}   NMPDGKVtNA GTAAQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
                 Consensus   *******_** ********** ********** ********** **********

                             101                                               150
   msa237615.2{328_1169NT}   NSGLLQDEPT VKnFNAMNVE YGTLGNHEFD EGLAEYNRIV TGKAPAPDSN
     msa237615.2{328_2603}   NSGLLQDEPT VKnFNAMNVE YGTLGNHEFD EGLAEYNRIV TGKAPAPDSN
     msa237615.2{328_A909}   NSGLLQDEPT VKtFNAMNVE YGTLGNHEFD EGLAEYNRIV TGKAPAPDSN
     msa237615.2{328_M732}   NSGLLQDEPT VKtFNAMNVE YGTLGNHEFD EGLAEYNRIV TGKAPAPDSN
     msa237615.2{328_COH1}   NSGLLQDEPT VKtFNAMNVE YGTLGNHEFD EGLAEYNRIV TGKAPAPDSN
     msa237615.2{328_M781}   NSGLLQDEPT VKtFNAMNVE YGTLGNHEFD EGLAEYNRIV TGKAPAPDSN
     msa237615.2{328_H36B}   NSGLLQDEPT VKtFNAMNVE YGTLGNHEFD EGLAEYNRIV TGKAPAPDSN
msa237615.2{328_JM9130013}   NSGLLQDEPT VKtFNAMNVE YGTLGNHEFD EGLAEYNRIV TGKAPAPDSN
   msa237615.2{328_18RS21}   NSGLLQDEPT VKtFNAMNVE YGTLGNHEFD EGLAEYNRIV TGKAPAPDSN
      msa237615.2{328_090}   NSGLLQDEPT VKtFNAMNVE YGTLGNHEFD EGLAEYNRIV TGKAPAPDSN
   msa237615.2{328_CJB110}   NSGLLQDEPT VKtFNAMNVE YGTLGNHEFD EGLAEYNRIV TGKAPAPDSN
                 Consensus   ********** **_******* ********** ********** **********

                             151                                               200
   msa237615.2{328_1169NT}   INNITKSYPH EAAKQEIVVA NVIDKVNKQI PYNWKPYaIK NIPVNNKSVN
     msa237615.2{328_2603}   INNITKSYPH EAAKQEIVVA NVIDKVNKQI PYNWKPYaIK NIPVNNKSVN
     msa237615.2{328_A909}   INNITKSYPH EAAKQEIVVA NVIDKVNKQI PYNWKPYtIK NIPVNNKSVN
     msa237615.2{328_M732}   INNITKSYPH EAAKQEIVVA NVIDKVNKQI PYNWKPYtIK NIPVNNKSVN
     msa237615.2{328_COH1}   INNITKSYPH EAAKQEIVVA NVIDKVNKQI PYNWKPYtIK NIPVNNKSVN
     msa237615.2{328_M781}   INNITKSYPH EAAKQEIVVA NVIDKVNKQI PYNWKPYtIK NIPVNNKSVN
```

Table 71: Comparative Sequences relating to SAG1333

```
      msa237615.2{328_H36B}   INNITKSYPH EAAKQEIVVA NVIDKVNKQI PYNWKPYtIK NIPVNNKSVN
  msa237615.2{328_JM9130013}  INNITKSYPH EAAKQEIVVA NVIDKVNKQI PYNWKPYtIK NIPVNNKSVN
     msa237615.2{328_18RS21}  INNITKSYPH EAAKQEIVVA NVIDKVNKQI PYNWKPYtIK NIPVNNKSVN
       msa237615.2{328_090}   INNITKSYPH EAAKQEIVVA NVIDKVNKQI PYNWKPYaIK NIPVNNKSVN
     msa237615.2{328_CJB110}  INNITKSYPH EAAKQEIVVA NVIDKVNKQI PYNWKPYaIK NIPVNNKSVN
                  Consensus   ********** ********** ********** *******-** **********

                              201                                              250
    msa237615.2{328_1169NT}   VGFIGIVTKD IPNLVLRKNY EQYEFLDEAE TIVKYAKELQ AKNVKAIVVL
      msa237615.2{328_2603}   VGFIGIVTKD IPNLVLRKNY EQYEFLDEAE TIVKYAKELQ AKNVKAIVVL
      msa237615.2{328_A909}   VGFIGIVTKD IPNLVLRKNY EQYEFLDEAE TIVKYAKELQ AKNVKAIVVL
      msa237615.2{328_M732}   VGFIGIVTKD IPNLVLRKNY EQYEFLDEAE TIVKYAKELQ AKNVKAIVVL
      msa237615.2{328_COH1}   VGFIGIVTKD IPNLVLRKNY EQYEFLDEAE TIVKYAKELQ AKNVKAIVVL
      msa237615.2{328_M781}   VGFIGIVTKD IPNLVLRKNY EQYEFLDEAE TIVKYAKELQ AKNVKAIVVL
      msa237615.2{328_H36B}   VGFIGIVTKD IPNLVLRKNY EQYEFLDEAE TIVKYAKELQ AKNVKAIVVL
  msa237615.2{328_JM9130013}  VGFIGIVTKD IPNLVLRKNY EQYEFLDEAE TIVKYAKELQ AKNVKAIVVL
     msa237615.2{328_18RS21}  VGFIGIVTKD IPNLVLRKNY EQYEFLDEAE TIVKYAKELQ AKNVKAIVVL
       msa237615.2{328_090}   VGFIGIVTKD IPNLVLRKNY EQYEFLDEAE TIVKYAKELQ AKNVKAIVVL
     msa237615.2{328_CJB110}  VGFIGIVTKD IPNLVLRKNY EQYEFLDEAE TIVKYAKELQ AKNVKAIVVL
                  Consensus   ********** ********** ********** ********** **********

                              251                                              300
    msa237615.2{328_1169NT}   AHVPATSKnD IAEGEAAEMM KKVNQLFPEN SVDIVFAGHN HQYTNGLVGK
      msa237615.2{328_2603}   AHVPATSKnD IAEGEAAEMM KKVNQLFPEN SVDIVFAGHN HQYTNGLVGK
      msa237615.2{328_A909}   AHVPATSKdD IAEGEAAEMM KKVNQLFPEN SVDIVFAGHN HQYTNGLVGK
      msa237615.2{328_M732}   AHVPATSKdD IAEGEAAEMM KKVNQLFPEN SVDIVFAGHN HQYTNGLVGK
      msa237615.2{328_COH1}   AHVPATSKdD IAEGEAAEMM KKVNQLFPEN SVDIVFAGHN HQYTNGLVGK
      msa237615.2{328_M781}   AHVPATSKdD IAEGEAAEMM KKVNQLFPEN SVDIVFAGHN HQYTNGLVGK
      msa237615.2{328_H36B}   AHVPATSKdD IAEGEAAEMM KKVNQLFPEN SVDIVFAGHN HQYTNGLVGK
  msa237615.2{328_JM9130013}  AHVPATSKdD IAEGEAAEMM KKVNQLFPEN SVDIVFAGHN HQYTNGLVGK
     msa237615.2{328_18RS21}  AHVPATSKdD IAEGEAAEMM KKVNQLFPEN SVDIVFAGHN HQYTNGLVGK
       msa237615.2{328_090}   AHVPATSKdD IAEGEAAEMM KKVNQLFPEN SVDIVFAGHN HQYTNGLVGK
     msa237615.2{328_CJB110}  AHVPATSKdD IAEGEAAEMM KKVNQLFPEN SVDIVFAGHN HQYTNGLVGK
                  Consensus   ********-* ********** ********** ********** **********

                              301                                              350
    msa237615.2{328_1169NT}   TRIVQALSQG KAYADVRGVL DTDTQDFIET PSAKViAVAP GKKTGSADIQ
      msa237615.2{328_2603}   TRIVQALSQG KAYADVRGVL DTDTQDFIET PSAKViAVAP GKKTGSADIQ
      msa237615.2{328_A909}   TRIVQALSQG KAYADVRGVL DTDTQDFIET PSAKViAVAP GKKTGSADIQ
      msa237615.2{328_M732}   TRIVQALSQG KAYADVRGVL DTDTQDFIET PSAKViAVAP GKKTGSADIQ
      msa237615.2{328_COH1}   TRIVQALSQG KAYADVRGVL DTDTQDFIET PSAKViAVAP GKKTGSADIQ
      msa237615.2{328_M781}   TRIVQALSQG KAYADVRGVL DTDTQDFIET PSAKViAVAP GKKTGSADIQ
      msa237615.2{328_H36B}   TRIVQALSQG KAYADVRGVL DTDTQDFIET PSAKViAVAP GKKTGSADIQ
  msa237615.2{328_JM9130013}  TRIVQALSQG KAYADVRGVL DTDTQDFIET PSAKViAVAP GKKTGSADIQ
     msa237615.2{328_18RS21}  TRIVQALSQG KAYADVRGVL DTDTQDFIET PSAKViAVAP GKKTGSADIQ
       msa237615.2{328_090}   TRIVQALSQG KAYADVRGVL DTDTQDFIET PSAKVvAVAP GKKTGSADIQ
     msa237615.2{328_CJB110}  TRIVQALSQG KAYADVRGVL DTDTQDFIET PSAKVvAVAP GKKTGSADIQ
                  Consensus   ********** ********** ********** *****-**** **********

                              351                                              400
    msa237615.2{328_1169NT}   AIVDQANTIV KQVTEAKIGT AEVSvMITRS VDQDNVSPVG SLITEAQLAI
      msa237615.2{328_2603}   AIVDQANTIV KQVTEAKIGT AEVSvMITRS VDQDNVSPVG SLITEAQLAI
      msa237615.2{328_A909}   AIVDQANTIV KQVTEAKIGT AEVSgMITRS VDQDNVSPVG SLITEAQLAI
      msa237615.2{328_M732}   AIVDQANTIV KQVTEAKIGT AEVSgMITRS VDQDNVSPVG SLITEAQLAI
      msa237615.2{328_COH1}   AIVDQANTIV KQVTEAKIGT AEVSgMITRS VDQDNVSPVG SLITEAQLAI
      msa237615.2{328_M781}   AIVDQANTIV KQVTEAKIGT AEVSgMITRS VDQDNVSPVG SLITEAQLAI
      msa237615.2{328_H36B}   AIVDQANTIV KQVTEAKIGT AEVSgMITRS VDQDNVSPVG SLITEAQLAI
  msa237615.2{328_JM9130013}  AIVDQANTIV KQVTEAKIGT AEVSgMITRS VDQDNVSPVG SLITEAQLAI
     msa237615.2{328_18RS21}  AIVDQANTIV KQVTEAKIGT AEVSgMITRS VDQDNVSPVG SLITEAQLAI
       msa237615.2{328_090}   AIVDQANTIV KQVTEAKIGT AEVSgMITRS VDQDNVSPVG SLITEAQLAI
     msa237615.2{328_CJB110}  AIVDQANTIV KQVTEAKIGT AEVSgMITRS VDQDNVSPVG SLITEAQLAI
                  Consensus   ********** ********** ****-***** ********** **********

                              401                                              450
    msa237615.2{328_1169NT}   ARKSWPDIDF AMTNNGGIRA DLLIKPDGTI TWGAAQAVQP FGNILQVVEI
      msa237615.2{328_2603}   ARKSWPDIDF AMTNNGGIRA DLLIKPDGTI TWGAAQAVQP FGNILQVVEI
      msa237615.2{328_A909}   ARKSWPDIDF AMTNNGGIRA DLLIKPDGTI TWGAAQAVQP FGNILQVVEI
      msa237615.2{328_M732}   ARKSWPDIDF AMTNNGGIRA DLLIKPDGTI TWGAAQAVQP FGNILQVVEI
      msa237615.2{328_COH1}   ARKSWPDIDF AMTNNGGIRA DLLIKPDGTI TWGAAQAVQP FGNILQVVEI
      msa237615.2{328_M781}   ARKSWPDIDF AMTNNGGIRA DLLIKPDGTI TWGAAQAVQP FGNILQVVEI
      msa237615.2{328_H36B}   ARKSWPDIDF AMTNNGGIRA DLLIKPDGTI TWGAAQAVQP FGNILQVVEI
  msa237615.2{328_JM9130013}  ARKSWPDIDF AMTNNGGIRA DLLIKPDGTI TWGAAQAVQP FGNILQVVEI
     msa237615.2{328_18RS21}  ARKSWPDIDF AMTNNGGIRA DLLIKPDGTI TWGAAQAVQP FGNILQVVEI
       msa237615.2{328_090}   ARKSWPDIDF AMTNNGGIRA DLLIKPDGTI TWGAAQAVQP FGNILQVVEI
     msa237615.2{328_CJB110}  ARKSWPDIDF AMTNNGGIRA DLLIKPDGTI TWGAAQAVQP FGNILQVVEI
                  Consensus   ********** ********** ********** ********** **********

                              451                                              500
    msa237615.2{328_1169NT}   TGRDLYKALN EQYDQKQNFF LQIAGLRYTY TDNKEGGEET PFKVVKAYKS
      msa237615.2{328_2603}   TGRDLYKALN EQYDQKQNFF LQIAGLRYTY TDNKEGGEET PFKVVKAYKS
      msa237615.2{328_A909}   TGRDLYKALN EQYDQKQNFF LQIAGLRYTY TDNKEGGEET PFKVVKAYKS
      msa237615.2{328_M732}   TGRDLYKALN EQYDQKQNFF LQIAGLRYTY TDNKEGGEET PFKVVKAYKS
      msa237615.2{328_COH1}   TGRDLYKALN EQYDQKQNFF LQIAGLRYTY TDNKEGGEET PFKVVKAYKS
```

Table 71: Comparative Sequences relating to SAG1333

```
     msa237615.2{328_M781}  TGRDLYKALN EQYDQKQNFF LQIAGLRYTY TDNKEGGEET PFKVVKAYKS
     msa237615.2{328_H36B}  TGRDLYKALN EQYDQKQNFF LQIAGLRYTY TDNKEGGEET PFKVVKAYKS
msa237615.2{328_JM9130013}  TGRDLYKALN EQYDQKQNFF LQIAGLRYTY TDNKEGGEET PFKVVKAYKS
   msa237615.2{328_18RS21}  TGRDLYKALN EQYDQKQNFF LQIAGLRYTY TDNKEGGEET PFKVVKAYKS
      msa237615.2{328_090}  TGRDLYKALN EQYDQKQNFF LQIAGLRYTY TDNKEGGEET PFKVVKAYKS
   msa237615.2{328_CJB110}  TGRDLYKALN EQYDQKQNFF LQIAGLRYTY TDNKEGGEET PFKVVKAYKS
                 Consensus  ********** ********** ********** ********** **********

                            501                                                550
   msa237615.2{328_1169NT}  NGEEINPDAK YKLVINDFLF GGGDGFASFR NAKLLGAINP DTEVFMAYIT
     msa237615.2{328_2603}  NGEEINPDAK YKLVINDFLF GGGDGFASFR NAKLLGAINP DTEVFMAYIT
     msa237615.2{328_A909}  NGEEINPDAK YKLVINDFLF GGGDGFASFR NAKLLGAINP DTEVFMAYIT
     msa237615.2{328_M732}  NGEEINPDAK YKLVINDFLF GGGDGFASFR NAKLLGAINP DTEVFMAYIT
     msa237615.2{328_COH1}  NGEEINPDAK YKLVINDFLF GGGDGFASFR NAKLLGAINP DTEVFMAYIT
     msa237615.2{328_M781}  NGEEINPDAK YKLVINDFLF GGGDGFASFR NAKLLGAINP DTEVFMAYIT
     msa237615.2{328_H36B}  NGEEINPDAK YKLVINDFLF GGGDGFASFR NAKLLGAINP DTEVFMAYIT
msa237615.2{328_JM9130013}  NGEEINPDAK YKLVINDFLF GGGDGFASFR NAKLLGAINP DTEVFMAYIT
   msa237615.2{328_18RS21}  NGEEINPDAK YKLVINDFLF GGGDGFASFR NAKLLGAINP DTEVFMAYIT
      msa237615.2{328_090}  NGEEINPDAK YKLVINDFLF GGGDGFASFR NAKLLGAINP DTEVFMAYIT
   msa237615.2{328_CJB110}  NGEEINPDAK YKLVINDFLF GGGDGFASFR NAKLLGAINP DTEVFMAYIT
                 Consensus  ********** ********** ********** ********** **********

                            551                                                600
   msa237615.2{328_1169NT}  DLEKAGKKVS vPNNKPKIYV TMKMVNETIT QNDGThSIIk KLYLDRQGNI
     msa237615.2{328_2603}  DLEKAGKKVS vPNNKPKIYV TMKMVNETIT QNDGThSIIk KLYLDRQGNI
     msa237615.2{328_A909}  DLEKAGKKVS vPNNKPKIYV TMKMVNETIT QNDGTySIIk KLYLDRQGNI
     msa237615.2{328_M732}  DLEKAGKKVS iPNNKPKIYV TMKMVNETIT QNDGTySIIk KLYLDRQGNI
     msa237615.2{328_COH1}  DLEKAGKKVS iPNNKPKIYV TMKMVNETIT QNDGTySIIk KLYLDRQGNI
     msa237615.2{328_M781}  DLEKAGKKVS iPNNKPKIYV TMKMVNETIT QNDGTySIIk KLYLDRQGNI
     msa237615.2{328_H36B}  DLEKAGKKVS vPNNKPKIYV TMKMVNETIT QNDGTySIIk KLYLDRQGNI
msa237615.2{328_JM9130013}  DLEKAGKKVS vPNNKPKIYV TMKMVNETIT QNDGTySIIe KLYLDRQGNI
   msa237615.2{328_18RS21}  DLEKAGKKVS vPNNKPKIYV TMKMVNETIT QNDGTySIIk KLYLDRQGNI
      msa237615.2{328_090}  DLEKAGKKVS vPNNKPKIYV TMKMVNETIT QNDGThSIIk KLYLDRQGNI
   msa237615.2{328_CJB110}  DLEKAGKKVS vPNNKPKIYV TMKMVNETIT QNDGThSIIk KLYLDRQGNI
                 Consensus  ********** -********* ********** *****-***- **********

                            601                                                650
   msa237615.2{328_1169NT}  VAQEIVSDTL NQTKSKSTKI NPVTTIHKKQ LHQFTAINPM RNYGKPSNST
     msa237615.2{328_2603}  VAQEIVSDTL NQTKSKSTKI NPVTTIHKKQ LHQFTAINPM RNYGKPSNST
     msa237615.2{328_A909}  VAQEIVSDTL NQTKSKSTKI NPVTTIHKKQ LHQFTAINPM RNYGKPSNST
     msa237615.2{328_M732}  VAQEIVSDTL NQTKSKSTKI NPVTTIHKKQ LHQFTAINPM RNYGKPSNST
     msa237615.2{328_COH1}  VAQEIVSDTL NQTKSKSTKI NPVTTIHKKQ LHQFTAINPM RNYGKPSNST
     msa237615.2{328_M781}  VAQEIVSDTL NQTKSKSTKI NPVTTIHKKQ LHQFTAINPM RNYGKPSNST
     msa237615.2{328_H36B}  VAQEIVSDTL NQTKSKSTKI NPVTTIHKKQ LHQFTAINPM RNYGKPSNST
msa237615.2{328_JM9130013}  VAQEIVSDTL NQTKSKSTKI NPVTTIHKKQ LHQFTAINPM RNYGKPSNST
   msa237615.2{328_18RS21}  VAQEIVSDTL NQTKSKSTKI NPVTTIHKKQ LHQFTAINPM RNYGKPSNST
      msa237615.2{328_090}  VAQEIVSDTL NQTKSKSTKI NPVTTIHKKQ LHQFTAINPM RNYGKPSNST
   msa237615.2{328_CJB110}  VAQEIVSDTL NQTKSKSTKI NPVTTIHKKQ LHQFTAINPM RNYGKPSNST
                 Consensus  ********** ********** ********** ********** **********

                            651                                     690
   msa237615.2{328_1169NT}  TVKS~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa237615.2{328_2603}  TVKSKQlpkt nseygqsflm svfgvgligi alntkkkhmk
     msa237615.2{328_A909}  TVKSKQ~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa237615.2{328_M732}  TVKSKQ~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa237615.2{328_COH1}  TVKS~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa237615.2{328_M781}  TVKS~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa237615.2{328_H36B}  TVKS~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa237615.2{328_JM9130013}  TVKSK~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa237615.2{328_18RS21}  TVKSK~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa237615.2{328_090}  TVKSKQ~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa237615.2{328_CJB110}  TVKS~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                 Consensus  ********** ********** ********** **********
```

Table 72: Comparative Sequences relating to SAG0941

SEQ ID NO. 7201
STRAIN 2603
ATGAATAAACGCGTAAAAATCGTTGCAACACTTGGTCCTGCGGTTGAATTCCGTGGTG
GTAAGAAGTTTGGTGAGTCTGGATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAG
AAAAAATTGCTCAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATG
GAGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTCGTAAAGCAGAAGAGATTGCAG
GACAAAAAGTTGGCTTCCTCCTTGATACTAAAGGACCTGAAATTCGTACAGAACTTTTTG
AAGATGGTGCAGATTTCCATTCATATACAACAGGTACAAAATTACGTGTTGCTACTAAGC
AAGGTATCAAATCAACTCCAGAAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCT
TTGATGACGTTGAAGTTGGTAAGCAAATCCTTGTTGATGATGGTAAACTAGGTCTTACTG
TGTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATGATGGCCTTA
TTGGTAAACAAAAAGGTGTAAACATCCCTTATACTAAAATTCCTTTCCCAGCACTTGCAG
AACGCGATAATGCTGATATCCGTTTTGGACTTGAGCAAGGACTTAACTTTATTGCTATCT
CATTTGTACGTACTGCTAAAGATGTTAATGAAGTTCGTGCTATTTGTGAAGAAACTGGsm
ATGGACACGTTAAGTTGTTTGCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATG
AGATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTATCGAAGTTC
CATTTGAAATGGTTCCAGTTTACCAAAAAATGATCATTACTAAAGTTAATGCAGCTGGTA
AAGCAGTTATTACAGCAACAAATATGCTTgAAACAATGACTGATAAACCACGTGCGACTC
GTTCAGAAGTATCTGATGTCTTCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTT
CAGGTGAGTCAGCTAATGGTAAATACCCAGTTGAGTCAGTTCGTACAATGGCTACTATTG
ATAAAAATGCTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTGCATTCCCAC
GTAATAACAAAACTGATGTTATTGCATCTGCGGTTAAAGATGCAACACACTCAATGGATA
TCAAACTTGTTGTAACAATTACTGAAACAGGTAATACAGCTCGTGCCATTTCTAAATTCC
GTCCAGATGCAGACATTTTGGCTGTTACATTTGATGAAAAAGTACAACGTTCATTGATGA
TTAACTGGGGTGTTATCCCTGTCCTTGCAGACAAACCAGCATCTACAGATGATATGTTTG
AGGTTGCAGAACGTGTAGCACTTGAAGCAGGATTTGTTGAATCAGGCGATAATATCGTTA
TCGTTGCAGGTGTTCCTGTAGGTACAGGTGGAACTAACACAATGCGTGTTCGTACTGTTA
AA

SEQ ID NO. 7202
STRAIN 090
AATAAACGCGTAAAAATCGTTGCAACACT
TGGTCCTGCGGTAGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTGGAT
ACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCTCAA
TTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGGAGA
TCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTCGTAAAGCAGAAGAGA
TTGCAGGACAAAAAGTTGGCTTCCTCCTTGATACTAAAGGACCTGAAATT
CGTACAGAACTTTTTGAAGATGGTTCAGATTTCCATTCATATACAACAGG
TACAGAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAGAAG
TGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTTGAA
GTTGGTAAGCAAATCCTTGTTGATGATGGTAAACTAGGTCTTACTGTGTT
TGCAAAAGATAAAGACACTCgTGAATTTGAAGTAGTTGTTGAGAATGATG
GCCTTATTGGTAAACAaaaaGGTGTAAACATCCCTTATACTAaAATTCCT
TTCCCAgCACTTGCAGAACGCGATAATGCTGATATCCGTTTTGGACTTGA
GCAAGGACTTAACTTTATTGCTATCTCATTTGTACGTACTGCTAAAGATG
TTAATGAAGTTCGTGCTATTTGTGAAGAAACTGGCAATGGACATGTTAAG
TTGTTTGCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATGAGAT
TATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTATCG
AAGTTCCATTTGAAATGGTTCCAGTTTACCAAAAAATGATCATTACTAAA
GTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGAAAC
AATGACTGATAAACCACGTGCGACTCGTTCAGAAGTATCTGATGTCTTCA
ATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCAGCT
AATGGTAAATACCCAGTTGAGTCAGTTCGTACAATGGCTACTATTGATAA
AAATGCTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTGCAT
TCCCACGTAATAACAAAACTGATGTTATTGCATCTGCGGTTAAAGATGCA
ACACACTCAATGGATATCAAACTTGTTGTGACAATTACTGAAACAGGTAA
TACAGCTCGTGCCATTTCTAAATTCCGTCCAGATGCAGACATTTTGGCTG
TTACATTTGATGAAAAAGTACAACGTTCATTGATGATTAACTGGGGTGTT
ATCCCTGTCCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGAGGT
TGCAGAACGTGTAGCACTTGAAGCAGGACTTGTTGAATCAGGCGATAATA
TCGTTATCGTTGCAGGTGTTCCTGTAGGTACAGGTGGAACTAACACAATG
CGTGTTCGTACTGTTAAA

SEQ ID NO. 7203
STRAIN A909
AATAAACGCGTAAAAATCGTTGCAACACTTGGTC
CTGCGGTTGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTGGATACTGG
GGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCTCAATTGAT
TAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGGAGATCATG
CTGAGCAAGGAGCTCGTATGGCTACTGTTCGTAAAGCAGAAGAGATTGCA
GGACAAAAAGTTGGCTTCCTCCTTGATACTAAAGGACCTGAAATTCGTAC
AGAACTTTTTGAAGATGGTGCAGATTTCCATTCATATACAACAGGTACAA
AATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAGAAGTGATT
GCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTTGAAGTTGG
TAAGCAAATCCTTGTTGATGATGGTAAACTAGGTCTTACTGTGTTTGCAA
AAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATGATGGCCTT
ATTGGTAAACAAAAAGGTGTAAACATCCCTTATACTAAAATTCCTTTCCC
AGCACTTGCAGAACGCGATAATGCTGATATCCGTTTTGGACTTGAGCAAG
GACTTAACTTTATTGCTATCTCATTTGTACGTACTGCTAAAgATGTTAAT
GAAGTTCGTGCTATTTGTGAAGAAACTGGCAATGGACACGTTAAGTTGTT
TGCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATGAGATTATCG
AAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTATCGAAGTT
CCATTTGAAATGGTTCCAGTTTACCAAAAAATGATCATTACTAAAGTTAA

Table 72: Comparative Sequences relating to SAG0941

TGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGAAACAATGA
CTGATAAACCACGTGCGACTCGTTCAGAAGTATCTGATGTCTTCAATGCT
GTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCAGCTAATGG
TAAATACCCAGTTGAGTCAGTTCGTACAATGGCTACTATTGATAAAAATG
CTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTGCATTCCCA
CGTAATAACAAAACTGATGTTATTGCATCTGCGGTTAAAGATGCAACACA
CTCAATGGATATCAAACTTGTTGTAACAATTACTGAAACAGGTAATACAG
CTCGTGCCATTTCTAAATTCCGTCCAGATGCAGACATTTTGGCTGTTACA
TTTGATGAAAAAGTACAACGTTCATTGATGATTAACTGGGGTGTTATCCC
TGTCCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGAGGTTGCAG
AACGTGTAGCACTTGAAGCAGGATTTGTTGAATCAGGCGATAATATCGTT
ATCGTTGCAGGTGTTCCTGTAGGTACAGGTGGAACTAACACAATGCGTGT
TCGTACTGTTAAA

SEQ ID NO. 7204
STRAIN H36B
AATAAACGCGTAAAAATCGTTGCAAC
ACTTGGTCCTGCGGTTGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTCGTAAAGCAGAAG
AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATACTAAAGGACCTGAA
ATTCGTACAGAACTTTTTGAAGATGGTGCAGATTTCCATTCATATACAAC
AGGTACAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
GAAGTTGGTAAGCAAATCCTTGTTGATGATGGTAAACTAGGTCTTACTGT
GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
ATGGCCTTATTGGTAAACAAAAAGGTGTAAACATCCCTTATACTAAAATT
CCTTTCCCAGCACTTGCAGAACGCGATAATGCTGATATCCGTTTTGGACT
TGAGCAAGGACTTAACTTTATTGCTATCTCATTTGTACGTACTGCTAAAG
ATGTTAATGAAGTTCGTGCTATTTGTGAAGAAACTGGCAATGGACACGTT
AAGTTGTTTGCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
TCGAAGTTCCATTTGAAATGGTTCCAGTTTACCAAAAAATGATCATTACT
AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
AACAATGAcTGATAAACCACGTGCGACTCGTTCAGAAGTATCTGATGTCT
TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
GCTAATGGTAAATACCCAGTTGAGTCAGTTCGTACAATGGCTACTATTGA
TAAAAATGCTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
CATTCCCACGTAATAACAAAACTGATGTTATTGCATCTGCGGTTAAAGAT
GCAACACACTCAATGGATATCAAACTTGTTGTAACAATTACTGaAACAGG
TAATACAGCTCGTGCCATTTCTAAATTCCGTCCAGATGCAGACATTTTGG
CTGTTACATTTGATGAAAAAGTACAACGTTCATTGATGATTAACTGGGGT
GTTATCCCTGTCCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGA
GGTTGCAGAACGTGTAGCACTTGAAGCAGGATTTGTTGAATCAGGCGATA
ATATCGTTATCGTTGCAGGTGTTCCTGTAgGTACAGGTGGAACTAACACA
ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7205
STRAIN 18RS21
AATAAACGCGTAAAAATCGTTGCAAC
ACTTGGTCCTGCGGTTGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
GATACTGGGGTGAAAGCCTTGACGTAgAAGCTTCAGCAGAAAAAATTGCT
CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTCGTAAAGCAGAAG
AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATACTAAAGGACCTGAA
ATTCGTACAGAACTTTTTGAAGATGGTGCAGATTTCCATTCATATACAAC
AGGTACAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
GAAGTTGGTAAGCAAATCCTTGTTGATGATGGTAAACTAGGTCTTACTGT
GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
ATGGCCTTATTGGTAAACAAAAAGGTGTAAACATCCCTTATACTAAAATT
CCTTTCCCAGCACTTGCAGAACGCGATAATGCTGATATCCGTTTTGGACT
TGAGCAAGGACTTAACTTTATTGCTATCTCATTtGTACGTACTGCTAAAG
ATGTTAATGAAGTTCGTGCTATTTGTGAAGAAACTGGCAATGGACACGTT
AAGTTGTTTGCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
TCGAAGTTCCATTTGAAATGGTTCCAGTTTACCAAAAAATGATCATTACT
AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
AACAATGaCTGATAAACCACGTGCGACTCGTTCAGAAGTATCTGATGTCT
TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
GCTAATGGTAAATACCCAGTTGAGTCAGTTCGTACAATGGCTACTATTGA
TAAAAATGCTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
CATTCCCACGTAATAACAAAACTGATGTTATTGCATCTGCGGTTAAAGAT
GCAACACACTCAATGGATATCAAACTTGTTGTAACAATTACTGAAACAGG
TAATACAGCTCGTGCCATTTCTAAATTCCGTCCAGATGCAGACATTTTGG
CTGTTACATTTGATGAAAAAGTACAACGTTCATTGATGATTAACTGGGGT
GTTATCCCTGTCCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGA
GGTTGCAGAACGTGTAgCACTTGAAGCAGGATTTGTTGAATCAGGCGATA
ATATCGTTATCGTTGCAGGTGTTCCTGTAgGTACAGGTGGAACTAACACA
ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7206

Table 72: Comparative Sequences relating to SAG0941

STRAIN M732
AATAAACGCGTAAAAATCGTTGCAAC
ACTTGGTCCTGCGGTAGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTCGTAAAGCAGAAG
AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATACTAAAGGACCTGAA
ATTCGTACAGAACTTTTTGAAGATGGTGCAGATTTCCATTCATATACAAC
AGGTACAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
GAAGTTGGTAAGCAAATCCTTGTTGATGATGGTAAACTAGGTCTTACTGT
GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
ATGGCCTTATTGGTAAACAAAAAGGTGTAAACATCCCTTATACTAAAATT
CCTTTCCCAGCACTTGCAGAACGCGATAATGCTGATATCCGTTTTGGACT
TGAGCAAGGACTTAACTTTATTGCTATCTCATTTGTACGTACTGCTAAAG
ATGTTAATGAAGTTCGTGCTATTTGTGAAGAAACTGGCAATGGACACGTT
AAGTTGTTTGCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
TCGAAGTTCCATTTGAAATGGTTCCAGTTTACCAAAAAATGATCATTACT
AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
AACAATGACTGATAAACCACGTGCGACTCGTTCAGAAGTATCTGATGTCT
TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
GCTAATGGTAAATACCCAGTTGAGTCAGTTCGTACAATGGCTACTATTGA
TAAAAATGCTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
CATTCCCACGTAATAACAAAACTGATGTTATTGCATCTGCGGTTAAAGAT
GCAACACACTCAATGGATATCAAACTTGTTGTAACAATTACTGAAACAGG
TAATACAGCTCGTGCCATTTCTAAATTCCGTCCAGATGCAGACATTTTGG
CTGTTACATTTGATGAAAAAGTACAACGTTCATTGATGATTAACTGGGGT
GTTATCCCTGTCCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGA
GGTTGCAGAACGTGTAgCACTTGAAGCAGGACTTGTTGAATCAGGCGATA
ATATCGTTATCGTTGCAGGTGTTCCTGTAGGTACAGGTGGAACTAACACA
ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7207
STRAIN COH1
AATAAACGCGTAAAAATCGTTGCAAC
ACTTGGTCCTGCGGTAGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTCGTAAAGCAGAAG
AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATACTAAAGGACCTGAA
ATTCGTACAGAACTTTTTGAAGATGGTGCAGATTTCCATTCATATACAAC
AGGTACAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
GAAGTTGGTAAGCAAATCCTTGTTGATGATGGTAAACTAGGTCTTACTGT
GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
ATGGCCTTAtTGGTAAACAAAAAGGTGTAAACATCCCTTATACTAAAATT
CCTTTCCCAGCACTTGCAGAACGCGATAATGCTGATATCCGTTTTGgACT
TGAGCAAGGACTTAACTTTATTGCTATCTCATTTGTACGTACTGCTAAAG
ATGTTAATGAAGTTCGTGCTATTTGTGAAGAAACTGGCAATGGACACGTT
AAGTTGTTTGCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
TCGAAGTTCCATTTGAAATGGTTCCAGTTTACCAAAAAATGATCATTACT
AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
AACAATGACTGATAAACCACGTGCGACTCGTTCAGaAGTATCTGATGTCT
TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTtTCAGGTGAGTCA
GCTAATGGTAAATACCCAGTTGAGTCAGTTCGTACAATGGCTACTATTGA
TAAAAATGCTCAAACATTACTCAATGAGTATGGTCGcTTAGACTCATCTG
CATTCCCACGTAATAACAAAACTGATGTTATTGCATCTGCGGTTAAAGAT
GCAACACACTCAATGGATATCAAACTTGTTGTAACAATTACTGAAACAGG
TAATACAGCTCGTGCCATTTCTAAATTCCGTCCAGATGCAGACATTTTGG
CTGTTACATTTGATGAAAAAGTACAACGTTCATTGATGATTAACTGGGGT
GTTATCCCTGTCCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGA
GGTTGCAGAACGTGTAGCACTTGAAGCAGGACTTGTTGAATCAGGCGATA
ATATCGTTATCGTTGCAGGTGTTCCTGTAGGTACAGGTGGAACTAACACA
ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7208
STRAIN M781
AATAAACGCGTAAAAATCGTTGCAAC
ACTTGGTCCTGCGGTAGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTCGTAAAGCAGAAG
AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATACTAAAGGACCTGAA
ATTCGTACAGAACTTTTTGAAGATGGTGCAGATTTCCATTCATATACAAC
AGGTACAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
GAAGTTGGTAAGCAAATCCTTGTTGATGATGGTAAACTAGGTCTTACTGT
GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
ATGGCCTTATTGgTAAACAAAAAGGTGTAAACATCCCTTATACTAAAATT
CCTTTCCCAGCACTTGCAGaaCGCGATAATGCTGATATCCGTTTTGGACT
TGAGCAAGGACTTAACTTTATTGCTATCTCATTTGTACGTACTGCTAAAG

Table 72: Comparative Sequences relating to SAG0941

ATGTTAATGAAGTTCGTGCTATTTGTGAAGAAACTGGCAATGGACACGTT
AAGTTGTTTGCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
TCGAAGTTCCATTTGAAATGGTTCCAGTTTACCAAAAAATGATCATTACT
AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
AACAATGACTGATAAACCACGTGCGACTCGTTCAGAAGTATCTGATGTCT
TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
GCTAATGGTAAATACCCAGTTGAGTCAGTTCGTACAATGGCTACTATTGA
TAAAAATGCTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
CATTCCCACGTAATAACAAAACTGATGTTATTGCATCTGCGGTTAAAGAT
GCAACACACTCAATGGATATCAAACTTGTTGTAACAATTACTGAAACAGG
TAATACAGCTCGTGCCATTTCTAAGTTCCGTCCAGATGCAGACATTTTGG
CTGTTACATTTGATGAAAAAGTACAACGTTCATTGATGATTAACTGGGGT
GTTATCCCTGTCCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGA
GGTTGCAGAACGTGTAGCACTTGAAGCAGGACTTGTTGAATCAGGCGATA
ATATCGTTATCGTTGCAGGTGTTCCTGTAGGTACAGGTGGAACTAACACA
ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7209
STRAIN CJB110
AATAAACGCGTAAAAATCGTTGCAAC
ACTTGGTCCTGCGGTTGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
GATACTGGGGTGAAAGCCTTGACGTAgAAGCTTCAGCAGAAAAAATTGCT
CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTCGTAAAGCAGAAG
AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATACTAAAGGACCTGAA
ATTCGTACAGAACTTTTTGAAGATGGTGCAGATTTCCATTCATATACAAC
AGGTACAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
GAAGTTGGTAAGCAAATCCTTGTTGATGATGGTAAACTAGGTCTTACTGT
GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
ATGGCCTTAtTGGTAAACAAAAAGGTGTAAACATCCCTTATACTAAAATT
CCTTTCCCAGCACTTGCAGAACGCGATAATGCTGATATCCGTTTTGGACT
TGAACAAGGACTTAACTTTATTGCTATCTCATTTGTACGTACTGCTAAAG
ATGTTAATGAAGTTCGTGCTATTTGTGAAGAAACTGGCAATGGACACGTT
AAGTTGTTTGCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
TCGAAGTTCCATTTGAAATGGTTCCAGTTTACCAAAAAATGATCATTACT
AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
AACAATGACTGATAAACCACGTGCGACTCGTTCAGAAGTATCTGATGTCT
TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
GCTAATGGTAAATACCCAGTTGAGTCAGTTCGTACAATGGCTACTATTGA
TAAAAATGCTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
CATTCCCACGTAATAACAAAACTGATGTTATTGCATCTGCGGTTAAAGAT
GCAACACACTCAATGGATATCAAACTTGTTGTAACAATTACTGAAACAGG
TAATACAGCTCGTGCCATTTCTAAATTCCGTCCAGATGCAGACATTTTGG
CTGTTACATTTGATGAAAAAGTACAACGTTCATTGATGATTAACTGGGGT
GTTATCCCTGTCCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGA
GGTTGCAGAACGTGTAGCACTTGAAGCAGGATTTGTTGAATCAGGCGATA
ATATCGtTATCGTTGCAGGTGTTCCTGTAGGTACAGGTGGAACTAACACA
ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7210
STRAIN 1169NT
AATAAACGCGTAAAAATCGTTGCAAC
ACTTGGTCCTGCGGTAGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTCGTAAAGCAGAAG
AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATACTAAAGGACCTGAA
ATTCGTACAGAACTTTTTGAAGATGGTGCAGATTTCCATTCATATACAAC
AGGTACAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
GAAGTTGGTAAGCAAATCCTTGTTGATGATGGTAAACTAGGTCTTACTGT
GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
ATGGCCTTATTGGTAAACAAAAAGGTGTAAACATCCCTTATACTAAAATT
CCTTTCCCAGCACTTGCAGAACGCGATAATGCTGATATCCGTTTTGGACT
TGAGCAAGGACTTAACTTTATTGCTATCTCATTTGTACGTACTGCTAAAG
ATGTTAATGAAGTTCGTGCTATTTGTGAAGAAACTGGCAATGGACACGTT
AAGTTGTTTGcTAAAATTGAAAATCAaCAAGGTATCGATAATATTGATGA
GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
TCGAAGTTCCATTTGAAATGGTTCCAGTTTACCAAAaAATGATCATTACT
AaAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
AACAATGACTGATAAACCACGTGCGACTCGTTCAGAAGTATCTGATGTCT
TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
GCTAATGGTAAATACCCAGTTGAGTCAGTTCGTACAATGGCTACTATTGA
TAAAAATGCTCAAACAttACTCAATGAGTATGGTCGTTTAGACTCATCTG
CATTCCCACGTAATAACAAAACTGATGTTATTGCATCTGCGGTTAAAGAT
GCAACACACTCAATGGATATCAAACTTGTTGTAACAATTACTGAAACAGG
TAATACAGCTCGTGCCATTTCTAAATTCCGTCCAGATGCAGACATTTTGG
CTGTTACATTTGATGAAAAAGTACAACGTTCATTGATGATTAACTGGGGT
GTTATCCCTGTCCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGA
GGTTGCAGAACGTGTAGCACTTGAAGCAGGACTTGTTGAATCAGGCGATA

Table 72: Comparative Sequences relating to SAG0941

ATATCGTTATCGTTGCAGGTGTTCCTGTAGGTACAGGTGGAACTAACACA
ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7211
STRAIN JM9130013
AATAAACGCGTAAAAATCGTTGCAAC
ACTTGGTCCTGCGGTAGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTCGTAAAGCAGAAG
AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATACTAAAGGACCTGAA
ATTCGTACAGAACTTTTTGAAGATGGTTCAGATTTCCATTCATATACAAC
AGGTACAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
GAAGTTGGTAAGCAAATCCTTGTTGATGATGGTAAACTAGGTCTTACTGT
GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
ATGGCCTTATTGGTAAACAAAAAGGTGTAAACATCCCTTATACTAAAATT
CCTTTCCCAGCACTTGCAGAACGCGATAATGCTGATATCCGTTTTGGACT
TGAGCAAGGACTTAACTTTATTGCTATCTCATTTGTACGTACTGCTAAAG
ATGTTAATGAAGTTCGTGCTATTTGTGAAGAAACTGGCAATGGACATGTT
AAGTTGTTTGCTAAAATTGaAAATCAaCAAGGTATCGATAATATTGATGA
GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
TCGAAGTTCCATTTGAAATGGTTCCAGTTTACCAAAAAATGATCATTACT
AAAGTTAATGCAGCTGGTAAAGCAGTTAttACAGCAACAAATATGCTTGA
AACAATGACTGATAAACCACGTGCGACTCGTTCAGAAGTATCTGATGTCT
TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
GCTAATGGTAAATACCCAGTTGAGTCAGTTCGTACAATGGCTACTATTGA
TAAAAATGCTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
CATTCCCACGTAATAaCAAAACTGATGTTATTGCATCTGCGGTTAAAGAT
GCAACACACTCAATGGATATCAAACTTGTTGTGACAATTACTGAAACAGG
TAATACAGCTCGTGCCATTTCTAAATTCCGTCCAGATGCAGACATTTTGG
CTGTTACATTTGATGAAAAAGTACAACGTTCATTGATGATTAACTGGGGT
GTTATCCCTGTCCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGA
GGTTGCAGAACGTGTAgcACTTGAAGCAGGACTTGTTGAATCAGGCGATA
ATATCGTTATCGTTGCAGGTGTTCCTGTAGGTACAGGTGGAACTAACACA
ATGCGTGTTCGTACTGTTAAA

```
PRETTY of: /biotmp/msa277466.2{*}   February 24, 2003 01:44  ..

                                1                                                   50
         msa277466.2{330_090}   ---AATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCTG CGGTaGAATT
    msa277466.2{330_JM9130013}  ---AATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCTG CGGTaGAATT
       msa277466.2{330_18RS21}  ---AATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCTG CGGTtGAATT
         msa277466.2{330_2603}  atgAATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCTG CGGTtGAATT
         msa277466.2{330_A909}  ---AATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCTG CGGTtGAATT
         msa277466.2{330_H36B}  ---AATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCTG CGGTtGAATT
       msa277466.2{330_CJB110}  ---AATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCTG CGGTtGAATT
         msa277466.2{330_COH1}  ---AATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCTG CGGTaGAATT
         msa277466.2{330_M732}  ---AATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCTG CGGTaGAATT
       msa277466.2{330_1169NT}  ---AATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCTG CGGTaGAATT
         msa277466.2{330_M781}  ---AATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCTG CGGTaGAATT
                     Consensus  ********** ********** ********** ********** ****_*****

                                51                                                 100
         msa277466.2{330_090}   CCGTGGTGGT AAGAAGTTTG GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
    msa277466.2{330_JM9130013}  CCGTGGTGGT AAGAAGTTTG GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
       msa277466.2{330_18RS21}  CCGTGGTGGT AAGAAGTTTG GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
         msa277466.2{330_2603}  CCGTGGTGGT AAGAAGTTTG GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
         msa277466.2{330_A909}  CCGTGGTGGT AAGAAGTTTG GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
         msa277466.2{330_H36B}  CCGTGGTGGT AAGAAGTTTG GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
       msa277466.2{330_CJB110}  CCGTGGTGGT AAGAAGTTTG GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
         msa277466.2{330_COH1}  CCGTGGTGGT AAGAAGTTTG GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
         msa277466.2{330_M732}  CCGTGGTGGT AAGAAGTTTG GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
       msa277466.2{330_1169NT}  CCGTGGTGGT AAGAAGTTTG GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
         msa277466.2{330_M781}  CCGTGGTGGT AAGAAGTTTG GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
                     Consensus  ********** ********** ********** ********** **********

                                101                                                150
         msa277466.2{330_090}   ACGTAGAAGC TTCAGCAGAA AAAATTGCTC AATTGATTAA AGAAGGTGCT
    msa277466.2{330_JM9130013}  ACGTAGAAGC TTCAGCAGAA AAAATTGCTC AATTGATTAA AGAAGGTGCT
       msa277466.2{330_18RS21}  ACGTAGAAGC TTCAGCAGAA AAAATTGCTC AATTGATTAA AGAAGGTGCT
         msa277466.2{330_2603}  ACGTAGAAGC TTCAGCAGAA AAAATTGCTC AATTGATTAA AGAAGGTGCT
         msa277466.2{330_A909}  ACGTAGAAGC TTCAGCAGAA AAAATTGCTC AATTGATTAA AGAAGGTGCT
         msa277466.2{330_H36B}  ACGTAGAAGC TTCAGCAGAA AAAATTGCTC AATTGATTAA AGAAGGTGCT
       msa277466.2{330_CJB110}  ACGTAGAAGC TTCAGCAGAA AAAATTGCTC AATTGATTAA AGAAGGTGCT
         msa277466.2{330_COH1}  ACGTAGAAGC TTCAGCAGAA AAAATTGCTC AATTGATTAA AGAAGGTGCT
         msa277466.2{330_M732}  ACGTAGAAGC TTCAGCAGAA AAAATTGCTC AATTGATTAA AGAAGGTGCT
       msa277466.2{330_1169NT}  ACGTAGAAGC TTCAGCAGAA AAAATTGCTC AATTGATTAA AGAAGGTGCT
         msa277466.2{330_M781}  ACGTAGAAGC TTCAGCAGAA AAAATTGCTC AATTGATTAA AGAAGGTGCT
                     Consensus  ********** ********** ********** ********** **********

                                151                                                200
         msa277466.2{330_090}   AACGTTTTCC GTTTCAACTT CTCACATGGA GATCATGCTG AGCAAGGAGC
```

Table 72: Comparative Sequences relating to SAG0941

```
msa277466.2{330_JM9130013}  AACGTTTTCC GTTTCAACTT CTCACATGGA GATCATGCTG AGCAAGGAGC
    msa277466.2{330_18RS21}  AACGTTTTCC GTTTCAACTT CTCACATGGA GATCATGCTG AGCAAGGAGC
      msa277466.2{330_2603}  AACGTTTTCC GTTTCAACTT CTCACATGGA GATCATGCTG AGCAAGGAGC
      msa277466.2{330_A909}  AACGTTTTCC GTTTCAACTT CTCACATGGA GATCATGCTG AGCAAGGAGC
      msa277466.2{330_H36B}  AACGTTTTCC GTTTCAACTT CTCACATGGA GATCATGCTG AGCAAGGAGC
    msa277466.2{330_CJB110}  AACGTTTTCC GTTTCAACTT CTCACATGGA GATCATGCTG AGCAAGGAGC
      msa277466.2{330_COH1}  AACGTTTTCC GTTTCAACTT CTCACATGGA GATCATGCTG AGCAAGGAGC
      msa277466.2{330_M732}  AACGTTTTCC GTTTCAACTT CTCACATGGA GATCATGCTG AGCAAGGAGC
    msa277466.2{330_1169NT}  AACGTTTTCC GTTTCAACTT CTCACATGGA GATCATGCTG AGCAAGGAGC
      msa277466.2{330_M781}  AACGTTTTCC GTTTCAACTT CTCACATGGA GATCATGCTG AGCAAGGAGC
                  Consensus  ********** ********** ********** ********** **********

                             201                                               250
       msa277466.2{330_090}  TCGTATGGCT ACTGTTCGTA AAGCAGAAGA GATTGCAGGA CAAAAAGTTG
msa277466.2{330_JM9130013}  TCGTATGGCT ACTGTTCGTA AAGCAGAAGA GATTGCAGGA CAAAAAGTTG
    msa277466.2{330_18RS21}  TCGTATGGCT ACTGTTCGTA AAGCAGAAGA GATTGCAGGA CAAAAAGTTG
      msa277466.2{330_2603}  TCGTATGGCT ACTGTTCGTA AAGCAGAAGA GATTGCAGGA CAAAAAGTTG
      msa277466.2{330_A909}  TCGTATGGCT ACTGTTCGTA AAGCAGAAGA GATTGCAGGA CAAAAAGTTG
      msa277466.2{330_H36B}  TCGTATGGCT ACTGTTCGTA AAGCAGAAGA GATTGCAGGA CAAAAAGTTG
    msa277466.2{330_CJB110}  TCGTATGGCT ACTGTTCGTA AAGCAGAAGA GATTGCAGGA CAAAAAGTTG
      msa277466.2{330_COH1}  TCGTATGGCT ACTGTTCGTA AAGCAGAAGA GATTGCAGGA CAAAAAGTTG
      msa277466.2{330_M732}  TCGTATGGCT ACTGTTCGTA AAGCAGAAGA GATTGCAGGA CAAAAAGTTG
    msa277466.2{330_1169NT}  TCGTATGGCT ACTGTTCGTA AAGCAGAAGA GATTGCAGGA CAAAAAGTTG
      msa277466.2{330_M781}  TCGTATGGCT ACTGTTCGTA AAGCAGAAGA GATTGCAGGA CAAAAAGTTG
                  Consensus  ********** ********** ********** ********** **********

                             251                                               300
       msa277466.2{330_090}  GCTTCCTCCT TGATACTAAA GGACCTGAAA TTCGTACAGA ACTTTTTGAA
msa277466.2{330_JM9130013}  GCTTCCTCCT TGATACTAAA GGACCTGAAA TTCGTACAGA ACTTTTTGAA
    msa277466.2{330_18RS21}  GCTTCCTCCT TGATACTAAA GGACCTGAAA TTCGTACAGA ACTTTTTGAA
      msa277466.2{330_2603}  GCTTCCTCCT TGATACTAAA GGACCTGAAA TTCGTACAGA ACTTTTTGAA
      msa277466.2{330_A909}  GCTTCCTCCT TGATACTAAA GGACCTGAAA TTCGTACAGA ACTTTTTGAA
      msa277466.2{330_H36B}  GCTTCCTCCT TGATACTAAA GGACCTGAAA TTCGTACAGA ACTTTTTGAA
    msa277466.2{330_CJB110}  GCTTCCTCCT TGATACTAAA GGACCTGAAA TTCGTACAGA ACTTTTTGAA
      msa277466.2{330_COH1}  GCTTCCTCCT TGATACTAAA GGACCTGAAA TTCGTACAGA ACTTTTTGAA
      msa277466.2{330_M732}  GCTTCCTCCT TGATACTAAA GGACCTGAAA TTCGTACAGA ACTTTTTGAA
    msa277466.2{330_1169NT}  GCTTCCTCCT TGATACTAAA GGACCTGAAA TTCGTACAGA ACTTTTTGAA
      msa277466.2{330_M781}  GCTTCCTCCT TGATACTAAA GGACCTGAAA TTCGTACAGA ACTTTTTGAA
                  Consensus  ********** ********** ********** ********** **********

                             301                                               350
       msa277466.2{330_090}  GATGGTtCAG ATTTCCATTC ATATACAACA GGTACAgAAT TACGTGTTGC
msa277466.2{330_JM9130013}  GATGGTtCAG ATTTCCATTC ATATACAACA GGTACAaAAT TACGTGTTGC
    msa277466.2{330_18RS21}  GATGGTgCAG ATTTCCATTC ATATACAACA GGTACAaAAT TACGTGTTGC
      msa277466.2{330_2603}  GATGGTgCAG ATTTCCATTC ATATACAACA GGTACAaAAT TACGTGTTGC
      msa277466.2{330_A909}  GATGGTgCAG ATTTCCATTC ATATACAACA GGTACAaAAT TACGTGTTGC
      msa277466.2{330_H36B}  GATGGTgCAG ATTTCCATTC ATATACAACA GGTACAaAAT TACGTGTTGC
    msa277466.2{330_CJB110}  GATGGTgCAG ATTTCCATTC ATATACAACA GGTACAaAAT TACGTGTTGC
      msa277466.2{330_COH1}  GATGGTgCAG ATTTCCATTC ATATACAACA GGTACAaAAT TACGTGTTGC
      msa277466.2{330_M732}  GATGGTgCAG ATTTCCATTC ATATACAACA GGTACAaAAT TACGTGTTGC
    msa277466.2{330_1169NT}  GATGGTgCAG ATTTCCATTC ATATACAACA GGTACAaAAT TACGTGTTGC
      msa277466.2{330_M781}  GATGGTgCAG ATTTCCATTC ATATACAACA GGTACAaAAT TACGTGTTGC
                  Consensus  ******_*** ********** ********** ******_*** **********

                             351                                               400
       msa277466.2{330_090}  TACTAAGCAA GGTATCAAAT CAACTCCAGA AGTGATTGCA TTGAATGTTG
msa277466.2{330_JM9130013}  TACTAAGCAA GGTATCAAAT CAACTCCAGA AGTGATTGCA TTGAATGTTG
    msa277466.2{330_18RS21}  TACTAAGCAA GGTATCAAAT CAACTCCAGA AGTGATTGCA TTGAATGTTG
      msa277466.2{330_2603}  TACTAAGCAA GGTATCAAAT CAACTCCAGA AGTGATTGCA TTGAATGTTG
      msa277466.2{330_A909}  TACTAAGCAA GGTATCAAAT CAACTCCAGA AGTGATTGCA TTGAATGTTG
      msa277466.2{330_H36B}  TACTAAGCAA GGTATCAAAT CAACTCCAGA AGTGATTGCA TTGAATGTTG
    msa277466.2{330_CJB110}  TACTAAGCAA GGTATCAAAT CAACTCCAGA AGTGATTGCA TTGAATGTTG
      msa277466.2{330_COH1}  TACTAAGCAA GGTATCAAAT CAACTCCAGA AGTGATTGCA TTGAATGTTG
      msa277466.2{330_M732}  TACTAAGCAA GGTATCAAAT CAACTCCAGA AGTGATTGCA TTGAATGTTG
    msa277466.2{330_1169NT}  TACTAAGCAA GGTATCAAAT CAACTCCAGA AGTGATTGCA TTGAATGTTG
      msa277466.2{330_M781}  TACTAAGCAA GGTATCAAAT CAACTCCAGA AGTGATTGCA TTGAATGTTG
                  Consensus  ********** ********** ********** ********** **********

                             401                                               450
       msa277466.2{330_090}  CTGGTGGACT TGACATCTTT GATGACGTTG AAGTTGGTAA GCAAATCCTT
msa277466.2{330_JM9130013}  CTGGTGGACT TGACATCTTT GATGACGTTG AAGTTGGTAA GCAAATCCTT
    msa277466.2{330_18RS21}  CTGGTGGACT TGACATCTTT GATGACGTTG AAGTTGGTAA GCAAATCCTT
      msa277466.2{330_2603}  CTGGTGGACT TGACATCTTT GATGACGTTG AAGTTGGTAA GCAAATCCTT
      msa277466.2{330_A909}  CTGGTGGACT TGACATCTTT GATGACGTTG AAGTTGGTAA GCAAATCCTT
      msa277466.2{330_H36B}  CTGGTGGACT TGACATCTTT GATGACGTTG AAGTTGGTAA GCAAATCCTT
    msa277466.2{330_CJB110}  CTGGTGGACT TGACATCTTT GATGACGTTG AAGTTGGTAA GCAAATCCTT
      msa277466.2{330_COH1}  CTGGTGGACT TGACATCTTT GATGACGTTG AAGTTGGTAA GCAAATCCTT
      msa277466.2{330_M732}  CTGGTGGACT TGACATCTTT GATGACGTTG AAGTTGGTAA GCAAATCCTT
    msa277466.2{330_1169NT}  CTGGTGGACT TGACATCTTT GATGACGTTG AAGTTGGTAA GCAAATCCTT
      msa277466.2{330_M781}  CTGGTGGACT TGACATCTTT GATGACGTTG AAGTTGGTAA GCAAATCCTT
                  Consensus  ********** ********** ********** ********** **********

                             451                                               500
```

Table 72: Comparative Sequences relating to SAG0941

```
      msa277466.2{330_090}  GTTGATGATG GTAAACTAGG TCTTACTGTG TTTGCAAAAG ATAAAGACAC
msa277466.2{330_JM9130013}  GTTGATGATG GTAAACTAGG TCTTACTGTG TTTGCAAAAG ATAAAGACAC
   msa277466.2{330_18RS21}  GTTGATGATG GTAAACTAGG TCTTACTGTG TTTGCAAAAG ATAAAGACAC
     msa277466.2{330_2603}  GTTGATGATG GTAAACTAGG TCTTACTGTG TTTGCAAAAG ATAAAGACAC
     msa277466.2{330_A909}  GTTGATGATG GTAAACTAGG TCTTACTGTG TTTGCAAAAG ATAAAGACAC
     msa277466.2{330_H36B}  GTTGATGATG GTAAACTAGG TCTTACTGTG TTTGCAAAAG ATAAAGACAC
   msa277466.2{330_CJB110}  GTTGATGATG GTAAACTAGG TCTTACTGTG TTTGCAAAAG ATAAAGACAC
     msa277466.2{330_COH1}  GTTGATGATG GTAAACTAGG TCTTACTGTG TTTGCAAAAG ATAAAGACAC
     msa277466.2{330_M732}  GTTGATGATG GTAAACTAGG TCTTACTGTG TTTGCAAAAG ATAAAGACAC
   msa277466.2{330_1169NT}  GTTGATGATG GTAAACTAGG TCTTACTGTG TTTGCAAAAG ATAAAGACAC
     msa277466.2{330_M781}  GTTGATGATG GTAAACTAGG TCTTACTGTG TTTGCAAAAG ATAAAGACAC
                 Consensus  ********** ********** ********** ********** **********

                            501                                                550
      msa277466.2{330_090}  TCGTGAATTT GAAGTAGTTG TTGAGAATGA TGGCCTTATT GGTAAACAAA
msa277466.2{330_JM9130013}  TCGTGAATTT GAAGTAGTTG TTGAGAATGA TGGCCTTATT GGTAAACAAA
   msa277466.2{330_18RS21}  TCGTGAATTT GAAGTAGTTG TTGAGAATGA TGGCCTTATT GGTAAACAAA
     msa277466.2{330_2603}  TCGTGAATTT GAAGTAGTTG TTGAGAATGA TGGCCTTATT GGTAAACAAA
     msa277466.2{330_A909}  TCGTGAATTT GAAGTAGTTG TTGAGAATGA TGGCCTTATT GGTAAACAAA
     msa277466.2{330_H36B}  TCGTGAATTT GAAGTAGTTG TTGAGAATGA TGGCCTTATT GGTAAACAAA
   msa277466.2{330_CJB110}  TCGTGAATTT GAAGTAGTTG TTGAGAATGA TGGCCTTATT GGTAAACAAA
     msa277466.2{330_COH1}  TCGTGAATTT GAAGTAGTTG TTGAGAATGA TGGCCTTATT GGTAAACAAA
     msa277466.2{330_M732}  TCGTGAATTT GAAGTAGTTG TTGAGAATGA TGGCCTTATT GGTAAACAAA
   msa277466.2{330_1169NT}  TCGTGAATTT GAAGTAGTTG TTGAGAATGA TGGCCTTATT GGTAAACAAA
     msa277466.2{330_M781}  TCGTGAATTT GAAGTAGTTG TTGAGAATGA TGGCCTTATT GGTAAACAAA
                 Consensus  ********** ********** ********** ********** **********

                            551                                                600
      msa277466.2{330_090}  AAGGTGTAAA CATCCCTTAT ACTAAAATTC CTTTCCCAGC ACTTGCAGAA
msa277466.2{330_JM9130013}  AAGGTGTAAA CATCCCTTAT ACTAAAATTC CTTTCCCAGC ACTTGCAGAA
   msa277466.2{330_18RS21}  AAGGTGTAAA CATCCCTTAT ACTAAAATTC CTTTCCCAGC ACTTGCAGAA
     msa277466.2{330_2603}  AAGGTGTAAA CATCCCTTAT ACTAAAATTC CTTTCCCAGC ACTTGCAGAA
     msa277466.2{330_A909}  AAGGTGTAAA CATCCCTTAT ACTAAAATTC CTTTCCCAGC ACTTGCAGAA
     msa277466.2{330_H36B}  AAGGTGTAAA CATCCCTTAT ACTAAAATTC CTTTCCCAGC ACTTGCAGAA
   msa277466.2{330_CJB110}  AAGGTGTAAA CATCCCTTAT ACTAAAATTC CTTTCCCAGC ACTTGCAGAA
     msa277466.2{330_COH1}  AAGGTGTAAA CATCCCTTAT ACTAAAATTC CTTTCCCAGC ACTTGCAGAA
     msa277466.2{330_M732}  AAGGTGTAAA CATCCCTTAT ACTAAAATTC CTTTCCCAGC ACTTGCAGAA
   msa277466.2{330_1169NT}  AAGGTGTAAA CATCCCTTAT ACTAAAATTC CTTTCCCAGC ACTTGCAGAA
     msa277466.2{330_M781}  AAGGTGTAAA CATCCCTTAT ACTAAAATTC CTTTCCCAGC ACTTGCAGAA
                 Consensus  ********** ********** ********** ********** **********

                            601                                                650
      msa277466.2{330_090}  CGCGATAATG CTGATATCCG TTTTGGACTT GAgCAAGGAC TTAACTTTAT
msa277466.2{330_JM9130013}  CGCGATAATG CTGATATCCG TTTTGGACTT GAgCAAGGAC TTAACTTTAT
   msa277466.2{330_18RS21}  CGCGATAATG CTGATATCCG TTTTGGACTT GAgCAAGGAC TTAACTTTAT
     msa277466.2{330_2603}  CGCGATAATG CTGATATCCG TTTTGGACTT GAgCAAGGAC TTAACTTTAT
     msa277466.2{330_A909}  CGCGATAATG CTGATATCCG TTTTGGACTT GAgCAAGGAC TTAACTTTAT
     msa277466.2{330_H36B}  CGCGATAATG CTGATATCCG TTTTGGACTT GAgCAAGGAC TTAACTTTAT
   msa277466.2{330_CJB110}  CGCGATAATG CTGATATCCG TTTTGGACTT GAaCAAGGAC TTAACTTTAT
     msa277466.2{330_COH1}  CGCGATAATG CTGATATCCG TTTTGGACTT GAgCAAGGAC TTAACTTTAT
     msa277466.2{330_M732}  CGCGATAATG CTGATATCCG TTTTGGACTT GAgCAAGGAC TTAACTTTAT
   msa277466.2{330_1169NT}  CGCGATAATG CTGATATCCG TTTTGGACTT GAgCAAGGAC TTAACTTTAT
     msa277466.2{330_M781}  CGCGATAATG CTGATATCCG TTTTGGACTT GAgCAAGGAC TTAACTTTAT
                 Consensus  ********** ********** ********** **-******* **********

                            651                                                700
      msa277466.2{330_090}  TGCTATCTCA TTTGTACGTA CTGCTAAAGA TGTTAATGAA GTTCGTGCTA
msa277466.2{330_JM9130013}  TGCTATCTCA TTTGTACGTA CTGCTAAAGA TGTTAATGAA GTTCGTGCTA
   msa277466.2{330_18RS21}  TGCTATCTCA TTTGTACGTA CTGCTAAAGA TGTTAATGAA GTTCGTGCTA
     msa277466.2{330_2603}  TGCTATCTCA TTTGTACGTA CTGCTAAAGA TGTTAATGAA GTTCGTGCTA
     msa277466.2{330_A909}  TGCTATCTCA TTTGTACGTA CTGCTAAAGA TGTTAATGAA GTTCGTGCTA
     msa277466.2{330_H36B}  TGCTATCTCA TTTGTACGTA CTGCTAAAGA TGTTAATGAA GTTCGTGCTA
   msa277466.2{330_CJB110}  TGCTATCTCA TTTGTACGTA CTGCTAAAGA TGTTAATGAA GTTCGTGCTA
     msa277466.2{330_COH1}  TGCTATCTCA TTTGTACGTA CTGCTAAAGA TGTTAATGAA GTTCGTGCTA
     msa277466.2{330_M732}  TGCTATCTCA TTTGTACGTA CTGCTAAAGA TGTTAATGAA GTTCGTGCTA
   msa277466.2{330_1169NT}  TGCTATCTCA TTTGTACGTA CTGCTAAAGA TGTTAATGAA GTTCGTGCTA
     msa277466.2{330_M781}  TGCTATCTCA TTTGTACGTA CTGCTAAAGA TGTTAATGAA GTTCGTGCTA
                 Consensus  ********** ********** ********** ********** **********

                            701                                                750
      msa277466.2{330_090}  TTTGTGAAGA AACTGGcaAT GGACAtGTTA AGTTGTTTGC TAAAATTGAA
msa277466.2{330_JM9130013}  TTTGTGAAGA AACTGGcaAT GGACAtGTTA AGTTGTTTGC TAAAATTGAA
   msa277466.2{330_18RS21}  TTTGTGAAGA AACTGGcaAT GGACAcGTTA AGTTGTTTGC TAAAATTGAA
     msa277466.2{330_2603}  TTTGTGAAGA AACTGGsmAT GGACAcGTTA AGTTGTTTGC TAAAATTGAA
     msa277466.2{330_A909}  TTTGTGAAGA AACTGGcaAT GGACAcGTTA AGTTGTTTGC TAAAATTGAA
     msa277466.2{330_H36B}  TTTGTGAAGA AACTGGcaAT GGACAcGTTA AGTTGTTTGC TAAAATTGAA
   msa277466.2{330_CJB110}  TTTGTGAAGA AACTGGcaAT GGACAcGTTA AGTTGTTTGC TAAAATTGAA
     msa277466.2{330_COH1}  TTTGTGAAGA AACTGGcaAT GGACAcGTTA AGTTGTTTGC TAAAATTGAA
     msa277466.2{330_M732}  TTTGTGAAGA AACTGGcaAT GGACAcGTTA AGTTGTTTGC TAAAATTGAA
   msa277466.2{330_1169NT}  TTTGTGAAGA AACTGGcaAT GGACAcGTTA AGTTGTTTGC TAAAATTGAA
     msa277466.2{330_M781}  TTTGTGAAGA AACTGGcaAT GGACAcGTTA AGTTGTTTGC TAAAATTGAA
                 Consensus  ********** ******--** *****-**** ********** **********
```

Table 72: Comparative Sequences relating to SAG0941

```
                                751                                                 800
      msa277466.2{330_090}      AATCAACAAG GTATCGATAA TATTGATGAG ATTATCGAAG CAGCAGATGG
msa277466.2{330_JM9130013}      AATCAACAAG GTATCGATAA TATTGATGAG ATTATCGAAG CAGCAGATGG
    msa277466.2{330_18RS21}     AATCAACAAG GTATCGATAA TATTGATGAG ATTATCGAAG CAGCAGATGG
      msa277466.2{330_2603}     AATCAACAAG GTATCGATAA TATTGATGAG ATTATCGAAG CAGCAGATGG
      msa277466.2{330_A909}     AATCAACAAG GTATCGATAA TATTGATGAG ATTATCGAAG CAGCAGATGG
      msa277466.2{330_H36B}     AATCAACAAG GTATCGATAA TATTGATGAG ATTATCGAAG CAGCAGATGG
    msa277466.2{330_CJB110}     AATCAACAAG GTATCGATAA TATTGATGAG ATTATCGAAG CAGCAGATGG
      msa277466.2{330_COH1}     AATCAACAAG GTATCGATAA TATTGATGAG ATTATCGAAG CAGCAGATGG
      msa277466.2{330_M732}     AATCAACAAG GTATCGATAA TATTGATGAG ATTATCGAAG CAGCAGATGG
    msa277466.2{330_1169NT}     AATCAACAAG GTATCGATAA TATTGATGAG ATTATCGAAG CAGCAGATGG
      msa277466.2{330_M781}     AATCAACAAG GTATCGATAA TATTGATGAG ATTATCGAAG CAGCAGATGG
                  Consensus     ********** ********** ********** ********** **********

                                801                                                 850
      msa277466.2{330_090}      TATTATGATT GCTCGTGGTG ATATGGGTAT CGAAGTTCCA TTTGAAATGG
msa277466.2{330_JM9130013}      TATTATGATT GCTCGTGGTG ATATGGGTAT CGAAGTTCCA TTTGAAATGG
    msa277466.2{330_18RS21}     TATTATGATT GCTCGTGGTG ATATGGGTAT CGAAGTTCCA TTTGAAATGG
      msa277466.2{330_2603}     TATTATGATT GCTCGTGGTG ATATGGGTAT CGAAGTTCCA TTTGAAATGG
      msa277466.2{330_A909}     TATTATGATT GCTCGTGGTG ATATGGGTAT CGAAGTTCCA TTTGAAATGG
      msa277466.2{330_H36B}     TATTATGATT GCTCGTGGTG ATATGGGTAT CGAAGTTCCA TTTGAAATGG
    msa277466.2{330_CJB110}     TATTATGATT GCTCGTGGTG ATATGGGTAT CGAAGTTCCA TTTGAAATGG
      msa277466.2{330_COH1}     TATTATGATT GCTCGTGGTG ATATGGGTAT CGAAGTTCCA TTTGAAATGG
      msa277466.2{330_M732}     TATTATGATT GCTCGTGGTG ATATGGGTAT CGAAGTTCCA TTTGAAATGG
    msa277466.2{330_1169NT}     TATTATGATT GCTCGTGGTG ATATGGGTAT CGAAGTTCCA TTTGAAATGG
      msa277466.2{330_M781}     TATTATGATT GCTCGTGGTG ATATGGGTAT CGAAGTTCCA TTTGAAATGG
                  Consensus     ********** ********** ********** ********** **********

                                851                                                 900
      msa277466.2{330_090}      TTCCAGTTTA CCAAAAAATG ATCATTACTA AAGTTAATGC AGCTGGTAAA
msa277466.2{330_JM9130013}      TTCCAGTTTA CCAAAAAATG ATCATTACTA AAGTTAATGC AGCTGGTAAA
    msa277466.2{330_18RS21}     TTCCAGTTTA CCAAAAAATG ATCATTACTA AAGTTAATGC AGCTGGTAAA
      msa277466.2{330_2603}     TTCCAGTTTA CCAAAAAATG ATCATTACTA AAGTTAATGC AGCTGGTAAA
      msa277466.2{330_A909}     TTCCAGTTTA CCAAAAAATG ATCATTACTA AAGTTAATGC AGCTGGTAAA
      msa277466.2{330_H36B}     TTCCAGTTTA CCAAAAAATG ATCATTACTA AAGTTAATGC AGCTGGTAAA
    msa277466.2{330_CJB110}     TTCCAGTTTA CCAAAAAATG ATCATTACTA AAGTTAATGC AGCTGGTAAA
      msa277466.2{330_COH1}     TTCCAGTTTA CCAAAAAATG ATCATTACTA AAGTTAATGC AGCTGGTAAA
      msa277466.2{330_M732}     TTCCAGTTTA CCAAAAAATG ATCATTACTA AAGTTAATGC AGCTGGTAAA
    msa277466.2{330_1169NT}     TTCCAGTTTA CCAAAAAATG ATCATTACTA AAGTTAATGC AGCTGGTAAA
      msa277466.2{330_M781}     TTCCAGTTTA CCAAAAAATG ATCATTACTA AAGTTAATGC AGCTGGTAAA
                  Consensus     ********** ********** ********** ********** **********

                                901                                                 950
      msa277466.2{330_090}      GCAGTTATTA CAGCAACAAA TATGCTTGAA ACAATGACTG ATAAACCACG
msa277466.2{330_JM9130013}      GCAGTTATTA CAGCAACAAA TATGCTTGAA ACAATGACTG ATAAACCACG
    msa277466.2{330_18RS21}     GCAGTTATTA CAGCAACAAA TATGCTTGAA ACAATGACTG ATAAACCACG
      msa277466.2{330_2603}     GCAGTTATTA CAGCAACAAA TATGCTTGAA ACAATGACTG ATAAACCACG
      msa277466.2{330_A909}     GCAGTTATTA CAGCAACAAA TATGCTTGAA ACAATGACTG ATAAACCACG
      msa277466.2{330_H36B}     GCAGTTATTA CAGCAACAAA TATGCTTGAA ACAATGACTG ATAAACCACG
    msa277466.2{330_CJB110}     GCAGTTATTA CAGCAACAAA TATGCTTGAA ACAATGACTG ATAAACCACG
      msa277466.2{330_COH1}     GCAGTTATTA CAGCAACAAA TATGCTTGAA ACAATGACTG ATAAACCACG
      msa277466.2{330_M732}     GCAGTTATTA CAGCAACAAA TATGCTTGAA ACAATGACTG ATAAACCACG
    msa277466.2{330_1169NT}     GCAGTTATTA CAGCAACAAA TATGCTTGAA ACAATGACTG ATAAACCACG
      msa277466.2{330_M781}     GCAGTTATTA CAGCAACAAA TATGCTTGAA ACAATGACTG ATAAACCACG
                  Consensus     ********** ********** ********** ********** **********

                                951                                                1000
      msa277466.2{330_090}      TGCGACTCGT TCAGAAGTAT CTGATGTCTT CAATGCTGTT ATTGATGGTA
msa277466.2{330_JM9130013}      TGCGACTCGT TCAGAAGTAT CTGATGTCTT CAATGCTGTT ATTGATGGTA
    msa277466.2{330_18RS21}     TGCGACTCGT TCAGAAGTAT CTGATGTCTT CAATGCTGTT ATTGATGGTA
      msa277466.2{330_2603}     TGCGACTCGT TCAGAAGTAT CTGATGTCTT CAATGCTGTT ATTGATGGTA
      msa277466.2{330_A909}     TGCGACTCGT TCAGAAGTAT CTGATGTCTT CAATGCTGTT ATTGATGGTA
      msa277466.2{330_H36B}     TGCGACTCGT TCAGAAGTAT CTGATGTCTT CAATGCTGTT ATTGATGGTA
    msa277466.2{330_CJB110}     TGCGACTCGT TCAGAAGTAT CTGATGTCTT CAATGCTGTT ATTGATGGTA
      msa277466.2{330_COH1}     TGCGACTCGT TCAGAAGTAT CTGATGTCTT CAATGCTGTT ATTGATGGTA
      msa277466.2{330_M732}     TGCGACTCGT TCAGAAGTAT CTGATGTCTT CAATGCTGTT ATTGATGGTA
    msa277466.2{330_1169NT}     TGCGACTCGT TCAGAAGTAT CTGATGTCTT CAATGCTGTT ATTGATGGTA
      msa277466.2{330_M781}     TGCGACTCGT TCAGAAGTAT CTGATGTCTT CAATGCTGTT ATTGATGGTA
                  Consensus     ********** ********** ********** ********** **********

                                1001                                               1050
      msa277466.2{330_090}      CTGATGCTAC AATGCTTTCA GGTGAGTCAG CTAATGGTAA ATACCCAGTT
msa277466.2{330_JM9130013}      CTGATGCTAC AATGCTTTCA GGTGAGTCAG CTAATGGTAA ATACCCAGTT
    msa277466.2{330_18RS21}     CTGATGCTAC AATGCTTTCA GGTGAGTCAG CTAATGGTAA ATACCCAGTT
      msa277466.2{330_2603}     CTGATGCTAC AATGCTTTCA GGTGAGTCAG CTAATGGTAA ATACCCAGTT
      msa277466.2{330_A909}     CTGATGCTAC AATGCTTTCA GGTGAGTCAG CTAATGGTAA ATACCCAGTT
      msa277466.2{330_H36B}     CTGATGCTAC AATGCTTTCA GGTGAGTCAG CTAATGGTAA ATACCCAGTT
    msa277466.2{330_CJB110}     CTGATGCTAC AATGCTTTCA GGTGAGTCAG CTAATGGTAA ATACCCAGTT
      msa277466.2{330_COH1}     CTGATGCTAC AATGCTTTCA GGTGAGTCAG CTAATGGTAA ATACCCAGTT
      msa277466.2{330_M732}     CTGATGCTAC AATGCTTTCA GGTGAGTCAG CTAATGGTAA ATACCCAGTT
    msa277466.2{330_1169NT}     CTGATGCTAC AATGCTTTCA GGTGAGTCAG CTAATGGTAA ATACCCAGTT
      msa277466.2{330_M781}     CTGATGCTAC AATGCTTTCA GGTGAGTCAG CTAATGGTAA ATACCCAGTT
                  Consensus     ********** ********** ********** ********** **********
```

Table 72: Comparative Sequences relating to SAG0941

```
                                 1051                                                  1100
         msa277466.2{330_090}    GAGTCAGTTC GTACAATGGC TACTATTGAT AAAAATGCTC AAACATTACT
    msa277466.2{330_JM9130013}   GAGTCAGTTC GTACAATGGC TACTATTGAT AAAAATGCTC AAACATTACT
       msa277466.2{330_18RS21}   GAGTCAGTTC GTACAATGGC TACTATTGAT AAAAATGCTC AAACATTACT
         msa277466.2{330_2603}   GAGTCAGTTC GTACAATGGC TACTATTGAT AAAAATGCTC AAACATTACT
         msa277466.2{330_A909}   GAGTCAGTTC GTACAATGGC TACTATTGAT AAAAATGCTC AAACATTACT
         msa277466.2{330_H36B}   GAGTCAGTTC GTACAATGGC TACTATTGAT AAAAATGCTC AAACATTACT
       msa277466.2{330_CJB110}   GAGTCAGTTC GTACAATGGC TACTATTGAT AAAAATGCTC AAACATTACT
         msa277466.2{330_COH1}   GAGTCAGTTC GTACAATGGC TACTATTGAT AAAAATGCTC AAACATTACT
         msa277466.2{330_M732}   GAGTCAGTTC GTACAATGGC TACTATTGAT AAAAATGCTC AAACATTACT
       msa277466.2{330_1169NT}   GAGTCAGTTC GTACAATGGC TACTATTGAT AAAAATGCTC AAACATTACT
         msa277466.2{330_M781}   GAGTCAGTTC GTACAATGGC TACTATTGAT AAAAATGCTC AAACATTACT
                     Consensus   ********** ********** ********** ********** **********

                                 1101                                                  1150
         msa277466.2{330_090}    CAATGAGTAT GGTCGcTTAG ACTCATCTGC ATTCCCACGT AATAACAAAA
    msa277466.2{330_JM9130013}   CAATGAGTAT GGTCGcTTAG ACTCATCTGC ATTCCCACGT AATAACAAAA
       msa277466.2{330_18RS21}   CAATGAGTAT GGTCGcTTAG ACTCATCTGC ATTCCCACGT AATAACAAAA
         msa277466.2{330_2603}   CAATGAGTAT GGTCGcTTAG ACTCATCTGC ATTCCCACGT AATAACAAAA
         msa277466.2{330_A909}   CAATGAGTAT GGTCGcTTAG ACTCATCTGC ATTCCCACGT AATAACAAAA
         msa277466.2{330_H36B}   CAATGAGTAT GGTCGcTTAG ACTCATCTGC ATTCCCACGT AATAACAAAA
       msa277466.2{330_CJB110}   CAATGAGTAT GGTCGcTTAG ACTCATCTGC ATTCCCACGT AATAACAAAA
         msa277466.2{330_COH1}   CAATGAGTAT GGTCGcTTAG ACTCATCTGC ATTCCCACGT AATAACAAAA
         msa277466.2{330_M732}   CAATGAGTAT GGTCGcTTAG ACTCATCTGC ATTCCCACGT AATAACAAAA
       msa277466.2{330_1169NT}   CAATGAGTAT GGTCGtTTAG ACTCATCTGC ATTCCCACGT AATAACAAAA
         msa277466.2{330_M781}   CAATGAGTAT GGTCGcTTAG ACTCATCTGC ATTCCCACGT AATAACAAAA
                     Consensus   ********** *****-**** ********** ********** **********

                                 1151                                                  1200
         msa277466.2{330_090}    CTGATGTTAT TGCATCTGCG GTTAAAGATG CAACACACTC AATGGATATC
    msa277466.2{330_JM9130013}   CTGATGTTAT TGCATCTGCG GTTAAAGATG CAACACACTC AATGGATATC
       msa277466.2{330_18RS21}   CTGATGTTAT TGCATCTGCG GTTAAAGATG CAACACACTC AATGGATATC
         msa277466.2{330_2603}   CTGATGTTAT TGCATCTGCG GTTAAAGATG CAACACACTC AATGGATATC
         msa277466.2{330_A909}   CTGATGTTAT TGCATCTGCG GTTAAAGATG CAACACACTC AATGGATATC
         msa277466.2{330_H36B}   CTGATGTTAT TGCATCTGCG GTTAAAGATG CAACACACTC AATGGATATC
       msa277466.2{330_CJB110}   CTGATGTTAT TGCATCTGCG GTTAAAGATG CAACACACTC AATGGATATC
         msa277466.2{330_COH1}   CTGATGTTAT TGCATCTGCG GTTAAAGATG CAACACACTC AATGGATATC
         msa277466.2{330_M732}   CTGATGTTAT TGCATCTGCG GTTAAAGATG CAACACACTC AATGGATATC
       msa277466.2{330_1169NT}   CTGATGTTAT TGCATCTGCG GTTAAAGATG CAACACACTC AATGGATATC
         msa277466.2{330_M781}   CTGATGTTAT TGCATCTGCG GTTAAAGATG CAACACACTC AATGGATATC
                     Consensus   ********** ********** ********** ********** **********

                                 1201                                                  1250
         msa277466.2{330_090}    AAACTTGTTG TgACAATTAC TGAAACAGGT AATACAGCTC GTGCCATTTC
    msa277466.2{330_JM9130013}   AAACTTGTTG TgACAATTAC TGAAACAGGT AATACAGCTC GTGCCATTTC
       msa277466.2{330_18RS21}   AAACTTGTTG TaACAATTAC TGAAACAGGT AATACAGCTC GTGCCATTTC
         msa277466.2{330_2603}   AAACTTGTTG TaACAATTAC TGAAACAGGT AATACAGCTC GTGCCATTTC
         msa277466.2{330_A909}   AAACTTGTTG TaACAATTAC TGAAACAGGT AATACAGCTC GTGCCATTTC
         msa277466.2{330_H36B}   AAACTTGTTG TaACAATTAC TGAAACAGGT AATACAGCTC GTGCCATTTC
       msa277466.2{330_CJB110}   AAACTTGTTG TaACAATTAC TGAAACAGGT AATACAGCTC GTGCCATTTC
         msa277466.2{330_COH1}   AAACTTGTTG TaACAATTAC TGAAACAGGT AATACAGCTC GTGCCATTTC
         msa277466.2{330_M732}   AAACTTGTTG TaACAATTAC TGAAACAGGT AATACAGCTC GTGCCATTTC
       msa277466.2{330_1169NT}   AAACTTGTTG TaACAATTAC TGAAACAGGT AATACAGCTC GTGCCATTTC
         msa277466.2{330_M781}   AAACTTGTTG TaACAATTAC TGAAACAGGT AATACAGCTC GTGCCATTTC
                     Consensus   ********** *-******** ********** ********** **********

                                 1251                                                  1300
         msa277466.2{330_090}    TAAaTTCCGT CCAGATGCAG ACATTTTGGC TGTTACATTT GATGAAAAAG
    msa277466.2{330_JM9130013}   TAAaTTCCGT CCAGATGCAG ACATTTTGGC TGTTACATTT GATGAAAAAG
       msa277466.2{330_18RS21}   TAAaTTCCGT CCAGATGCAG ACATTTTGGC TGTTACATTT GATGAAAAAG
         msa277466.2{330_2603}   TAAaTTCCGT CCAGATGCAG ACATTTTGGC TGTTACATTT GATGAAAAAG
         msa277466.2{330_A909}   TAAaTTCCGT CCAGATGCAG ACATTTTGGC TGTTACATTT GATGAAAAAG
         msa277466.2{330_H36B}   TAAaTTCCGT CCAGATGCAG ACATTTTGGC TGTTACATTT GATGAAAAAG
       msa277466.2{330_CJB110}   TAAaTTCCGT CCAGATGCAG ACATTTTGGC TGTTACATTT GATGAAAAAG
         msa277466.2{330_COH1}   TAAaTTCCGT CCAGATGCAG ACATTTTGGC TGTTACATTT GATGAAAAAG
         msa277466.2{330_M732}   TAAaTTCCGT CCAGATGCAG ACATTTTGGC TGTTACATTT GATGAAAAAG
       msa277466.2{330_1169NT}   TAAaTTCCGT CCAGATGCAG ACATTTTGGC TGTTACATTT GATGAAAAAG
         msa277466.2{330_M781}   TAAgTTCCGT CCAGATGCAG ACATTTTGGC TGTTACATTT GATGAAAAAG
                     Consensus   ***-****** ********** ********** ********** **********

                                 1301                                                  1350
         msa277466.2{330_090}    TACAACGTTC ATTGATGATT AACTGGGGTG TTATCCCTGT CCTTGCAGAC
    msa277466.2{330_JM9130013}   TACAACGTTC ATTGATGATT AACTGGGGTG TTATCCCTGT CCTTGCAGAC
       msa277466.2{330_18RS21}   TACAACGTTC ATTGATGATT AACTGGGGTG TTATCCCTGT CCTTGCAGAC
         msa277466.2{330_2603}   TACAACGTTC ATTGATGATT AACTGGGGTG TTATCCCTGT CCTTGCAGAC
         msa277466.2{330_A909}   TACAACGTTC ATTGATGATT AACTGGGGTG TTATCCCTGT CCTTGCAGAC
         msa277466.2{330_H36B}   TACAACGTTC ATTGATGATT AACTGGGGTG TTATCCCTGT CCTTGCAGAC
       msa277466.2{330_CJB110}   TACAACGTTC ATTGATGATT AACTGGGGTG TTATCCCTGT CCTTGCAGAC
         msa277466.2{330_COH1}   TACAACGTTC ATTGATGATT AACTGGGGTG TTATCCCTGT CCTTGCAGAC
         msa277466.2{330_M732}   TACAACGTTC ATTGATGATT AACTGGGGTG TTATCCCTGT CCTTGCAGAC
       msa277466.2{330_1169NT}   TACAACGTTC ATTGATGATT AACTGGGGTG TTATCCCTGT CCTTGCAGAC
         msa277466.2{330_M781}   TACAACGTTC ATTGATGATT AACTGGGGTG TTATCCCTGT CCTTGCAGAC
```

Table 72: Comparative Sequences relating to SAG0941

```
                Consensus  ********** ********** ********** ********** **********

                           1351                                              1400
      msa277466.2{330_090} AAACCAGCAT CTACAGATGA TATGTTTGAG GTTGCAGAAC GTGTAGCACT
msa277466.2{330_JM9130013} AAACCAGCAT CTACAGATGA TATGTTTGAG GTTGCAGAAC GTGTAGCACT
   msa277466.2{330_18RS21} AAACCAGCAT CTACAGATGA TATGTTTGAG GTTGCAGAAC GTGTAGCACT
     msa277466.2{330_2603} AAACCAGCAT CTACAGATGA TATGTTTGAG GTTGCAGAAC GTGTAGCACT
     msa277466.2{330_A909} AAACCAGCAT CTACAGATGA TATGTTTGAG GTTGCAGAAC GTGTAGCACT
     msa277466.2{330_H36B} AAACCAGCAT CTACAGATGA TATGTTTGAG GTTGCAGAAC GTGTAGCACT
   msa277466.2{330_CJB110} AAACCAGCAT CTACAGATGA TATGTTTGAG GTTGCAGAAC GTGTAGCACT
     msa277466.2{330_COH1} AAACCAGCAT CTACAGATGA TATGTTTGAG GTTGCAGAAC GTGTAGCACT
     msa277466.2{330_M732} AAACCAGCAT CTACAGATGA TATGTTTGAG GTTGCAGAAC GTGTAGCACT
   msa277466.2{330_1169NT} AAACCAGCAT CTACAGATGA TATGTTTGAG GTTGCAGAAC GTGTAGCACT
     msa277466.2{330_M781} AAACCAGCAT CTACAGATGA TATGTTTGAG GTTGCAGAAC GTGTAGCACT
                Consensus  ********** ********** ********** ********** **********

                           1401                                              1450
      msa277466.2{330_090} TGAAGCAGGA cTTGTTGAAT CAGGCGATAA TATCGTTATC GTTGCAGGTG
msa277466.2{330_JM9130013} TGAAGCAGGA cTTGTTGAAT CAGGCGATAA TATCGTTATC GTTGCAGGTG
   msa277466.2{330_18RS21} TGAAGCAGGA tTTGTTGAAT CAGGCGATAA TATCGTTATC GTTGCAGGTG
     msa277466.2{330_2603} TGAAGCAGGA tTTGTTGAAT CAGGCGATAA TATCGTTATC GTTGCAGGTG
     msa277466.2{330_A909} TGAAGCAGGA tTTGTTGAAT CAGGCGATAA TATCGTTATC GTTGCAGGTG
     msa277466.2{330_H36B} TGAAGCAGGA tTTGTTGAAT CAGGCGATAA TATCGTTATC GTTGCAGGTG
   msa277466.2{330_CJB110} TGAAGCAGGA tTTGTTGAAT CAGGCGATAA TATCGTTATC GTTGCAGGTG
     msa277466.2{330_COH1} TGAAGCAGGA cTTGTTGAAT CAGGCGATAA TATCGTTATC GTTGCAGGTG
     msa277466.2{330_M732} TGAAGCAGGA cTTGTTGAAT CAGGCGATAA TATCGTTATC GTTGCAGGTG
   msa277466.2{330_1169NT} TGAAGCAGGA cTTGTTGAAT CAGGCGATAA TATCGTTATC GTTGCAGGTG
     msa277466.2{330_M781} TGAAGCAGGA cTTGTTGAAT CAGGCGATAA TATCGTTATC GTTGCAGGTG
                Consensus  ********** _********* ********** ********** **********

                           1451                                              1500
      msa277466.2{330_090} TTCCTGTAGG TACAGGTGGA ACTAACACAA TGCGTGTTCG TACTGTTAAA
msa277466.2{330_JM9130013} TTCCTGTAGG TACAGGTGGA ACTAACACAA TGCGTGTTCG TACTGTTAAA
   msa277466.2{330_18RS21} TTCCTGTAGG TACAGGTGGA ACTAACACAA TGCGTGTTCG TACTGTTAAA
     msa277466.2{330_2603} TTCCTGTAGG TACAGGTGGA ACTAACACAA TGCGTGTTCG TACTGTTAAA
     msa277466.2{330_A909} TTCCTGTAGG TACAGGTGGA ACTAACACAA TGCGTGTTCG TACTGTTAAA
     msa277466.2{330_H36B} TTCCTGTAGG TACAGGTGGA ACTAACACAA TGCGTGTTCG TACTGTTAAA
   msa277466.2{330_CJB110} TTCCTGTAGG TACAGGTGGA ACTAACACAA TGCGTGTTCG TACTGTTAAA
     msa277466.2{330_COH1} TTCCTGTAGG TACAGGTGGA ACTAACACAA TGCGTGTTCG TACTGTTAAA
     msa277466.2{330_M732} TTCCTGTAGG TACAGGTGGA ACTAACACAA TGCGTGTTCG TACTGTTAAA
   msa277466.2{330_1169NT} TTCCTGTAGG TACAGGTGGA ACTAACACAA TGCGTGTTCG TACTGTTAAA
     msa277466.2{330_M781} TTCCTGTAGG TACAGGTGGA ACTAACACAA TGCGTGTTCG TACTGTTAAA
                Consensus  ********** ********** ********** ********** **********
```

SEQ ID NO. 7212
STRAIN 2603 frame: 1
MNKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHG
DHAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDGADFHSYTTGTKLRVATKQ
GIKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVVENDGLI
GKQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGX
GHVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGK
AVITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATID
KNAQTLLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFR
PDADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIVI
VAGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7213
STRAIN 090 frame: 1
NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDGSDFHSYTTGTELRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVVENDGLIG
KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFRP
DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7214
STRAIN A909 frame: 1
NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDGADFHSYTTGTKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVVENDGLIG
KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFRP
DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIVIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7215
STRAIN H36B frame: 1

Table 72: Comparative Sequences relating to SAG0941

NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDGADFHSYTTGTKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVVENDGLIG
KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFRP
DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIVIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7216
STRAIN 18RS21 frame: 1
NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDGADFHSYTTGTKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVVENDGLIG
KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFRP
DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIVIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7217
STRAIN M732 frame: 1
NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDGADFHSYTTGTKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVVENDGLIG
KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFRP
DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7218
STRAIN COH1 frame: 1
NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDGADFHSYTTGTKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVVENDGLIG
KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFRP
DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7219
STRAIN M781 frame: 1
NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDGADFHSYTTGTKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVVENDGLIG
KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFRP
DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7220
STRAIN CJB110 frame: 1
NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDGADFHSYTTGTKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVVENDGLIG
KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFRP
DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIVIV
AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7221
STRAIN 1169NT frame: 1
NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDGADFHSYTTGTKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVVENDGLIG
KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFRP
DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
AGVPVGTGGTNTMRVRTVK

Table 72: Comparative Sequences relating to SAG0941

SEQ ID NO. 7222
STRAIN JM9130013 frame: 1
NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDGSDFHSYTTGTKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVVENDGLIG
KQKGVNIPYTKIPFPALAERDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRLDSSAFPRNNKTDVIASAVKDATHSMDIKLVVTITETGNTARAISKFRP
DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
AGVPVGTGGTNTMRVRTVK

```
PRETTY of: /biotmp/msa277662.2{*}   February 24, 2003 01:49  ..

                            1                                                  50
   msa277662.2{330_18RS21}  ~NKRVKIVAT LGPAVEFRGG KKFGESGYWG ESLDVEASAE KIAQLIKEGA
     msa277662.2{330_A909}  ~NKRVKIVAT LGPAVEFRGG KKFGESGYWG ESLDVEASAE KIAQLIKEGA
   msa277662.2{330_CJB110}  ~NKRVKIVAT LGPAVEFRGG KKFGESGYWG ESLDVEASAE KIAQLIKEGA
     msa277662.2{330_H36B}  ~NKRVKIVAT LGPAVEFRGG KKFGESGYWG ESLDVEASAE KIAQLIKEGA
   msa277662.2{330_1169NT}  ~NKRVKIVAT LGPAVEFRGG KKFGESGYWG ESLDVEASAE KIAQLIKEGA
     msa277662.2{330_COH1}  ~NKRVKIVAT LGPAVEFRGG KKFGESGYWG ESLDVEASAE KIAQLIKEGA
     msa277662.2{330_M732}  ~NKRVKIVAT LGPAVEFRGG KKFGESGYWG ESLDVEASAE KIAQLIKEGA
     msa277662.2{330_M781}  ~NKRVKIVAT LGPAVEFRGG KKFGESGYWG ESLDVEASAE KIAQLIKEGA
msa277662.2{330_JM9130013}  ~NKRVKIVAT LGPAVEFRGG KKFGESGYWG ESLDVEASAE KIAQLIKEGA
      msa277662.2{330_090}  ~NKRVKIVAT LGPAVEFRGG KKFGESGYWG ESLDVEASAE KIAQLIKEGA
     msa277662.2{330_2603}  mNKRVKIVAT LGPAVEFRGG KKFGESGYWG ESLDVEASAE KIAQLIKEGA
                 Consensus  ********** ********** ********** ********** **********

                            51                                                100
   msa277662.2{330_18RS21}  NVFRFNFSHG DHAEQGARMA TVRKAEEIAG QKVGFLLDTK GPEIRTELFE
     msa277662.2{330_A909}  NVFRFNFSHG DHAEQGARMA TVRKAEEIAG QKVGFLLDTK GPEIRTELFE
   msa277662.2{330_CJB110}  NVFRFNFSHG DHAEQGARMA TVRKAEEIAG QKVGFLLDTK GPEIRTELFE
     msa277662.2{330_H36B}  NVFRFNFSHG DHAEQGARMA TVRKAEEIAG QKVGFLLDTK GPEIRTELFE
   msa277662.2{330_1169NT}  NVFRFNFSHG DHAEQGARMA TVRKAEEIAG QKVGFLLDTK GPEIRTELFE
     msa277662.2{330_COH1}  NVFRFNFSHG DHAEQGARMA TVRKAEEIAG QKVGFLLDTK GPEIRTELFE
     msa277662.2{330_M732}  NVFRFNFSHG DHAEQGARMA TVRKAEEIAG QKVGFLLDTK GPEIRTELFE
     msa277662.2{330_M781}  NVFRFNFSHG DHAEQGARMA TVRKAEEIAG QKVGFLLDTK GPEIRTELFE
msa277662.2{330_JM9130013}  NVFRFNFSHG DHAEQGARMA TVRKAEEIAG QKVGFLLDTK GPEIRTELFE
      msa277662.2{330_090}  NVFRFNFSHG DHAEQGARMA TVRKAEEIAG QKVGFLLDTK GPEIRTELFE
     msa277662.2{330_2603}  NVFRFNFSHG DHAEQGARMA TVRKAEEIAG QKVGFLLDTK GPEIRTELFE
                 Consensus  ********** ********** ********** ********** **********

                            101                                               150
   msa277662.2{330_18RS21}  DGaDFHSYTT GTkLRVATKQ GIKSTPEVIA LNVAGGLDIF DDVEVGKQIL
     msa277662.2{330_A909}  DGaDFHSYTT GTkLRVATKQ GIKSTPEVIA LNVAGGLDIF DDVEVGKQIL
   msa277662.2{330_CJB110}  DGaDFHSYTT GTkLRVATKQ GIKSTPEVIA LNVAGGLDIF DDVEVGKQIL
     msa277662.2{330_H36B}  DGaDFHSYTT GTkLRVATKQ GIKSTPEVIA LNVAGGLDIF DDVEVGKQIL
   msa277662.2{330_1169NT}  DGaDFHSYTT GTkLRVATKQ GIKSTPEVIA LNVAGGLDIF DDVEVGKQIL
     msa277662.2{330_COH1}  DGaDFHSYTT GTkLRVATKQ GIKSTPEVIA LNVAGGLDIF DDVEVGKQIL
     msa277662.2{330_M732}  DGaDFHSYTT GTkLRVATKQ GIKSTPEVIA LNVAGGLDIF DDVEVGKQIL
     msa277662.2{330_M781}  DGaDFHSYTT GTkLRVATKQ GIKSTPEVIA LNVAGGLDIF DDVEVGKQIL
msa277662.2{330_JM9130013}  DGsDFHSYTT GTkLRVATKQ GIKSTPEVIA LNVAGGLDIF DDVEVGKQIL
      msa277662.2{330_090}  DGsDFHSYTT GTeLRVATKQ GIKSTPEVIA LNVAGGLDIF DDVEVGKQIL
     msa277662.2{330_2603}  DGaDFHSYTT GTkLRVATKQ GIKSTPEVIA LNVAGGLDIF DDVEVGKQIL
                 Consensus  **_******* **_******* ********** ********** **********

                            151                                               200
   msa277662.2{330_18RS21}  VDDGKLGLTV FAKDKDTREF EVVVENDGLI GKQKGVNIPY TKIPFPALAE
     msa277662.2{330_A909}  VDDGKLGLTV FAKDKDTREF EVVVENDGLI GKQKGVNIPY TKIPFPALAE
   msa277662.2{330_CJB110}  VDDGKLGLTV FAKDKDTREF EVVVENDGLI GKQKGVNIPY TKIPFPALAE
     msa277662.2{330_H36B}  VDDGKLGLTV FAKDKDTREF EVVVENDGLI GKQKGVNIPY TKIPFPALAE
   msa277662.2{330_1169NT}  VDDGKLGLTV FAKDKDTREF EVVVENDGLI GKQKGVNIPY TKIPFPALAE
     msa277662.2{330_COH1}  VDDGKLGLTV FAKDKDTREF EVVVENDGLI GKQKGVNIPY TKIPFPALAE
     msa277662.2{330_M732}  VDDGKLGLTV FAKDKDTREF EVVVENDGLI GKQKGVNIPY TKIPFPALAE
     msa277662.2{330_M781}  VDDGKLGLTV FAKDKDTREF EVVVENDGLI GKQKGVNIPY TKIPFPALAE
msa277662.2{330_JM9130013}  VDDGKLGLTV FAKDKDTREF EVVVENDGLI GKQKGVNIPY TKIPFPALAE
      msa277662.2{330_090}  VDDGKLGLTV FAKDKDTREF EVVVENDGLI GKQKGVNIPY TKIPFPALAE
     msa277662.2{330_2603}  VDDGKLGLTV FAKDKDTREF EVVVENDGLI GKQKGVNIPY TKIPFPALAE
                 Consensus  ********** ********** ********** ********** **********

                            201                                               250
   msa277662.2{330_18RS21}  RDNADIRFGL EQGLNFIAIS FVRTAKDVNE VRAICEETGn GHVKLFAKIE
     msa277662.2{330_A909}  RDNADIRFGL EQGLNFIAIS FVRTAKDVNE VRAICEETGn GHVKLFAKIE
   msa277662.2{330_CJB110}  RDNADIRFGL EQGLNFIAIS FVRTAKDVNE VRAICEETGn GHVKLFAKIE
     msa277662.2{330_H36B}  RDNADIRFGL EQGLNFIAIS FVRTAKDVNE VRAICEETGn GHVKLFAKIE
   msa277662.2{330_1169NT}  RDNADIRFGL EQGLNFIAIS FVRTAKDVNE VRAICEETGn GHVKLFAKIE
     msa277662.2{330_COH1}  RDNADIRFGL EQGLNFIAIS FVRTAKDVNE VRAICEETGn GHVKLFAKIE
     msa277662.2{330_M732}  RDNADIRFGL EQGLNFIAIS FVRTAKDVNE VRAICEETGn GHVKLFAKIE
     msa277662.2{330_M781}  RDNADIRFGL EQGLNFIAIS FVRTAKDVNE VRAICEETGn GHVKLFAKIE
msa277662.2{330_JM9130013}  RDNADIRFGL EQGLNFIAIS FVRTAKDVNE VRAICEETGn GHVKLFAKIE
      msa277662.2{330_090}  RDNADIRFGL EQGLNFIAIS FVRTAKDVNE VRAICEETGn GHVKLFAKIE
     msa277662.2{330_2603}  RDNADIRFGL EQGLNFIAIS FVRTAKDVNE VRAICEETGx GHVKLFAKIE
                 Consensus  ********** ********** ********** *********_ **********
```

Table 72: Comparative Sequences relating to SAG0941

```
                             251                                                300
   msa277662.2{330_18RS21}   NQQGIDNIDE IIEAADGIMI ARGDMGIEVP FEMVPVYQKM IITKVNAAGK
     msa277662.2{330_A909}   NQQGIDNIDE IIEAADGIMI ARGDMGIEVP FEMVPVYQKM IITKVNAAGK
   msa277662.2{330_CJB110}   NQQGIDNIDE IIEAADGIMI ARGDMGIEVP FEMVPVYQKM IITKVNAAGK
     msa277662.2{330_H36B}   NQQGIDNIDE IIEAADGIMI ARGDMGIEVP FEMVPVYQKM IITKVNAAGK
   msa277662.2{330_1169NT}   NQQGIDNIDE IIEAADGIMI ARGDMGIEVP FEMVPVYQKM IITKVNAAGK
     msa277662.2{330_COH1}   NQQGIDNIDE IIEAADGIMI ARGDMGIEVP FEMVPVYQKM IITKVNAAGK
     msa277662.2{330_M732}   NQQGIDNIDE IIEAADGIMI ARGDMGIEVP FEMVPVYQKM IITKVNAAGK
     msa277662.2{330_M781}   NQQGIDNIDE IIEAADGIMI ARGDMGIEVP FEMVPVYQKM IITKVNAAGK
msa277662.2{330_JM9130013}   NQQGIDNIDE IIEAADGIMI ARGDMGIEVP FEMVPVYQKM IITKVNAAGK
      msa277662.2{330_090}   NQQGIDNIDE IIEAADGIMI ARGDMGIEVP FEMVPVYQKM IITKVNAAGK
     msa277662.2{330_2603}   NQQGIDNIDE IIEAADGIMI ARGDMGIEVP FEMVPVYQKM IITKVNAAGK
                 Consensus   ********** ********** ********** ********** **********

                             301                                                350
   msa277662.2{330_18RS21}   AVITATNMLE TMTDKPRATR SEVSDVFNAV IDGTDATMLS GESANGKYPV
     msa277662.2{330_A909}   AVITATNMLE TMTDKPRATR SEVSDVFNAV IDGTDATMLS GESANGKYPV
   msa277662.2{330_CJB110}   AVITATNMLE TMTDKPRATR SEVSDVFNAV IDGTDATMLS GESANGKYPV
     msa277662.2{330_H36B}   AVITATNMLE TMTDKPRATR SEVSDVFNAV IDGTDATMLS GESANGKYPV
   msa277662.2{330_1169NT}   AVITATNMLE TMTDKPRATR SEVSDVFNAV IDGTDATMLS GESANGKYPV
     msa277662.2{330_COH1}   AVITATNMLE TMTDKPRATR SEVSDVFNAV IDGTDATMLS GESANGKYPV
     msa277662.2{330_M732}   AVITATNMLE TMTDKPRATR SEVSDVFNAV IDGTDATMLS GESANGKYPV
     msa277662.2{330_M781}   AVITATNMLE TMTDKPRATR SEVSDVFNAV IDGTDATMLS GESANGKYPV
msa277662.2{330_JM9130013}   AVITATNMLE TMTDKPRATR SEVSDVFNAV IDGTDATMLS GESANGKYPV
      msa277662.2{330_090}   AVITATNMLE TMTDKPRATR SEVSDVFNAV IDGTDATMLS GESANGKYPV
     msa277662.2{330_2603}   AVITATNMLE TMTDKPRATR SEVSDVFNAV IDGTDATMLS GESANGKYPV
                 Consensus   ********** ********** ********** ********** **********

                             351                                                400
   msa277662.2{330_18RS21}   ESVRTMATID KNAQTLLNEY GRLDSSAFPR NNKTDVIASA VKDATHSMDI
     msa277662.2{330_A909}   ESVRTMATID KNAQTLLNEY GRLDSSAFPR NNKTDVIASA VKDATHSMDI
   msa277662.2{330_CJB110}   ESVRTMATID KNAQTLLNEY GRLDSSAFPR NNKTDVIASA VKDATHSMDI
     msa277662.2{330_H36B}   ESVRTMATID KNAQTLLNEY GRLDSSAFPR NNKTDVIASA VKDATHSMDI
   msa277662.2{330_1169NT}   ESVRTMATID KNAQTLLNEY GRLDSSAFPR NNKTDVIASA VKDATHSMDI
     msa277662.2{330_COH1}   ESVRTMATID KNAQTLLNEY GRLDSSAFPR NNKTDVIASA VKDATHSMDI
     msa277662.2{330_M732}   ESVRTMATID KNAQTLLNEY GRLDSSAFPR NNKTDVIASA VKDATHSMDI
     msa277662.2{330_M781}   ESVRTMATID KNAQTLLNEY GRLDSSAFPR NNKTDVIASA VKDATHSMDI
msa277662.2{330_JM9130013}   ESVRTMATID KNAQTLLNEY GRLDSSAFPR NNKTDVIASA VKDATHSMDI
      msa277662.2{330_090}   ESVRTMATID KNAQTLLNEY GRLDSSAFPR NNKTDVIASA VKDATHSMDI
     msa277662.2{330_2603}   ESVRTMATID KNAQTLLNEY GRLDSSAFPR NNKTDVIASA VKDATHSMDI
                 Consensus   ********** ********** ********** ********** **********

                             401                                                450
   msa277662.2{330_18RS21}   KLVVTITETG NTARAISKFR PDADILAVTF DEKVQRSLMI NWGVIPVLAD
     msa277662.2{330_A909}   KLVVTITETG NTARAISKFR PDADILAVTF DEKVQRSLMI NWGVIPVLAD
   msa277662.2{330_CJB110}   KLVVTITETG NTARAISKFR PDADILAVTF DEKVQRSLMI NWGVIPVLAD
     msa277662.2{330_H36B}   KLVVTITETG NTARAISKFR PDADILAVTF DEKVQRSLMI NWGVIPVLAD
   msa277662.2{330_1169NT}   KLVVTITETG NTARAISKFR PDADILAVTF DEKVQRSLMI NWGVIPVLAD
     msa277662.2{330_COH1}   KLVVTITETG NTARAISKFR PDADILAVTF DEKVQRSLMI NWGVIPVLAD
     msa277662.2{330_M732}   KLVVTITETG NTARAISKFR PDADILAVTF DEKVQRSLMI NWGVIPVLAD
     msa277662.2{330_M781}   KLVVTITETG NTARAISKFR PDADILAVTF DEKVQRSLMI NWGVIPVLAD
msa277662.2{330_JM9130013}   KLVVTITETG NTARAISKFR PDADILAVTF DEKVQRSLMI NWGVIPVLAD
      msa277662.2{330_090}   KLVVTITETG NTARAISKFR PDADILAVTF DEKVQRSLMI NWGVIPVLAD
     msa277662.2{330_2603}   KLVVTITETG NTARAISKFR PDADILAVTF DEKVQRSLMI NWGVIPVLAD
                 Consensus   ********** ********** ********** ********** **********

                             451                                                500
   msa277662.2{330_18RS21}   KPASTDDMFE VAERVALEAG fVESGDNIVI VAGVPVGTGG TNTMRVRTVK
     msa277662.2{330_A909}   KPASTDDMFE VAERVALEAG fVESGDNIVI VAGVPVGTGG TNTMRVRTVK
   msa277662.2{330_CJB110}   KPASTDDMFE VAERVALEAG fVESGDNIVI VAGVPVGTGG TNTMRVRTVK
     msa277662.2{330_H36B}   KPASTDDMFE VAERVALEAG fVESGDNIVI VAGVPVGTGG TNTMRVRTVK
   msa277662.2{330_1169NT}   KPASTDDMFE VAERVALEAG lVESGDNIVI VAGVPVGTGG TNTMRVRTVK
     msa277662.2{330_COH1}   KPASTDDMFE VAERVALEAG lVESGDNIVI VAGVPVGTGG TNTMRVRTVK
     msa277662.2{330_M732}   KPASTDDMFE VAERVALEAG lVESGDNIVI VAGVPVGTGG TNTMRVRTVK
     msa277662.2{330_M781}   KPASTDDMFE VAERVALEAG lVESGDNIVI VAGVPVGTGG TNTMRVRTVK
msa277662.2{330_JM9130013}   KPASTDDMFE VAERVALEAG lVESGDNIVI VAGVPVGTGG TNTMRVRTVK
      msa277662.2{330_090}   KPASTDDMFE VAERVALEAG lVESGDNIVI VAGVPVGTGG TNTMRVRTVK
     msa277662.2{330_2603}   KPASTDDMFE VAERVALEAG fVESGDNIVI VAGVPVGTGG TNTMRVRTVK
                 Consensus   ********** ********** _********* ********** **********
```

Table 73: Comparative Sequences relating to SAG0981

SEQ ID NO. 7301
STRAIN 2603
TTGTCTGCTATAATAGACAAAAAGGTGGTGATATTTATGTATTTAGCATTAATCGGTGAT
ATCATTAATTCAAAACAGATACTTGAACGTGAAACTTTCCAACAGTCTTTTCAGCAACTA
ATGACCGAACTATCTGATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCT
GGTGATGAATTTCAAGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTATTGACCAT
ATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCGGCCTCGGTACAGGAAACATTATA
ACATCCATCAATTCAAATGAAAGTATCGGTGCTGATGGTCCTGCCTACTGGCATGCTCGC
TCAGCTATTAATCATATACATGATAAAAATGATTATGGAACAGTTCAAGTAGCTATTTGC
CTTGATGATGAAGACCAAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGAT
TTTATCAAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAA
GATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTGGAAAATATTGAACCT
AGTGCGCTGACTAAACGCCTTAAAGCAAGCGGTCTGAAGATTTACTTAAGAACGAGAACA
CAGGCAGCCGATCTATTAGTTAAAAGTTGCACTCAAACTAAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7302
STRAIN 090
TCTGCTATAATAGACAAAAAGGTGGTGATATTTATGTATTT
AGCATTAATCGGTGATATCATTAATTCAAAACAGATACTTGAACGTGAAA
CTTTCCAACAGTCTTTTCAGCAAcTAATGACCGAACTATcTGATGTATAT
GGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGATGAATTTCA
AGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTATTGACCATATTC
AACTAGCTCTAAAACCTGTTAATGTAAGGTTCGGCCTCGGtACAGGAAAC
ATTATAACATCCATCAATTTAAATGAAAGTATCGGTGCTGATGGTCCTGC
CTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATAAAAATGATT
ATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACCAAAACCTT
GAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTATCAAGTCAAA
ATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAAGATA
ATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTGGAAAATATT
GAACCTAGTGCGCTGACTAAACGCCTTAAAGCAAGCGGTCTGAAGATTTA
CTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAAGTTGCACTC
AAACTAAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7303
STRAIN A909
TCTGCTATAATAGACAAAAAGGTGGTGATATTTATGTAT
TTAGCATTAATCGGTGATATCATTAATTCAAAACAGATACTTGAACGTGA
AACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTGATGTAT
ATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGATGAATTT
CAAGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTATTGACCATAT
TCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCGGCCTCGGTACAGGAA
ACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGATGGTCCT
GCCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATAAAAATGA
TTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACCAAAACC
TTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTATCAAGTCA
AAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAAGA
TAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTGGAAAATA
TTGAACCTAGTGCGCTGACTAAACGCCTTAAAGCAAGCGGTCTGAAGATT
TACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAAGTTGCAC
TCAAACTAAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7304
STRAIN H36B
TCTGCTATAATAGACAAAAAGGTGGTGATATTT
ATGTATTTAGCATTAATCGGTGATATCATTAATTCAAAACAGATACTTGA
ACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG
ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
GAATTTCAAGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTATTGA
CCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCGGCCTCGGTA
CAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT
GGTCCTGCCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATAA
AAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACC
AAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTATC
AAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT
TCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTGG
AAAATATTGAACCTAGTGCGCTGACTAAACGCCTTAAAGCAAGCGGTCTG
AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAAG
TTGCACTCAAACTAAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7305
STRAIN 18RS21
TCTGCTATAATAGACAAAAAGGTGGTGATATTT
ATGTATTTAGCATTAATCGGTGATATCATTAATTCAAAACAGATACTTGA
ACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG
ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
GAATTTCAAGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTATTGA
CCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCGGCCTCGGTA
CAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT
GGTCCTGCCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATAA
AAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACC
AAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTATC
AAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT

Table 73: Comparative Sequences relating to SAG0981

TCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTGG
AAAATATTGAACCTAGTGCGCTGACTAAACGCCTTAAAGCAAGCGGTCTG
AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAAG
TTGCACTCAAACTAAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7306
STRAIN M732
TCTGCTATAATAGACAAAAAGGTGGTGATATT
TATGTATTTAGCATTAATCGGTGATATCATTAATTCAAAACAGATACTTG
AACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCT
GATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGA
TGAATTTCAAGCTTTATTGAAACaATCAAAAAAGGTATTTCAAATTATTG
ACCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCGGCCTCGGT
ACAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGA
TGGTCCTGCCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATA
AAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGAC
CAAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTAT
CAAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATAC
TTCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTG
GAAAATATTGAACCTAGTGCGCTGACTAAACGCCTTAAAGCAAGCGGTCT
GAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAA
GTTGCACTCAAACTAAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7307
STRAIN COH1
TCTGCTATAATAGACAAAAAGGTGGTGATATT
TATGTATTTAGCATTAATCGGTGATATCATTAATTCAAAACAGATACTTG
AACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCT
GATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGA
TGAATTTCAAGCTTTATTGAAACaATCAAAAAAGGTATTTCAAATTATTG
ACCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCGGCCTCGGT
ACAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGA
TGGTCCTGCCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATA
AAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGAC
CAAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTAT
CAAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATAC
TTCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTG
GAAAATATTGAACCTAGTGCGCTGACTAAACGCCTTAAAGCAAGCGGTCT
GAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAA
GTTGCACTCAAACTAAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7308
STRAIN M781
TCTGCTATAATAGACAAAAAGGTGGTGATATTT
ATGTATTTAGCATTAATCGGTGATATCATTAATTCAAAACAGATACTTGA
ACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG
ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
GAATTTCAAGCTTTATTGAAACAATCAAAAAAGGTATTTCAAATTATTGA
CCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCGGCCTCGGTA
CAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT
GGTCCTGCCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATAA
AAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACC
AAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTATC
AAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT
TCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTGG
AAAATATTGAACCTAGTGCGCTGACTAAACGCCTTAAAGCAAGCGGTCTG
AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAAG
TTGCACTCAAACTAAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7309
STRAIN CJB110
TCTGCTATAATAGACAAAAAGGTGGTGGTA
TTTATGTATTTAGCATTAATCGGTGATATCATTAATTCAAAACAGATACT
TGAACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTAT
CTGATGTATATGGTGAAGAGCTGATTTCTCTATTCACTATTACAGCTGGT
GATGAATTTCAAGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTAT
TGACCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCGGCCTCG
GTACAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCT
GATGGTCCTGCCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGA
TAAAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAG
ACCAAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTT
ATCAAGTCAAAATGGACTACTAACCATTTTCAAATGCTTGAGCACTTAAT
ACTTCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAAC
TGGAAAATATTGAACCTAGTGCGCTGACTAAACGCCTTAAAGCAAGCGGT
CTGAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAA
AAGTTGCACTCAAACTAAAGGGGGAAGCTATGATTTc

SEQ ID NO. 7310
STRAIN JM9130013
TCTGCTATAATAGACAAAAAGGTGGTGATATTT
ATGTATTTAGCATTAATCGGTGATATCATTAATTCAAAACAGATACTTGA
ACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG

Table 73: Comparative Sequences relating to SAG0981

```
ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
GAATTTCAAGCTTTATTGAAACCATCAAAAAAGGTATTTCAAATTATTGA
CCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCGGCCTCGGTA
CAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT
GGTCCTGCCTACTGGCATGCTCGCTCAGCTATTAATCATATACATGATAA
AAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACC
AAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTATC
AAGTCAAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT
TCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCAACTGG
AAAATATTGAACCTAGTGCGCTGACTAAACGCCTTAAAGCAAGCGGTCTG
AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAAG
TTGCACTCAAACTAAAGGGGGAAGCTATGATTTC
```

```
PRETTY of: /biotmp/msa31912.2{*}   February 18, 2003 08:19  ..

                           1                                                  50
   msa31912.2{338_18RS21}  ---TCTGCTA TAATAGACAA AAAGGTGGTG aTATTTATGT ATTTAGCATT
     msa31912.2{338_2603}  ttgTCTGCTA TAATAGACAA AAAGGTGGTG aTATTTATGT ATTTAGCATT
     msa31912.2{338_A909}  ---TCTGCTA TAATAGACAA AAAGGTGGTG aTATTTATGT ATTTAGCATT
     msa31912.2{338_H36B}  ---TCTGCTA TAATAGACAA AAAGGTGGTG aTATTTATGT ATTTAGCATT
msa31912.2{338_JM9130013}  ---TCTGCTA TAATAGACAA AAAGGTGGTG aTATTTATGT ATTTAGCATT
     msa31912.2{338_COH1}  ---TCTGCTA TAATAGACAA AAAGGTGGTG aTATTTATGT ATTTAGCATT
     msa31912.2{338_M732}  ---TCTGCTA TAATAGACAA AAAGGTGGTG aTATTTATGT ATTTAGCATT
     msa31912.2{338_M781}  ---TCTGCTA TAATAGACAA AAAGGTGGTG aTATTTATGT ATTTAGCATT
      msa31912.2{338_090}  ---TCTGCTA TAATAGACAA AAAGGTGGTG aTATTTATGT ATTTAGCATT
   msa31912.2{338_CJB110}  ---TCTGCTA TAATAGACAA AAAGGTGGTG gTATTTATGT ATTTAGCATT
                Consensus  ********** ********** ********** _********* **********

                           51                                                100
   msa31912.2{338_18RS21}  AATCGGTGAT ATCATTAATT CAAAACAGAT ACTTGAACGT GAAACTTTCC
     msa31912.2{338_2603}  AATCGGTGAT ATCATTAATT CAAAACAGAT ACTTGAACGT GAAACTTTCC
     msa31912.2{338_A909}  AATCGGTGAT ATCATTAATT CAAAACAGAT ACTTGAACGT GAAACTTTCC
     msa31912.2{338_H36B}  AATCGGTGAT ATCATTAATT CAAAACAGAT ACTTGAACGT GAAACTTTCC
msa31912.2{338_JM9130013}  AATCGGTGAT ATCATTAATT CAAAACAGAT ACTTGAACGT GAAACTTTCC
     msa31912.2{338_COH1}  AATCGGTGAT ATCATTAATT CAAAACAGAT ACTTGAACGT GAAACTTTCC
     msa31912.2{338_M732}  AATCGGTGAT ATCATTAATT CAAAACAGAT ACTTGAACGT GAAACTTTCC
     msa31912.2{338_M781}  AATCGGTGAT ATCATTAATT CAAAACAGAT ACTTGAACGT GAAACTTTCC
      msa31912.2{338_090}  AATCGGTGAT ATCATTAATT CAAAACAGAT ACTTGAACGT GAAACTTTCC
   msa31912.2{338_CJB110}  AATCGGTGAT ATCATTAATT CAAAACAGAT ACTTGAACGT GAAACTTTCC
                Consensus  ********** ********** ********** ********** **********

                           101                                               150
   msa31912.2{338_18RS21}  AACAGTCTTT TCAGCAACTA ATGACCGAAC TATCTGATGT ATATGGTGAA
     msa31912.2{338_2603}  AACAGTCTTT TCAGCAACTA ATGACCGAAC TATCTGATGT ATATGGTGAA
     msa31912.2{338_A909}  AACAGTCTTT TCAGCAACTA ATGACCGAAC TATCTGATGT ATATGGTGAA
     msa31912.2{338_H36B}  AACAGTCTTT TCAGCAACTA ATGACCGAAC TATCTGATGT ATATGGTGAA
msa31912.2{338_JM9130013}  AACAGTCTTT TCAGCAACTA ATGACCGAAC TATCTGATGT ATATGGTGAA
     msa31912.2{338_COH1}  AACAGTCTTT TCAGCAACTA ATGACCGAAC TATCTGATGT ATATGGTGAA
     msa31912.2{338_M732}  AACAGTCTTT TCAGCAACTA ATGACCGAAC TATCTGATGT ATATGGTGAA
     msa31912.2{338_M781}  AACAGTCTTT TCAGCAACTA ATGACCGAAC TATCTGATGT ATATGGTGAA
      msa31912.2{338_090}  AACAGTCTTT TCAGCAACTA ATGACCGAAC TATCTGATGT ATATGGTGAA
   msa31912.2{338_CJB110}  AACAGTCTTT TCAGCAACTA ATGACCGAAC TATCTGATGT ATATGGTGAA
                Consensus  ********** ********** ********** ********** **********

                           151                                               200
   msa31912.2{338_18RS21}  GAGCTGATTT CTCcATTCAC TATTACAGCT GGTGATGAAT TTCAAGCTTT
     msa31912.2{338_2603}  GAGCTGATTT CTCcATTCAC TATTACAGCT GGTGATGAAT TTCAAGCTTT
     msa31912.2{338_A909}  GAGCTGATTT CTCcATTCAC TATTACAGCT GGTGATGAAT TTCAAGCTTT
     msa31912.2{338_H36B}  GAGCTGATTT CTCcATTCAC TATTACAGCT GGTGATGAAT TTCAAGCTTT
msa31912.2{338_JM9130013}  GAGCTGATTT CTCcATTCAC TATTACAGCT GGTGATGAAT TTCAAGCTTT
     msa31912.2{338_COH1}  GAGCTGATTT CTCcATTCAC TATTACAGCT GGTGATGAAT TTCAAGCTTT
     msa31912.2{338_M732}  GAGCTGATTT CTCcATTCAC TATTACAGCT GGTGATGAAT TTCAAGCTTT
     msa31912.2{338_M781}  GAGCTGATTT CTCcATTCAC TATTACAGCT GGTGATGAAT TTCAAGCTTT
      msa31912.2{338_090}  GAGCTGATTT CTCcATTCAC TATTACAGCT GGTGATGAAT TTCAAGCTTT
   msa31912.2{338_CJB110}  GAGCTGATTT CTCtATTCAC TATTACAGCT GGTGATGAAT TTCAAGCTTT
                Consensus  ********** ***_****** ********** ********** **********

                           201                                               250
   msa31912.2{338_18RS21}  ATTGAAACcA TCAAAAAAGG TATTTCAAAT TATTGACCAT ATTCAACTAG
     msa31912.2{338_2603}  ATTGAAACcA TCAAAAAAGG TATTTCAAAT TATTGACCAT ATTCAACTAG
     msa31912.2{338_A909}  ATTGAAACcA TCAAAAAAGG TATTTCAAAT TATTGACCAT ATTCAACTAG
     msa31912.2{338_H36B}  ATTGAAACcA TCAAAAAAGG TATTTCAAAT TATTGACCAT ATTCAACTAG
msa31912.2{338_JM9130013}  ATTGAAACcA TCAAAAAAGG TATTTCAAAT TATTGACCAT ATTCAACTAG
     msa31912.2{338_COH1}  ATTGAAACaA TCAAAAAAGG TATTTCAAAT TATTGACCAT ATTCAACTAG
     msa31912.2{338_M732}  ATTGAAACaA TCAAAAAAGG TATTTCAAAT TATTGACCAT ATTCAACTAG
     msa31912.2{338_M781}  ATTGAAACaA TCAAAAAAGG TATTTCAAAT TATTGACCAT ATTCAACTAG
      msa31912.2{338_090}  ATTGAAACcA TCAAAAAAGG TATTTCAAAT TATTGACCAT ATTCAACTAG
   msa31912.2{338_CJB110}  ATTGAAACcA TCAAAAAAGG TATTTCAAAT TATTGACCAT ATTCAACTAG
                Consensus  ********_* ********** ********** ********** **********

                           251                                               300
   msa31912.2{338_18RS21}  CTCTAAAACC TGTTAATGTA AGGTTCGGCC TCGGTACAGG AAACATTATA
     msa31912.2{338_2603}  CTCTAAAACC TGTTAATGTA AGGTTCGGCC TCGGTACAGG AAACATTATA
```

Table 73: Comparative Sequences relating to SAG0981

```
      msa31912.2{338_A909}  CTCTAAAACC TGTTAATGTA AGGTTCGGCC TCGGTACAGG AAACATTATA
      msa31912.2{338_H36B}  CTCTAAAACC TGTTAATGTA AGGTTCGGCC TCGGTACAGG AAACATTATA
 msa31912.2{338_JM9130013}  CTCTAAAACC TGTTAATGTA AGGTTCGGCC TCGGTACAGG AAACATTATA
      msa31912.2{338_COH1}  CTCTAAAACC TGTTAATGTA AGGTTCGGCC TCGGTACAGG AAACATTATA
      msa31912.2{338_M732}  CTCTAAAACC TGTTAATGTA AGGTTCGGCC TCGGTACAGG AAACATTATA
      msa31912.2{338_M781}  CTCTAAAACC TGTTAATGTA AGGTTCGGCC TCGGTACAGG AAACATTATA
       msa31912.2{338_090}  CTCTAAAACC TGTTAATGTA AGGTTCGGCC TCGGTACAGG AAACATTATA
    msa31912.2{338_CJB110}  CTCTAAAACC TGTTAATGTA AGGTTCGGCC TCGGTACAGG AAACATTATA
                 Consensus  ********** ********** ********** ********** **********

                            301                                               350
    msa31912.2{338_18RS21}  ACATCCATCA ATTcAAATGA AAGTATCGGT GCTGATGGTC CTGCCTACTG
      msa31912.2{338_2603}  ACATCCATCA ATTcAAATGA AAGTATCGGT GCTGATGGTC CTGCCTACTG
      msa31912.2{338_A909}  ACATCCATCA ATTcAAATGA AAGTATCGGT GCTGATGGTC CTGCCTACTG
      msa31912.2{338_H36B}  ACATCCATCA ATTcAAATGA AAGTATCGGT GCTGATGGTC CTGCCTACTG
 msa31912.2{338_JM9130013}  ACATCCATCA ATTcAAATGA AAGTATCGGT GCTGATGGTC CTGCCTACTG
      msa31912.2{338_COH1}  ACATCCATCA ATTcAAATGA AAGTATCGGT GCTGATGGTC CTGCCTACTG
      msa31912.2{338_M732}  ACATCCATCA ATTcAAATGA AAGTATCGGT GCTGATGGTC CTGCCTACTG
      msa31912.2{338_M781}  ACATCCATCA ATTcAAATGA AAGTATCGGT GCTGATGGTC CTGCCTACTG
       msa31912.2{338_090}  ACATCCATCA ATTtAAATGA AAGTATCGGT GCTGATGGTC CTGCCTACTG
    msa31912.2{338_CJB110}  ACATCCATCA ATTcAAATGA AAGTATCGGT GCTGATGGTC CTGCCTACTG
                 Consensus  ********** ***-****** ********** ********** **********

                            351                                               400
    msa31912.2{338_18RS21}  GCATGCTCGC TCAGCTATTA ATCATATACA TGATAAAAAT GATTATGGAA
      msa31912.2{338_2603}  GCATGCTCGC TCAGCTATTA ATCATATACA TGATAAAAAT GATTATGGAA
      msa31912.2{338_A909}  GCATGCTCGC TCAGCTATTA ATCATATACA TGATAAAAAT GATTATGGAA
      msa31912.2{338_H36B}  GCATGCTCGC TCAGCTATTA ATCATATACA TGATAAAAAT GATTATGGAA
 msa31912.2{338_JM9130013}  GCATGCTCGC TCAGCTATTA ATCATATACA TGATAAAAAT GATTATGGAA
      msa31912.2{338_COH1}  GCATGCTCGC TCAGCTATTA ATCATATACA TGATAAAAAT GATTATGGAA
      msa31912.2{338_M732}  GCATGCTCGC TCAGCTATTA ATCATATACA TGATAAAAAT GATTATGGAA
      msa31912.2{338_M781}  GCATGCTCGC TCAGCTATTA ATCATATACA TGATAAAAAT GATTATGGAA
       msa31912.2{338_090}  GCATGCTCGC TCAGCTATTA ATCATATACA TGATAAAAAT GATTATGGAA
    msa31912.2{338_CJB110}  GCATGCTCGC TCAGCTATTA ATCATATACA TGATAAAAAT GATTATGGAA
                 Consensus  ********** ********** ********** ********** **********

                            401                                               450
    msa31912.2{338_18RS21}  CAGTTCAAGT AGCTATTTGC CTTGATGATG AAGACCAAAA CCTTGAATTA
      msa31912.2{338_2603}  CAGTTCAAGT AGCTATTTGC CTTGATGATG AAGACCAAAA CCTTGAATTA
      msa31912.2{338_A909}  CAGTTCAAGT AGCTATTTGC CTTGATGATG AAGACCAAAA CCTTGAATTA
      msa31912.2{338_H36B}  CAGTTCAAGT AGCTATTTGC CTTGATGATG AAGACCAAAA CCTTGAATTA
 msa31912.2{338_JM9130013}  CAGTTCAAGT AGCTATTTGC CTTGATGATG AAGACCAAAA CCTTGAATTA
      msa31912.2{338_COH1}  CAGTTCAAGT AGCTATTTGC CTTGATGATG AAGACCAAAA CCTTGAATTA
      msa31912.2{338_M732}  CAGTTCAAGT AGCTATTTGC CTTGATGATG AAGACCAAAA CCTTGAATTA
      msa31912.2{338_M781}  CAGTTCAAGT AGCTATTTGC CTTGATGATG AAGACCAAAA CCTTGAATTA
       msa31912.2{338_090}  CAGTTCAAGT AGCTATTTGC CTTGATGATG AAGACCAAAA CCTTGAATTA
    msa31912.2{338_CJB110}  CAGTTCAAGT AGCTATTTGC CTTGATGATG AAGACCAAAA CCTTGAATTA
                 Consensus  ********** ********** ********** ********** **********

                            451                                               500
    msa31912.2{338_18RS21}  ACACTAAATA GTCTCATTTC AGCTGGTGAT TTTATCAAGT CAAAATGGAC
      msa31912.2{338_2603}  ACACTAAATA GTCTCATTTC AGCTGGTGAT TTTATCAAGT CAAAATGGAC
      msa31912.2{338_A909}  ACACTAAATA GTCTCATTTC AGCTGGTGAT TTTATCAAGT CAAAATGGAC
      msa31912.2{338_H36B}  ACACTAAATA GTCTCATTTC AGCTGGTGAT TTTATCAAGT CAAAATGGAC
 msa31912.2{338_JM9130013}  ACACTAAATA GTCTCATTTC AGCTGGTGAT TTTATCAAGT CAAAATGGAC
      msa31912.2{338_COH1}  ACACTAAATA GTCTCATTTC AGCTGGTGAT TTTATCAAGT CAAAATGGAC
      msa31912.2{338_M732}  ACACTAAATA GTCTCATTTC AGCTGGTGAT TTTATCAAGT CAAAATGGAC
      msa31912.2{338_M781}  ACACTAAATA GTCTCATTTC AGCTGGTGAT TTTATCAAGT CAAAATGGAC
       msa31912.2{338_090}  ACACTAAATA GTCTCATTTC AGCTGGTGAT TTTATCAAGT CAAAATGGAC
    msa31912.2{338_CJB110}  ACACTAAATA GTCTCATTTC AGCTGGTGAT TTTATCAAGT CAAAATGGAC
                 Consensus  ********** ********** ********** ********** **********

                            501                                               550
    msa31912.2{338_18RS21}  TACaAACCAT TTTCAAATGC TTGAGCACTT AATACTTCAA GATAATTATC
      msa31912.2{338_2603}  TACaAACCAT TTTCAAATGC TTGAGCACTT AATACTTCAA GATAATTATC
      msa31912.2{338_A909}  TACaAACCAT TTTCAAATGC TTGAGCACTT AATACTTCAA GATAATTATC
      msa31912.2{338_H36B}  TACaAACCAT TTTCAAATGC TTGAGCACTT AATACTTCAA GATAATTATC
 msa31912.2{338_JM9130013}  TACaAACCAT TTTCAAATGC TTGAGCACTT AATACTTCAA GATAATTATC
      msa31912.2{338_COH1}  TACaAACCAT TTTCAAATGC TTGAGCACTT AATACTTCAA GATAATTATC
      msa31912.2{338_M732}  TACaAACCAT TTTCAAATGC TTGAGCACTT AATACTTCAA GATAATTATC
      msa31912.2{338_M781}  TACaAACCAT TTTCAAATGC TTGAGCACTT AATACTTCAA GATAATTATC
       msa31912.2{338_090}  TACaAACCAT TTTCAAATGC TTGAGCACTT AATACTTCAA GATAATTATC
    msa31912.2{338_CJB110}  TACtAACCAT TTTCAAATGC TTGAGCACTT AATACTTCAA GATAATTATC
                 Consensus  ***-****** ********** ********** ********** **********

                            551                                               600
    msa31912.2{338_18RS21}  AAGAACAATT TCAACATCAA AAGTTAGCCC AACTGGAAAA TATTGAACCT
      msa31912.2{338_2603}  AAGAACAATT TCAACATCAA AAGTTAGCCC AACTGGAAAA TATTGAACCT
      msa31912.2{338_A909}  AAGAACAATT TCAACATCAA AAGTTAGCCC AACTGGAAAA TATTGAACCT
      msa31912.2{338_H36B}  AAGAACAATT TCAACATCAA AAGTTAGCCC AACTGGAAAA TATTGAACCT
 msa31912.2{338_JM9130013}  AAGAACAATT TCAACATCAA AAGTTAGCCC AACTGGAAAA TATTGAACCT
      msa31912.2{338_COH1}  AAGAACAATT TCAACATCAA AAGTTAGCCC AACTGGAAAA TATTGAACCT
      msa31912.2{338_M732}  AAGAACAATT TCAACATCAA AAGTTAGCCC AACTGGAAAA TATTGAACCT
```

Table 73: Comparative Sequences relating to SAG0981

```
     msa31912.2{338_M781}  AAGAACAATT TCAACATCAA AAGTTAGCCC AACTGGAAAA TATTGAACCT
      msa31912.2{338_090}  AAGAACAATT TCAACATCAA AAGTTAGCCC AACTGGAAAA TATTGAACCT
   msa31912.2{338_CJB110}  AAGAACAATT TCAACATCAA AAGTTAGCCC AACTGGAAAA TATTGAACCT
                Consensus  ********** ********** ********** ********** **********

                           601                                                650
   msa31912.2{338_18RS21}  AGTGCGCTGA CTAAACGCCT TAAAGCAAGC GGTCTGAAGA TTTACTTAAG
     msa31912.2{338_2603}  AGTGCGCTGA CTAAACGCCT TAAAGCAAGC GGTCTGAAGA TTTACTTAAG
     msa31912.2{338_A909}  AGTGCGCTGA CTAAACGCCT TAAAGCAAGC GGTCTGAAGA TTTACTTAAG
     msa31912.2{338_H36B}  AGTGCGCTGA CTAAACGCCT TAAAGCAAGC GGTCTGAAGA TTTACTTAAG
msa31912.2{338_JM9130013}  AGTGCGCTGA CTAAACGCCT TAAAGCAAGC GGTCTGAAGA TTTACTTAAG
     msa31912.2{338_COH1}  AGTGCGCTGA CTAAACGCCT TAAAGCAAGC GGTCTGAAGA TTTACTTAAG
     msa31912.2{338_M732}  AGTGCGCTGA CTAAACGCCT TAAAGCAAGC GGTCTGAAGA TTTACTTAAG
     msa31912.2{338_M781}  AGTGCGCTGA CTAAACGCCT TAAAGCAAGC GGTCTGAAGA TTTACTTAAG
      msa31912.2{338_090}  AGTGCGCTGA CTAAACGCCT TAAAGCAAGC GGTCTGAAGA TTTACTTAAG
   msa31912.2{338_CJB110}  AGTGCGCTGA CTAAACGCCT TAAAGCAAGC GGTCTGAAGA TTTACTTAAG
                Consensus  ********** ********** ********** ********** **********

                           651                                                700
   msa31912.2{338_18RS21}  AACGAGAACA CAGGCAGCCG ATCTATTAGT TAAAAGTTGC ACTCAAACTA
     msa31912.2{338_2603}  AACGAGAACA CAGGCAGCCG ATCTATTAGT TAAAAGTTGC ACTCAAACTA
     msa31912.2{338_A909}  AACGAGAACA CAGGCAGCCG ATCTATTAGT TAAAAGTTGC ACTCAAACTA
     msa31912.2{338_H36B}  AACGAGAACA CAGGCAGCCG ATCTATTAGT TAAAAGTTGC ACTCAAACTA
msa31912.2{338_JM9130013}  AACGAGAACA CAGGCAGCCG ATCTATTAGT TAAAAGTTGC ACTCAAACTA
     msa31912.2{338_COH1}  AACGAGAACA CAGGCAGCCG ATCTATTAGT TAAAAGTTGC ACTCAAACTA
     msa31912.2{338_M732}  AACGAGAACA CAGGCAGCCG ATCTATTAGT TAAAAGTTGC ACTCAAACTA
     msa31912.2{338_M781}  AACGAGAACA CAGGCAGCCG ATCTATTAGT TAAAAGTTGC ACTCAAACTA
      msa31912.2{338_090}  AACGAGAACA CAGGCAGCCG ATCTATTAGT TAAAAGTTGC ACTCAAACTA
   msa31912.2{338_CJB110}  AACGAGAACA CAGGCAGCCG ATCTATTAGT TAAAAGTTGC ACTCAAACTA
                Consensus  ********** ********** ********** ********** **********

                           701                  720
   msa31912.2{338_18RS21}  AAGGGGGAAG CTATGATTTC
     msa31912.2{338_2603}  AAGGGGGAAG CTATGATTTC
     msa31912.2{338_A909}  AAGGGGGAAG CTATGATTTC
     msa31912.2{338_H36B}  AAGGGGGAAG CTATGATTTC
msa31912.2{338_JM9130013}  AAGGGGGAAG CTATGATTTC
     msa31912.2{338_COH1}  AAGGGGGAAG CTATGATTTC
     msa31912.2{338_M732}  AAGGGGGAAG CTATGATTTC
     msa31912.2{338_M781}  AAGGGGGAAG CTATGATTTC
      msa31912.2{338_090}  AAGGGGGAAG CTATGATTTC
   msa31912.2{338_CJB110}  AAGGGGGAAG CTATGATTTC
                Consensus  ********** **********
```

SEQ ID NO. 7311
STRAIN 2603 frame: 1
LSAIIDKKVVIFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFTITA
GDEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHAR
SAINHIHDKNDYGTVQVAICLDDEDQNLELTLNSLISAGDFIKSKWTTNHFQMLEHLILQ
DNYQEQFQHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7312
STRAIN 090 frame: 1
SAIIDKKVVIFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFTITAG
DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINLNESIGADGPAYWHARS
AINHIHDKNDYGTVQVAICLDDEDQNLELTLNSLISAGDFIKSKWTTNHFQMLEHLILQD
NYQEQFQHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7313
STRAIN A909 frame: 1
SAIIDKKVVIFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFTITAG
DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS
AINHIHDKNDYGTVQVAICLDDEDQNLELTLNSLISAGDFIKSKWTTNHFQMLEHLILQD
NYQEQFQHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7314
STRAIN H36B frame: 1
SAIIDKKVVIFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFTITAG
DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS
AINHIHDKNDYGTVQVAICLDDEDQNLELTLNSLISAGDFIKSKWTTNHFQMLEHLILQD
NYQEQFQHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7315
STRAIN 18RS21 frame: 1
SAIIDKKVVIFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFTITAG
DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS
AINHIHDKNDYGTVQVAICLDDEDQNLELTLNSLISAGDFIKSKWTTNHFQMLEHLILQD
NYQEQFQHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7316
STRAIN M732 frame: 1
SAIIDKKVVIFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFTITAG

Table 73: Comparative Sequences relating to SAG0981

DEFQALLKQSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS
AINHIHDKNDYGTVQVAICLDDEDQNLELTLNSLISAGDFIKSKWTTNHFQMLEHLILQD
NYQEQFQHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7317
STRAIN COH1 frame: 1
SAIIDKKVVIFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFTITAG
DEFQALLKQSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS
AINHIHDKNDYGTVQVAICLDDEDQNLELTLNSLISAGDFIKSKWTTNHFQMLEHLILQD
NYQEQFQHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7318
STRAIN M781 frame: 1
SAIIDKKVVIFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFTITAG
DEFQALLKQSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS
AINHIHDKNDYGTVQVAICLDDEDQNLELTLNSLISAGDFIKSKWTTNHFQMLEHLILQD
NYQEQFQHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7319
STRAIN CJB110 frame: 1
SAIIDKKVVVFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISLFTITAG
DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS
AINHIHDKNDYGTVQVAICLDDEDQNLELTLNSLISAGDFIKSKWTTNHFQMLEHLILQD
NYQEQFQHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7320
STRAIN JM9130013 frame: 1
SAIIDKKVVIFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFTITAG
DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS
AINHIHDKNDYGTVQVAICLDDEDQNLELTLNSLISAGDFIKSKWTTNHFQMLEHLILQD
NYQEQFQHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

```
PRETTY of: /biotmp/msa32053.2{*}   February 18, 2003 08:25  ..

                                 1                                                    50
     msa32053.2{338_18RS21}   ~SAIIDKKVV iFMYLALIGD IINSKQILER ETFQQSFQQL MTELSDVYGE
       msa32053.2{338_2603}   1SAIIDKKVV iFMYLALIGD IINSKQILER ETFQQSFQQL MTELSDVYGE
       msa32053.2{338_A909}   ~SAIIDKKVV iFMYLALIGD IINSKQILER ETFQQSFQQL MTELSDVYGE
     msa32053.2{338_CJB110}   ~SAIIDKKVV vFMYLALIGD IINSKQILER ETFQQSFQQL MTELSDVYGE
       msa32053.2{338_COH1}   ~SAIIDKKVV iFMYLALIGD IINSKQILER ETFQQSFQQL MTELSDVYGE
       msa32053.2{338_H36B}   ~SAIIDKKVV iFMYLALIGD IINSKQILER ETFQQSFQQL MTELSDVYGE
  msa32053.2{338_JM9130013}   ~SAIIDKKVV iFMYLALIGD IINSKQILER ETFQQSFQQL MTELSDVYGE
       msa32053.2{338_M732}   ~SAIIDKKVV iFMYLALIGD IINSKQILER ETFQQSFQQL MTELSDVYGE
       msa32053.2{338_M781}   ~SAIIDKKVV iFMYLALIGD IINSKQILER ETFQQSFQQL MTELSDVYGE
        msa32053.2{338_090}   ~SAIIDKKVV iFMYLALIGD IINSKQILER ETFQQSFQQL MTELSDVYGE
                  Consensus   ********** _********* ********** ********** **********

                              51                                                  100
     msa32053.2{338_18RS21}   ELISpFTITA GDEFQALLKp SKKVFQIIDH IQLALKPVNV RFGLGTGNII
       msa32053.2{338_2603}   ELISpFTITA GDEFQALLKp SKKVFQIIDH IQLALKPVNV RFGLGTGNII
       msa32053.2{338_A909}   ELISpFTITA GDEFQALLKp SKKVFQIIDH IQLALKPVNV RFGLGTGNII
     msa32053.2{338_CJB110}   ELISlFTITA GDEFQALLKp SKKVFQIIDH IQLALKPVNV RFGLGTGNII
       msa32053.2{338_COH1}   ELISpFTITA GDEFQALLKq SKKVFQIIDH IQLALKPVNV RFGLGTGNII
       msa32053.2{338_H36B}   ELISpFTITA GDEFQALLKp SKKVFQIIDH IQLALKPVNV RFGLGTGNII
  msa32053.2{338_JM9130013}   ELISpFTITA GDEFQALLKp SKKVFQIIDH IQLALKPVNV RFGLGTGNII
       msa32053.2{338_M732}   ELISpFTITA GDEFQALLKq SKKVFQIIDH IQLALKPVNV RFGLGTGNII
       msa32053.2{338_M781}   ELISpFTITA GDEFQALLKq SKKVFQIIDH IQLALKPVNV RFGLGTGNII
        msa32053.2{338_090}   ELISpFTITA GDEFQALLKp SKKVFQIIDH IQLALKPVNV RFGLGTGNII
                  Consensus   ****_***** *********_ ********** ********** **********

                              101                                                 150
     msa32053.2{338_18RS21}   TSINsNESIG ADGPAYWHAR SAINHIHDKN DYGTVQVAIC LDDEDQNLEL
       msa32053.2{338_2603}   TSINsNESIG ADGPAYWHAR SAINHIHDKN DYGTVQVAIC LDDEDQNLEL
       msa32053.2{338_A909}   TSINsNESIG ADGPAYWHAR SAINHIHDKN DYGTVQVAIC LDDEDQNLEL
     msa32053.2{338_CJB110}   TSINsNESIG ADGPAYWHAR SAINHIHDKN DYGTVQVAIC LDDEDQNLEL
       msa32053.2{338_COH1}   TSINsNESIG ADGPAYWHAR SAINHIHDKN DYGTVQVAIC LDDEDQNLEL
       msa32053.2{338_H36B}   TSINsNESIG ADGPAYWHAR SAINHIHDKN DYGTVQVAIC LDDEDQNLEL
  msa32053.2{338_JM9130013}   TSINsNESIG ADGPAYWHAR SAINHIHDKN DYGTVQVAIC LDDEDQNLEL
       msa32053.2{338_M732}   TSINsNESIG ADGPAYWHAR SAINHIHDKN DYGTVQVAIC LDDEDQNLEL
       msa32053.2{338_M781}   TSINsNESIG ADGPAYWHAR SAINHIHDKN DYGTVQVAIC LDDEDQNLEL
        msa32053.2{338_090}   TSINlNESIG ADGPAYWHAR SAINHIHDKN DYGTVQVAIC LDDEDQNLEL
                  Consensus   ****_***** ********** ********** ********** **********

                              151                                                 200
     msa32053.2{338_18RS21}   TLNSLISAGD FIKSKWTTNH FQMLEHLILQ DNYQEQFQHQ KLAQLENIEP
       msa32053.2{338_2603}   TLNSLISAGD FIKSKWTTNH FQMLEHLILQ DNYQEQFQHQ KLAQLENIEP
       msa32053.2{338_A909}   TLNSLISAGD FIKSKWTTNH FQMLEHLILQ DNYQEQFQHQ KLAQLENIEP
     msa32053.2{338_CJB110}   TLNSLISAGD FIKSKWTTNH FQMLEHLILQ DNYQEQFQHQ KLAQLENIEP
       msa32053.2{338_COH1}   TLNSLISAGD FIKSKWTTNH FQMLEHLILQ DNYQEQFQHQ KLAQLENIEP
       msa32053.2{338_H36B}   TLNSLISAGD FIKSKWTTNH FQMLEHLILQ DNYQEQFQHQ KLAQLENIEP
  msa32053.2{338_JM9130013}   TLNSLISAGD FIKSKWTTNH FQMLEHLILQ DNYQEQFQHQ KLAQLENIEP
       msa32053.2{338_M732}   TLNSLISAGD FIKSKWTTNH FQMLEHLILQ DNYQEQFQHQ KLAQLENIEP
       msa32053.2{338_M781}   TLNSLISAGD FIKSKWTTNH FQMLEHLILQ DNYQEQFQHQ KLAQLENIEP
```

Table 73: Comparative Sequences relating to SAG0981

```
      msa32053.2{338_090}  TLNSLISAGD FIKSKWTTNH FQMLEHLILQ DNYQEQFQHQ KLAQLENIEP
                Consensus  ********** ********** ********** ********** **********

                           201                                    240
    msa32053.2{338_18RS21}  SALTKRLKAS GLKIYLRTRT QAADLLVKSC TQTKGGSYDF
      msa32053.2{338_2603}  SALTKRLKAS GLKIYLRTRT QAADLLVKSC TQTKGGSYDF
      msa32053.2{338_A909}  SALTKRLKAS GLKIYLRTRT QAADLLVKSC TQTKGGSYDF
    msa32053.2{338_CJB110}  SALTKRLKAS GLKIYLRTRT QAADLLVKSC TQTKGGSYDF
      msa32053.2{338_COH1}  SALTKRLKAS GLKIYLRTRT QAADLLVKSC TQTKGGSYDF
      msa32053.2{338_H36B}  SALTKRLKAS GLKIYLRTRT QAADLLVKSC TQTKGGSYDF
 msa32053.2{338_JM9130013}  SALTKRLKAS GLKIYLRTRT QAADLLVKSC TQTKGGSYDF
      msa32053.2{338_M732}  SALTKRLKAS GLKIYLRTRT QAADLLVKSC TQTKGGSYDF
      msa32053.2{338_M781}  SALTKRLKAS GLKIYLRTRT QAADLLVKSC TQTKGGSYDF
       msa32053.2{338_090}  SALTKRLKAS GLKIYLRTRT QAADLLVKSC TQTKGGSYDF
                 Consensus  ********** ********** ********** **********
```

Table 74: Comparative Sequences relating to SAG1572

SEQ ID NO. 7401
STRAIN 2603
ATGGAAATGCAAGTTCAAAAAAGTTTTAAATCAAATATACATTACGGAACACTCTAT
CTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGCCATTAGGATTTTA
AGAGAAGTTGATTTTATTTGTGCAGAGGATACACGAAATACGGGACTTTTACTCAAGCAC
TTTGATATTACTACTAAACAAATTAGTTTTCACGAACACAATGCTTACGATAAAATCTCT
GGGTTAATTGATTTGTTAAAAGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATG
CCCTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCCA
GTTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTCAGGTTTAGCT
CCACAACCTCATATTTTTTATGGCTTCTTACCTCGTAAGAAAGGTCAACAAATAACTTTC
TTTGAAACAAAGCAAGATTACCCTGAAACACAAATCTTTTATGAGTCACCGTTTCGAGTC
TCTGATACGCTAAAACACATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTTAGTACGC
GAATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAGAGCAT
ATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGGTAAGAGAGATACC
GAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTAGTATTAGTAAAAGAATATATCGCT
AATGGTGATAAAACTAATCAAGCGATAAAAAAAGTAGCAAAAGAATTTAATCTCAATAGA
CAAGAACTCTATGCTAGTTTCCATGATTTA

SEQ ID NO. 7402
STRAIN 090
GAAATGCAAGTTCAAAAAAGTTTTAAATCAAATACACATTACGGGACACT
CTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTG
CCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGAGGATACACGA
AATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTAG
TTTTCACGAACACAATGCTTACGATAAAATCTCTGGGTTAATTGATTTGT
TAAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCT
ATTTCTGACCCAGgACATGACCTTGTCAAGGCTGCTATTGAAGGGGGGAT
CCCGGTCGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCG
CTTCAGGTTTAGCTCCACAACCTCATATTTTTTATGGCTTCTTACCGCGT
AAGAAAGGTCAACAAATAACTTTTTTTGAAACAAAGAAAGATTACCCTGa
AACACAAATCTTTTATGAGTCACCGtTTCGAGTCTcTGATACGCTAAAAC
ACATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTTAGTACGCGAATTG
ACGAAaCTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAGG
GCATATTGAAAAAGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATG
GTAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTA
GTATTAGTAA

SEQ ID NO. 7403
STRAIN A909
AGTTCAAAAAAGTTTTAAATCAAATATACATTACGGAACACTCTATCTAG
TCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGCCATTAGG
ATTTTAAGAGAAGTTGATTTTATTTGTGCAGAGGATACACGAAATACGGG
ACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTAGTTTTCACG
AACACAATGCTTACGATAAAATCTCTGGGTTAATTGATTTGTTAAAAGAA
GGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCTATTTCTGA
CCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCCAGTTG
TATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTCAGGT
TTAGCTCCACAACCTCATATTTTTTATGGCTTCTTACCACGTAAGAAAGG
TCAACAAATAACTTTCTTTgAAACAAAGCAAGATTACCCTGAAACACAAA
TCTTTTATGAGTCACCGTTTCGAGTCTCtGATACGCTAAAACACATGAAA
GAGATTTACGGAGATCGCCAAGTTGTTTTAGTACGCGAATTGACGAAACT
CTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAGAGCATATTG
AAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGGTAAGAGA
GATACCGAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTAGTATTAGT
AA

SEQ ID NO. 7404
STRAIN H36B
GAAATGCAAGTTCAAAAAAGTTTTAAATCAAATACACATT
ACGGGACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATG
ACTTTTCGTGCCATTAGGATTTTAAGAgAAGTTGATTTTATTTGTGCAGA
GGATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTA
AACAAATTAGTTTTCACGAACACAATGCTTATGATAAAATCTCTGGGTTA
ATTGATTTGTTAAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGG
AATGCCCTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTG
AAGGGGATATCCCGGTCGTATCTATACCAGGAGCTAGCGCTGGTATTACT
GCTCTCATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTTTATGGCTT
CTTACCGCGTAAGCAAGGTCAACAAATAACTTTTTTTGAAACAAAGAAAG
ATTACCCTGAAACACAAATCTTTTATGAGTCACCGtTTCGAGTCTCTGAT
ACGCTAAAACACATGAAAGAGATTTATGGAGATCGCCAAGTTGTTTTAGT
ACGCGAATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTC
AACTTTTAGGGCATATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATT
ATTGTTGATGGTAAGAGAGATACTGAGCGAGTGAAAGACAGTAGCCAACA
AGATCCACTAGTATTAGTAA

SEQ ID NO. 7405
STRAIN 18RS21
GAAATGCAAGTTCAAAAAAGTTTTAAATCAAATATACATT
ACGGAACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAgATGATATG
ACTTTtCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGA
GgATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTA
AACAAATTAGTTTTCACGAACACAATGCTTACGATAAAATCTCTGGGTTA
ATTGATTTGTTAAAAGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGG

Table 74: Comparative Sequences relating to SAG1572

AATGCCCTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTG
AAGGGGATATCCCAGTTGTATCTATACCAGGAGCTAGCGCTGGTATTACT
GCTCTCATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTTTATGGCTT
CTTACCACGTAAGAAAGGTCAACAAATAACTTTCtTTGAAACAAAGCAAG
ATTACCCTGAAACACAAATCTTTTATGAGTCACCGtTTCGAGTCTCTGAT
ACGCTAAAACACATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTTAGT
ACGCGAATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTC
AACTTTTAGAGCATATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATT
ATTGTTGATGGTAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACA
AGATCCACTAGTATTAGTAA

SEQ ID NO. 7406
STRAIN M732
GAAATGCAAGTTCAAAAAAGTTTTAAATCAAAT
ATACATTACGGAACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAGA
TGATATGACTTTTCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTT
GTGCAGAGGATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATT
ACTACTAAACAAATTAGTTTTCACGAACACAATGCTTACGATAAAATCTC
TGGGTTAATTGATTTGTTAAAAGAAGGGAAATCTTTAGCCCAAGTATCTG
ATGCAGGAATGCCCTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCT
GCTATTGAAGGGGATATCCCAGTTGTATCTATACCAGGAGCTAGCGCTGG
TATTACTGCTCTCATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTTT
ATGGCTTCTTACCACGTAAGAAAGGTCAACAAATAACTTTCTTTGAAACA
AAGCAAGATTACCCTGAAACACAAATCTTTTATGAGTCACCGtTTCGAGT
CTCTGATACGCTAAAACACATGAAAGAGATTTACGGAGATCGCCAAGTTG
TTTTAGTACGCGAATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACC
ATTAGTCAACTTTTAGAGCATATTGAAAAGGTCCCTCTCAAAGGTGAATG
CTTAATTATTGTTGATGGTAAGAGAGATACCGAGCGAGTGAAAGACAGTA
GCCAACAAGATCCACTAGTATTAGTAA

SEQ ID NO. 7407
STRAIN COH1
GAAATGCAAGTTCAAAAAAGTTTTaAATCAAATATACATTAC
GGAACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGAC
TTTTCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGAGG
ATACACGAAATACGGGAcTTTTACTCAAGCACTTTGATATTACTACTAAA
CAAATTAGTTTTCACGAACACAATGCTTACGATAAAATCTCTGGGTTAAT
TGATTTGTTAAAAGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGGAA
TGCCCTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAA
GGGGATATCCCAGTTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGC
TCTCATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTTTATGGCTTCT
TACCACGTAAGAAAGGTCAACAAATAACTTTCTTTGAAACAAAGCAAGAT
TACCCTGAAACACAAATCTTTTATGAGTCACCGtTTCGAGTCTCTGATAC
GCTAAAACACATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTTAGTAC
GCGAATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAA
CTTTTAGAGCATATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTAT
TGTTGATGGTAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACAAG
ATCCACTAGTATTAGTAA

SEQ ID NO. 7408
STRAIN M781
AAATGCAAGTTCAAAAAAGTTTTAAATCAAATATACATTACGGAACACTC
TATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGC
CATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGAGGATACACGAA
ATACGGgACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTAGT
TTTCACGAACACAATGCTTACGATAAAATCTCTGGGTTAATTGATTTGTT
AAAAGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTcTA
TTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATC
CCAGTTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCGC
TTCAGGTTTAGCTCCACAACCTCATATTTTTTATGGCTTCTTACCACGTA
AGAAAGGTCAACAAATAACTTTCTTTGAAACAAAGCAAGATTACCCTGAA
ACACAAATCTTTTATGAGTCACCGTTTCGAGTcTcTGATACGCTAAAACA
CATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTTAGTACGCGAATTGA
CGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAGAG
CATATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGG
TAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTAG
TATTAGTAA
A

SEQ ID NO. 7409
STRAIN CJB110
GAAATGCAAGTTCAAAAAAGTTTTAAATCAAATACACATTACGGGACAC
TCTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGT
GCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGAGGATACACG
AAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTA
GTTTTCACGAACACAATGCTTACGATAAAATCTCTGGGTTAATTGATTTG
TTAAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTC
TATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGGGA
TCCCGGTCGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATC
GCTTCAGGTTTAGCTCCACAACCTCATATTTTTTATGGCTTCTTACCGCG
TAAGAAAGGTCAACAAATAACTTTtTTTGAAACAAAGAAAGATTACCCTG
AAACACAAATCTTtTTATGAGTCACCGtTTcGAGTCTCTGATACGCTAAAA
CACATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTTAGTACGCGAATT

Table 74: Comparative Sequences relating to SAG1572

GACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAG
GGCATATTGAAAAAGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGAT
GGTAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACAAGATCCACT
AGTATTAGTAA

SEQ ID NO. 7410
STRAIN 1169NT
TGCAAGTTCAAAAAAGTTTTAAATCAAATACACATTATGGGACACTCTAT
CTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGCCAT
TAGGATTTTAAGAgAAGTTGaTTTTATTTGTGCAGAGGATACACGAAATA
CGGGACTTTTACTCAAGCACTTTGATaTTACTACTAAACAAATTAGtTTT
cACGAACACAATGCTTACGATAAAATCTCTGGGTTAATTGATTtGTTAAA
AGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCTATTT
CTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCCA
GTTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTC
AGGTTTAGCTCCACAACCTCATATTTTTTATGGCTTCTTACCACGTAAGA
AAGGTCAACAAATAACTTTTTTTGAAACAAAGCAAGATTATCCTGAAACA
CAAATCTTTTATGAGTCACCGtTTCGAGTCTCTGATACGCTAAAACACAT
GAAAGAGATTTACGGAGATCGCCAAGTTGTTTTAGTACGCGAATTGACgA
AACTCTATGAAGAGTATCAAAGAGGAACCATTaGTCAACTTTTAGAGCAT
ATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGtTGATGGTAA
GAGAGAtaCCGAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTAGTAT
TAGTAA

SEQ ID NO. 7411
STRAIN JM9130013
GAAATGCAAGTTCAAAAAAGTTTTAAATCAAATACACATTACGGGA
CACTCTATCTAGTCCCAACTCCAATTGGTAATCTAgATGATATGACTTTT
CGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGAGGATAC
ACGAAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAACAAA
TTAGTTTTCACGAACACAATGCTTATGATAAAATCTCTGGGTTAATTGAT
TTGTTAAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGGAATGCC
CTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCtGCTATTGAAGGGG
ATATCCCGGTCGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTC
ATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTTTATGGCTTCTTACC
GCGTAAGCAAGGTCAACAAATAACtTTTTTTGAAACAAAGAAAGATTACC
CTGAAACACAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTA
AAACACATGAAAGAGATTTATGGAGATCGCCAAGTTGTTTTAGTACGCGA
ATTGACGAAACTCTATGAAGAGTATCAAaGAGGAACCATTAGTCAACTTT
TAGGGCATATTGaAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTT
GATGGTAAGAGAGATACTGAGCGAGTGAAAGACAGTAGCCAACAAGATCC
AGTAGTATTAGTAA

```
 PRETTY of: /biotmp/msa323014.2{*}   March 28, 2003 02:40  ..

                               1                                                  50
    msa323014.2{343_18RS21}   ---gaaatgc aAGTTCAAAA AAGTTTTAAA TCAAATAtAC ATTAcGGaAC
      msa323014.2{343_A909}   ---------- -AGTTCAAAA AAGTTTTAAA TCAAATAtAC ATTAcGGaAC
      msa323014.2{343_COH1}   ---gaaatgc aAGTTCAAAA AAGTTTTAAA TCAAATAtAC ATTAcGGaAC
      msa323014.2{343_M732}   ---gaaatgc aAGTTCAAAA AAGTTTTAAA TCAAATAtAC ATTAcGGaAC
      msa323014.2{343_M781}   ----aaatgc aAGTTCAAAA AAGTTTTAAA TCAAATAtAC ATTAcGGaAC
      msa323014.2{343_2603}   atggaaatgc aAGTTCAAAA AAGTTTTAAA TCAAATAtAC ATTAcGGaAC
    msa323014.2{343_1169NT}   -------tgc aAGTTCAAAA AAGTTTTAAA TCAAATAcAC ATTAtGGgAC
       msa323014.2{343_090}   ---gaaatgc aAGTTCAAAA AAGTTTTAAA TCAAATAcAC ATTAcGGgAC
    msa323014.2{343_CJB110}   ---gaaatgc aAGTTCAAAA AAGTTTTAAA TCAAATAcAC ATTAcGGgAC
      msa323014.2{343_H36B}   ---gaaatgc aAGTTCAAAA AAGTTTTAAA TCAAATAcAC ATTAcGGgAC
 msa323014.2{343_JM9130013}   ---gaaatgc aAGTTCAAAA AAGTTTTAAA TCAAATAcAC ATTAcGGgAC
                  Consensus   ***------- -********* ********** *******-** ****-**-**

                              51                                                 100
    msa323014.2{343_18RS21}   ACTCTATCTA GTCCCAACTC CAATTGGTAA TCTAGATGAT ATGACTTTTC
      msa323014.2{343_A909}   ACTCTATCTA GTCCCAACTC CAATTGGTAA TCTAGATGAT ATGACTTTTC
      msa323014.2{343_COH1}   ACTCTATCTA GTCCCAACTC CAATTGGTAA TCTAGATGAT ATGACTTTTC
      msa323014.2{343_M732}   ACTCTATCTA GTCCCAACTC CAATTGGTAA TCTAGATGAT ATGACTTTTC
      msa323014.2{343_M781}   ACTCTATCTA GTCCCAACTC CAATTGGTAA TCTAGATGAT ATGACTTTTC
      msa323014.2{343_2603}   ACTCTATCTA GTCCCAACTC CAATTGGTAA TCTAGATGAT ATGACTTTTC
    msa323014.2{343_1169NT}   ACTCTATCTA GTCCCAACTC CAATTGGTAA TCTAGATGAT ATGACTTTTC
       msa323014.2{343_090}   ACTCTATCTA GTCCCAACTC CAATTGGTAA TCTAGATGAT ATGACTTTTC
    msa323014.2{343_CJB110}   ACTCTATCTA GTCCCAACTC CAATTGGTAA TCTAGATGAT ATGACTTTTC
      msa323014.2{343_H36B}   ACTCTATCTA GTCCCAACTC CAATTGGTAA TCTAGATGAT ATGACTTTTC
 msa323014.2{343_JM9130013}   ACTCTATCTA GTCCCAACTC CAATTGGTAA TCTAGATGAT ATGACTTTTC
                  Consensus   ********** ********** ********** ********** **********

                              101                                                150
    msa323014.2{343_18RS21}   GTGCCATTAG GATTTTAAGA GAAGTTGATT TTATTTGTGC AGAGGATACA
      msa323014.2{343_A909}   GTGCCATTAG GATTTTAAGA GAAGTTGATT TTATTTGTGC AGAGGATACA
      msa323014.2{343_COH1}   GTGCCATTAG GATTTTAAGA GAAGTTGATT TTATTTGTGC AGAGGATACA
      msa323014.2{343_M732}   GTGCCATTAG GATTTTAAGA GAAGTTGATT TTATTTGTGC AGAGGATACA
      msa323014.2{343_M781}   GTGCCATTAG GATTTTAAGA GAAGTTGATT TTATTTGTGC AGAGGATACA
      msa323014.2{343_2603}   GTGCCATTAG GATTTTAAGA GAAGTTGATT TTATTTGTGC AGAGGATACA
    msa323014.2{343_1169NT}   GTGCCATTAG GATTTTAAGA GAAGTTGATT TTATTTGTGC AGAGGATACA
       msa323014.2{343_090}   GTGCCATTAG GATTTTAAGA GAAGTTGATT TTATTTGTGC AGAGGATACA
```

Table 74: Comparative Sequences relating to SAG1572

```
  msa323014.2{343_CJB110}  GTGCCATTAG GATTTTAAGA GAAGTTGATT TTATTTGTGC AGAGGATACA
    msa323014.2{343_H36B}  GTGCCATTAG GATTTTAAGA GAAGTTGATT TTATTTGTGC AGAGGATACA
msa323014.2{343_JM9130013}  GTGCCATTAG GATTTTAAGA GAAGTTGATT TTATTTGTGC AGAGGATACA
                Consensus  ********** ********** ********** ********** **********

                           151                                                200
  msa323014.2{343_18RS21}  CGAAATACGG GACTTTTACT CAAGCACTTT GATATTACTA CTAAACAAAT
    msa323014.2{343_A909}  CGAAATACGG GACTTTTACT CAAGCACTTT GATATTACTA CTAAACAAAT
    msa323014.2{343_COH1}  CGAAATACGG GACTTTTACT CAAGCACTTT GATATTACTA CTAAACAAAT
    msa323014.2{343_M732}  CGAAATACGG GACTTTTACT CAAGCACTTT GATATTACTA CTAAACAAAT
    msa323014.2{343_M781}  CGAAATACGG GACTTTTACT CAAGCACTTT GATATTACTA CTAAACAAAT
    msa323014.2{343_2603}  CGAAATACGG GACTTTTACT CAAGCACTTT GATATTACTA CTAAACAAAT
  msa323014.2{343_1169NT}  CGAAATACGG GACTTTTACT CAAGCACTTT GATATTACTA CTAAACAAAT
     msa323014.2{343_090}  CGAAATACGG GACTTTTACT CAAGCACTTT GATATTACTA CTAAACAAAT
  msa323014.2{343_CJB110}  CGAAATACGG GACTTTTACT CAAGCACTTT GATATTACTA CTAAACAAAT
    msa323014.2{343_H36B}  CGAAATACGG GACTTTTACT CAAGCACTTT GATATTACTA CTAAACAAAT
msa323014.2{343_JM9130013}  CGAAATACGG GACTTTTACT CAAGCACTTT GATATTACTA CTAAACAAAT
                Consensus  ********** ********** ********** ********** **********

                           201                                                250
  msa323014.2{343_18RS21}  TAGTTTTCAC GAACACAATG CTTAcGATAA AATCTCTGGG TTAATTGATT
    msa323014.2{343_A909}  TAGTTTTCAC GAACACAATG CTTAcGATAA AATCTCTGGG TTAATTGATT
    msa323014.2{343_COH1}  TAGTTTTCAC GAACACAATG CTTAcGATAA AATCTCTGGG TTAATTGATT
    msa323014.2{343_M732}  TAGTTTTCAC GAACACAATG CTTAcGATAA AATCTCTGGG TTAATTGATT
    msa323014.2{343_M781}  TAGTTTTCAC GAACACAATG CTTAcGATAA AATCTCTGGG TTAATTGATT
    msa323014.2{343_2603}  TAGTTTTCAC GAACACAATG CTTAcGATAA AATCTCTGGG TTAATTGATT
  msa323014.2{343_1169NT}  TAGTTTTCAC GAACACAATG CTTAcGATAA AATCTCTGGG TTAATTGATT
     msa323014.2{343_090}  TAGTTTTCAC GAACACAATG CTTAcGATAA AATCTCTGGG TTAATTGATT
  msa323014.2{343_CJB110}  TAGTTTTCAC GAACACAATG CTTAcGATAA AATCTCTGGG TTAATTGATT
    msa323014.2{343_H36B}  TAGTTTTCAC GAACACAATG CTTAtGATAA AATCTCTGGG TTAATTGATT
msa323014.2{343_JM9130013}  TAGTTTTCAC GAACACAATG CTTAtGATAA AATCTCTGGG TTAATTGATT
                Consensus  ********** ********** ****-***** ********** **********

                           251                                                300
  msa323014.2{343_18RS21}  TGTTAAAAGA AGGGAaATCT TTAGCCCAAG TATCTGATGC AGGAATGCCC
    msa323014.2{343_A909}  TGTTAAAAGA AGGGAaATCT TTAGCCCAAG TATCTGATGC AGGAATGCCC
    msa323014.2{343_COH1}  TGTTAAAAGA AGGGAaATCT TTAGCCCAAG TATCTGATGC AGGAATGCCC
    msa323014.2{343_M732}  TGTTAAAAGA AGGGAaATCT TTAGCCCAAG TATCTGATGC AGGAATGCCC
    msa323014.2{343_M781}  TGTTAAAAGA AGGGAaATCT TTAGCCCAAG TATCTGATGC AGGAATGCCC
    msa323014.2{343_2603}  TGTTAAAAGA AGGGAaATCT TTAGCCCAAG TATCTGATGC AGGAATGCCC
  msa323014.2{343_1169NT}  TGTTAAAAGA AGGGAaATCT TTAGCCCAAG TATCTGATGC AGGAATGCCC
     msa323014.2{343_090}  TGTTAAAAGA AGGGAgATCT TTAGCCCAAG TATCTGATGC AGGAATGCCC
  msa323014.2{343_CJB110}  TGTTAAAAGA AGGGAgATCT TTAGCCCAAG TATCTGATGC AGGAATGCCC
    msa323014.2{343_H36B}  TGTTAAAAGA AGGGAgATCT TTAGCCCAAG TATCTGATGC AGGAATGCCC
msa323014.2{343_JM9130013}  TGTTAAAAGA AGGGAgATCT TTAGCCCAAG TATCTGATGC AGGAATGCCC
                Consensus  ********** *****-**** ********** ********** **********

                           301                                                350
  msa323014.2{343_18RS21}  TCTATTTCTG ACCCAGGACA TGACCTTGTC AAGGCTGCTA TTGAAGGGGa
    msa323014.2{343_A909}  TCTATTTCTG ACCCAGGACA TGACCTTGTC AAGGCTGCTA TTGAAGGGGa
    msa323014.2{343_COH1}  TCTATTTCTG ACCCAGGACA TGACCTTGTC AAGGCTGCTA TTGAAGGGGa
    msa323014.2{343_M732}  TCTATTTCTG ACCCAGGACA TGACCTTGTC AAGGCTGCTA TTGAAGGGGa
    msa323014.2{343_M781}  TCTATTTCTG ACCCAGGACA TGACCTTGTC AAGGCTGCTA TTGAAGGGGa
    msa323014.2{343_2603}  TCTATTTCTG ACCCAGGACA TGACCTTGTC AAGGCTGCTA TTGAAGGGGa
  msa323014.2{343_1169NT}  TCTATTTCTG ACCCAGGACA TGACCTTGTC AAGGCTGCTA TTGAAGGGGa
     msa323014.2{343_090}  TCTATTTCTG ACCCAGGACA TGACCTTGTC AAGGCTGCTA TTGAAGGGGg
  msa323014.2{343_CJB110}  TCTATTTCTG ACCCAGGACA TGACCTTGTC AAGGCTGCTA TTGAAGGGGg
    msa323014.2{343_H36B}  TCTATTTCTG ACCCAGGACA TGACCTTGTC AAGGCTGCTA TTGAAGGGGa
msa323014.2{343_JM9130013}  TCTATTTCTG ACCCAGGACA TGACCTTGTC AAGGCTGCTA TTGAAGGGGa
                Consensus  ********** ********** ********** ********** *********-

                           351                                                400
  msa323014.2{343_18RS21}  tATCCCaGTt GTATCTATAC CAGGAGCTAG CGCTGGTATT ACTGCTCTCA
    msa323014.2{343_A909}  tATCCCaGTt GTATCTATAC CAGGAGCTAG CGCTGGTATT ACTGCTCTCA
    msa323014.2{343_COH1}  tATCCCaGTt GTATCTATAC CAGGAGCTAG CGCTGGTATT ACTGCTCTCA
    msa323014.2{343_M732}  tATCCCaGTt GTATCTATAC CAGGAGCTAG CGCTGGTATT ACTGCTCTCA
    msa323014.2{343_M781}  tATCCCaGTt GTATCTATAC CAGGAGCTAG CGCTGGTATT ACTGCTCTCA
    msa323014.2{343_2603}  tATCCCaGTt GTATCTATAC CAGGAGCTAG CGCTGGTATT ACTGCTCTCA
  msa323014.2{343_1169NT}  tATCCCaGTt GTATCTATAC CAGGAGCTAG CGCTGGTATT ACTGCTCTCA
     msa323014.2{343_090}  gATCCCgGTc GTATCTATAC CAGGAGCTAG CGCTGGTATT ACTGCTCTCA
  msa323014.2{343_CJB110}  gATCCCgGTc GTATCTATAC CAGGAGCTAG CGCTGGTATT ACTGCTCTCA
    msa323014.2{343_H36B}  tATCCCgGTc GTATCTATAC CAGGAGCTAG CGCTGGTATT ACTGCTCTCA
msa323014.2{343_JM9130013}  tATCCCgGTc GTATCTATAC CAGGAGCTAG CGCTGGTATT ACTGCTCTCA
                Consensus  -*****-**- ********** ********** ********** **********

                           401                                                450
  msa323014.2{343_18RS21}  TCGCTTCAGG TTTAGCTCCA CAACCTCATA TTTTTTATGG CTTCTTACCa
    msa323014.2{343_A909}  TCGCTTCAGG TTTAGCTCCA CAACCTCATA TTTTTTATGG CTTCTTACCa
    msa323014.2{343_COH1}  TCGCTTCAGG TTTAGCTCCA CAACCTCATA TTTTTTATGG CTTCTTACCa
    msa323014.2{343_M732}  TCGCTTCAGG TTTAGCTCCA CAACCTCATA TTTTTTATGG CTTCTTACCa
    msa323014.2{343_M781}  TCGCTTCAGG TTTAGCTCCA CAACCTCATA TTTTTTATGG CTTCTTACCa
    msa323014.2{343_2603}  TCGCTTCAGG TTTAGCTCCA CAACCTCATA TTTTTTATGG CTTCTTACCt
  msa323014.2{343_1169NT}  TCGCTTCAGG TTTAGCTCCA CAACCTCATA TTTTTTATGG CTTCTTACCa
```

Table 74: Comparative Sequences relating to SAG1572

```
     msa323014.2{343_090}  TCGCTTCAGG TTTAGCTCCA CAACCTCATA TTTTTTATGG CTTCTTACCg
   msa323014.2{343_CJB110}  TCGCTTCAGG TTTAGCTCCA CAACCTCATA TTTTTTATGG CTTCTTACCg
     msa323014.2{343_H36B}  TCGCTTCAGG TTTAGCTCCA CAACCTCATA TTTTTTATGG CTTCTTACCg
msa323014.2{343_JM9130013}  TCGCTTCAGG TTTAGCTCCA CAACCTCATA TTTTTTATGG CTTCTTACCg
                 Consensus  ********** ********** ********** ********** *********-

                            451                                               500
   msa323014.2{343_18RS21}  CGTAAGaAAG GTCAACAAAT AACTTTcTTT GAAACAAAGc AAGATTAcCC
     msa323014.2{343_A909}  CGTAAGaAAG GTCAACAAAT AACTTTcTTT GAAACAAAGc AAGATTAcCC
     msa323014.2{343_COH1}  CGTAAGaAAG GTCAACAAAT AACTTTcTTT GAAACAAAGc AAGATTAcCC
     msa323014.2{343_M732}  CGTAAGaAAG GTCAACAAAT AACTTTcTTT GAAACAAAGc AAGATTAcCC
     msa323014.2{343_M781}  CGTAAGaAAG GTCAACAAAT AACTTTcTTT GAAACAAAGc AAGATTAcCC
     msa323014.2{343_2603}  CGTAAGaAAG GTCAACAAAT AACTTTcTTT GAAACAAAGc AAGATTAcCC
   msa323014.2{343_1169NT}  CGTAAGaAAG GTCAACAAAT AACTTTtTTT GAAACAAAGc AAGATTAtCC
      msa323014.2{343_090}  CGTAAGaAAG GTCAACAAAT AACTTTtTTT GAAACAAAGa AAGATTAcCC
   msa323014.2{343_CJB110}  CGTAAGaAAG GTCAACAAAT AACTTTtTTT GAAACAAAGa AAGATTAcCC
     msa323014.2{343_H36B}  CGTAAGcAAG GTCAACAAAT AACTTTtTTT GAAACAAAGa AAGATTAcCC
msa323014.2{343_JM9130013}  CGTAAGcAAG GTCAACAAAT AACTTTtTTT GAAACAAAGa AAGATTAcCC
                 Consensus  ******-*** ********** ******-*** *********- *******-**

                            501                                               550
   msa323014.2{343_18RS21}  TGAAACACAA ATCTTTTATG AGTCACCGTT TCGAGTCTCT GATACGCTAA
     msa323014.2{343_A909}  TGAAACACAA ATCTTTTATG AGTCACCGTT TCGAGTCTCT GATACGCTAA
     msa323014.2{343_COH1}  TGAAACACAA ATCTTTTATG AGTCACCGTT TCGAGTCTCT GATACGCTAA
     msa323014.2{343_M732}  TGAAACACAA ATCTTTTATG AGTCACCGTT TCGAGTCTCT GATACGCTAA
     msa323014.2{343_M781}  TGAAACACAA ATCTTTTATG AGTCACCGTT TCGAGTCTCT GATACGCTAA
     msa323014.2{343_2603}  TGAAACACAA ATCTTTTATG AGTCACCGTT TCGAGTCTCT GATACGCTAA
   msa323014.2{343_1169NT}  TGAAACACAA ATCTTTTATG AGTCACCGTT TCGAGTCTCT GATACGCTAA
      msa323014.2{343_090}  TGAAACACAA ATCTTTTATG AGTCACCGTT TCGAGTCTCT GATACGCTAA
   msa323014.2{343_CJB110}  TGAAACACAA ATCTTTTATG AGTCACCGTT TCGAGTCTCT GATACGCTAA
     msa323014.2{343_H36B}  TGAAACACAA ATCTTTTATG AGTCACCGTT TCGAGTCTCT GATACGCTAA
msa323014.2{343_JM9130013}  TGAAACACAA ATCTTTTATG AGTCACCGTT TCGAGTCTCT GATACGCTAA
                 Consensus  ********** ********** ********** ********** **********

                            551                                               600
   msa323014.2{343_18RS21}  AACACATGAA AGAGATTTAc GGAGATCGCC AAGTTGTTTT AGTACGCGAA
     msa323014.2{343_A909}  AACACATGAA AGAGATTTAc GGAGATCGCC AAGTTGTTTT AGTACGCGAA
     msa323014.2{343_COH1}  AACACATGAA AGAGATTTAc GGAGATCGCC AAGTTGTTTT AGTACGCGAA
     msa323014.2{343_M732}  AACACATGAA AGAGATTTAc GGAGATCGCC AAGTTGTTTT AGTACGCGAA
     msa323014.2{343_M781}  AACACATGAA AGAGATTTAc GGAGATCGCC AAGTTGTTTT AGTACGCGAA
     msa323014.2{343_2603}  AACACATGAA AGAGATTTAc GGAGATCGCC AAGTTGTTTT AGTACGCGAA
   msa323014.2{343_1169NT}  AACACATGAA AGAGATTTAc GGAGATCGCC AAGTTGTTTT AGTACGCGAA
      msa323014.2{343_090}  AACACATGAA AGAGATTTAc GGAGATCGCC AAGTTGTTTT AGTACGCGAA
   msa323014.2{343_CJB110}  AACACATGAA AGAGATTTAc GGAGATCGCC AAGTTGTTTT AGTACGCGAA
     msa323014.2{343_H36B}  AACACATGAA AGAGATTTAt GGAGATCGCC AAGTTGTTTT AGTACGCGAA
msa323014.2{343_JM9130013}  AACACATGAA AGAGATTTAt GGAGATCGCC AAGTTGTTTT AGTACGCGAA
                 Consensus  ********** *********- ********** ********** **********

                            601                                               650
   msa323014.2{343_18RS21}  TTGACGAAAC TCTATGAAGA GTATCAAAGA GGAACCATTA GTCAACTTTT
     msa323014.2{343_A909}  TTGACGAAAC TCTATGAAGA GTATCAAAGA GGAACCATTA GTCAACTTTT
     msa323014.2{343_COH1}  TTGACGAAAC TCTATGAAGA GTATCAAAGA GGAACCATTA GTCAACTTTT
     msa323014.2{343_M732}  TTGACGAAAC TCTATGAAGA GTATCAAAGA GGAACCATTA GTCAACTTTT
     msa323014.2{343_M781}  TTGACGAAAC TCTATGAAGA GTATCAAAGA GGAACCATTA GTCAACTTTT
     msa323014.2{343_2603}  TTGACGAAAC TCTATGAAGA GTATCAAAGA GGAACCATTA GTCAACTTTT
   msa323014.2{343_1169NT}  TTGACGAAAC TCTATGAAGA GTATCAAAGA GGAACCATTA GTCAACTTTT
      msa323014.2{343_090}  TTGACGAAAC TCTATGAAGA GTATCAAAGA GGAACCATTA GTCAACTTTT
   msa323014.2{343_CJB110}  TTGACGAAAC TCTATGAAGA GTATCAAAGA GGAACCATTA GTCAACTTTT
     msa323014.2{343_H36B}  TTGACGAAAC TCTATGAAGA GTATCAAAGA GGAACCATTA GTCAACTTTT
msa323014.2{343_JM9130013}  TTGACGAAAC TCTATGAAGA GTATCAAAGA GGAACCATTA GTCAACTTTT
                 Consensus  ********** ********** ********** ********** **********

                            651                                               700
   msa323014.2{343_18RS21}  AGaGCATATT GAAAAgGTCC CTCTCAAAGG TGAATGCTTA ATTATTGTTG
     msa323014.2{343_A909}  AGaGCATATT GAAAAgGTCC CTCTCAAAGG TGAATGCTTA ATTATTGTTG
     msa323014.2{343_COH1}  AGaGCATATT GAAAAgGTCC CTCTCAAAGG TGAATGCTTA ATTATTGTTG
     msa323014.2{343_M732}  AGaGCATATT GAAAAgGTCC CTCTCAAAGG TGAATGCTTA ATTATTGTTG
     msa323014.2{343_M781}  AGaGCATATT GAAAAgGTCC CTCTCAAAGG TGAATGCTTA ATTATTGTTG
     msa323014.2{343_2603}  AGaGCATATT GAAAAgGTCC CTCTCAAAGG TGAATGCTTA ATTATTGTTG
   msa323014.2{343_1169NT}  AGaGCATATT GAAAAgGTCC CTCTCAAAGG TGAATGCTTA ATTATTGTTG
      msa323014.2{343_090}  AGgGCATATT GAAAAaGTCC CTCTCAAAGG TGAATGCTTA ATTATTGTTG
   msa323014.2{343_CJB110}  AGgGCATATT GAAAAaGTCC CTCTCAAAGG TGAATGCTTA ATTATTGTTG
     msa323014.2{343_H36B}  AGgGCATATT GAAAAgGTCC CTCTCAAAGG TGAATGCTTA ATTATTGTTG
msa323014.2{343_JM9130013}  AGgGCATATT GAAAAgGTCC CTCTCAAAGG TGAATGCTTA ATTATTGTTG
                 Consensus  **-******* *****-**** ********** ********** **********

                            701                                               750
   msa323014.2{343_18RS21}  ATGGTAAGAG AGATACcGAG CGAGTGAAAG ACAGTAGCCA ACAAGATCCA
     msa323014.2{343_A909}  ATGGTAAGAG AGATACcGAG CGAGTGAAAG ACAGTAGCCA ACAAGATCCA
     msa323014.2{343_COH1}  ATGGTAAGAG AGATACcGAG CGAGTGAAAG ACAGTAGCCA ACAAGATCCA
     msa323014.2{343_M732}  ATGGTAAGAG AGATACcGAG CGAGTGAAAG ACAGTAGCCA ACAAGATCCA
     msa323014.2{343_M781}  ATGGTAAGAG AGATACcGAG CGAGTGAAAG ACAGTAGCCA ACAAGATCCA
     msa323014.2{343_2603}  ATGGTAAGAG AGATACcGAG CGAGTGAAAG ACAGTAGCCA ACAAGATCCA
```

Table 74: Comparative Sequences relating to SAG1572

```
   msa323014.2{343_1169NT}  ATGGTAAGAG AGATACcGAG CGAGTGAAAG ACAGTAGCCA ACAAGATCCA
      msa323014.2{343_090}  ATGGTAAGAG AGATACcGAG CGAGTGAAAG ACAGTAGCCA ACAAGATCCA
   msa323014.2{343_CJB110}  ATGGTAAGAG AGATACcGAG CGAGTGAAAG ACAGTAGCCA ACAAGATCCA
     msa323014.2{343_H36B}  ATGGTAAGAG AGATACtGAG CGAGTGAAAG ACAGTAGCCA ACAAGATCCA
msa323014.2{343_JM9130013}  ATGGTAAGAG AGATACtGAG CGAGTGAAAG ACAGTAGCCA ACAAGATCCA
                 Consensus  ********** ******-*** ********** ********** **********

                            751                                              800
   msa323014.2{343_18RS21}  cTAGTATTAG TAA~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa323014.2{343_A909}  cTAGTATTAG TAA~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa323014.2{343_COH1}  cTAGTATTAG TAA~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa323014.2{343_M732}  cTAGTATTAG TAA~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa323014.2{343_M781}  cTAGTATTAG TAAA~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa323014.2{343_2603}  cTAGTATTAG TAAAagaata tatcgctaat ggtgataaaa ctaatcaagc
   msa323014.2{343_1169NT}  cTAGTATTAG TAA~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa323014.2{343_090}  cTAGTATTAG TAA~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa323014.2{343_CJB110}  cTAGTATTAG TAA~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa323014.2{343_H36B}  cTAGTATTAG TAA~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa323014.2{343_JM9130013}  gTAGTATTAG TAA~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                 Consensus  -********* ********** ********** ********** **********

                            801                                              850
   msa323014.2{343_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa323014.2{343_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa323014.2{343_COH1}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa323014.2{343_M732}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa323014.2{343_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa323014.2{343_2603}  gataaaaaaa gtagcaaaag aatttaatct caatagacaa gaactctatg
   msa323014.2{343_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa323014.2{343_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa323014.2{343_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa323014.2{343_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa323014.2{343_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                 Consensus  ********** ********** ********** ********** **********

                            851        867
   msa323014.2{343_18RS21}  ~~~~~~~~~~ ~~~~~~~
     msa323014.2{343_A909}  ~~~~~~~~~~ ~~~~~~~
     msa323014.2{343_COH1}  ~~~~~~~~~~ ~~~~~~~
     msa323014.2{343_M732}  ~~~~~~~~~~ ~~~~~~~
     msa323014.2{343_M781}  ~~~~~~~~~~ ~~~~~~~
     msa323014.2{343_2603}  ctagtttcca tgattta
   msa323014.2{343_1169NT}  ~~~~~~~~~~ ~~~~~~~
      msa323014.2{343_090}  ~~~~~~~~~~ ~~~~~~~
   msa323014.2{343_CJB110}  ~~~~~~~~~~ ~~~~~~~
     msa323014.2{343_H36B}  ~~~~~~~~~~ ~~~~~~~
msa323014.2{343_JM9130013}  ~~~~~~~~~~ ~~~~~~~
                 Consensus  ********** *******
```

SEQ ID NO. 7412
STRAIN 2603 frame: 1

```
MEMQVQKSFKSNIHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHF
DITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAAIEGDIPV
VSIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVS
DTLKHMKEIYGDRQVVLVRELTKLYEEYQRGTISQLLEHIEKVPLKGECLIIVDGKRDTE
RVKDSSQQDPLVLVKEYIANGDKTNQAIKKVAKEFNLNRQELYASFHDL
```

SEQ ID NO. 7413
STRAIN 090 frame: 1

```
EMQVQKSFKSNTHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLLKEGRSLAQVSDAGMPSISDPGHDLVKAAIEGGIPVV
SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKKDYPETQIFYESPFRVSD
TLKHMKEIYGDRQVVLVRELTKLYEEYQRGTISQLLGHIEKVPLKGECLIIVDGKRDTER
VKDSSQQDPLVLV
```

SEQ ID NO. 7414
STRAIN A909 frame: 2

```
VQKSFKSNIHYGTLYLVPTP,IGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFDITT
KQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAAIEGDIPVVSIP
GASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSDTLK
HMKEIYGDRQVVLVRELTKLYEEYQRGTISQLLEHIEKVPLKGECLIIVDGKRDTERVKD
SSQQDPLVLV
```

SEQ ID NO. 7415
STRAIN H36B frame: 1

```
EMQVQKSFKSNTHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLLKEGRSLAQVSDAGMPSISDPGHDLVKAAIEGDIPVV
SIPGASAGITALIASGLAPQPHIFYGFLPRKQGQQITFFETKKDYPETQIFYESPFRVSD
TLKHMKEIYGDRQVVLVRELTKLYEEYQRGTISQLLGHIEKVPLKGECLIIVDGKRDTER
VKDSSQQDPLVLV
```

SEQ ID NO. 7416

Table 74: Comparative Sequences relating to SAG1572

STRAIN 18RS21 frame: 1
EMQVQKSFKSNIHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAAIEGDIPVV
SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
TLKHMKEIYGDRQVVLVRELTKLYEEYQRGTISQLLEHIEKVPLKGECLIIVDGKRDTER
VKDSSQQDPLVLV

SEQ ID NO. 7417
STRAIN M732 frame: 1
EMQVQKSFKSNIHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAAIEGDIPVV
SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
TLKHMKEIYGDRQVVLVRELTKLYEEYQRGTISQLLEHIEKVPLKGECLIIVDGKRDTER
VKDSSQQDPLVLV

SEQ ID NO. 7418
STRAIN COH1 frame: 1
EMQVQKSFKSNIHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAAIEGDIPVV
SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
TLKHMKEIYGDRQVVLVRELTKLYEEYQRGTISQLLEHIEKVPLKGECLIIVDGKRDTER
VKDSSQQDPLVLV

SEQ ID NO. 7419
STRAIN M781 frame: 3
MQVQKSFKSNIHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFDI
TTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAAIEGDIPVVS
IPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSDT
LKHMKEIYGDRQVVLVRELTKLYEEYQRGTISQLLEHIEKVPLKGECLIIVDGKRDTERV
KDSSQQDPLVLV

SEQ ID NO. 7420
STRAIN CJB110 frame: 1
EMQVQKSFKSNTHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLLKEGRSLAQVSDAGMPSISDPGHDLVKAAIEGGIPVV
SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKKDYPETQIFYESPFRVSD
TLKHMKEIYGDRQVVLVRELTKLYEEYQRGTISQLLGHIEKVPLKGECLIIVDGKRDTER
VKDSSQQDPLVLV

SEQ ID NO. 7421
STRAIN 1169NT frame: 3
QVQKSFKSNTHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFDIT
TKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSISDPGHDLVKAAIEGDIPVVSI
PGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSDTL
KHMKEIYGDRQVVLVRELTKLYEEYQRGTISQLLEHIEKVPLKGECLIIVDGKRDTERVK
DSSQQDPLVLV

SEQ ID NO. 7422
STRAIN JM9130013 frame: 1
EMQVQKSFKSNTHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLLKEGRSLAQVSDAGMPSISDPGHDLVKAAIEGDIPVV
SIPGASAGITALIASGLAPQPHIFYGFLPRKQGQQITFFETKKDYPETQIFYESPFRVSD
TLKHMKEIYGDRQVVLVRELTKLYEEYQRGTISQLLGHIEKVPLKGECLIIVDGKRDTER
VKDSSQQDPVVLV

```
                           1                                                  50
     msa324064.2{343_18RS21}   ~emqVQKSFK SNiHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT
       msa324064.2{343_A909}   ----VQKSFK SNiHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT
       msa324064.2{343_M781}   --mqVQKSFK SNiHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT
       msa324064.2{343_2603}   memqVQKSFK SNiHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT
       msa324064.2{343_COH1}   ~emqVQKSFK SNiHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT
       msa324064.2{343_M732}   ~emqVQKSFK SNiHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT
     msa324064.2{343_1169NT}   ---qVQKSFK SNtHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT
        msa324064.2{343_090}   ~emqVQKSFK SNtHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT
     msa324064.2{343_CJB110}   ~emqVQKSFK SNtHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT
       msa324064.2{343_H36B}   ~emqVQKSFK SNtHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT
  msa324064.2{343_JM9130013}   ~emqVQKSFK SNtHYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT
                   Consensus   *---****** **-******* ********** ********** **********

                           51                                                100
     msa324064.2{343_18RS21}   RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLLKEGkS LAQVSDAGMP
       msa324064.2{343_A909}   RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLLKEGkS LAQVSDAGMP
       msa324064.2{343_M781}   RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLLKEGkS LAQVSDAGMP
       msa324064.2{343_2603}   RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLLKEGkS LAQVSDAGMP
       msa324064.2{343_COH1}   RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLLKEGkS LAQVSDAGMP
       msa324064.2{343_M732}   RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLLKEGkS LAQVSDAGMP
     msa324064.2{343_1169NT}   RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLLKEGkS LAQVSDAGMP
        msa324064.2{343_090}   RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLLKEGrS LAQVSDAGMP
     msa324064.2{343_CJB110}   RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLLKEGrS LAQVSDAGMP
       msa324064.2{343_H36B}   RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLLKEGrS LAQVSDAGMP
  msa324064.2{343_JM9130013}   RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLLKEGrS LAQVSDAGMP
                   Consensus   ********** ********** ********** ********-* **********
```

Table 74: Comparative Sequences relating to SAG1572

```
                                 101                                                150
      msa324064.2{343_18RS21}    SISDPGHDLV KAAIEGdIPV VSIPGASAGI TALIASGLAP QPHIFYGFLP
        msa324064.2{343_A909}    SISDPGHDLV KAAIEGdIPV VSIPGASAGI TALIASGLAP QPHIFYGFLP
        msa324064.2{343_M781}    SISDPGHDLV KAAIEGdIPV VSIPGASAGI TALIASGLAP QPHIFYGFLP
        msa324064.2{343_2603}    SISDPGHDLV KAAIEGdIPV VSIPGASAGI TALIASGLAP QPHIFYGFLP
        msa324064.2{343_COH1}    SISDPGHDLV KAAIEGdIPV VSIPGASAGI TALIASGLAP QPHIFYGFLP
        msa324064.2{343_M732}    SISDPGHDLV KAAIEGdIPV VSIPGASAGI TALIASGLAP QPHIFYGFLP
      msa324064.2{343_1169NT}    SISDPGHDLV KAAIEGdIPV VSIPGASAGI TALIASGLAP QPHIFYGFLP
         msa324064.2{343_090}    SISDPGHDLV KAAIEGgIPV VSIPGASAGI TALIASGLAP QPHIFYGFLP
      msa324064.2{343_CJB110}    SISDPGHDLV KAAIEGgIPV VSIPGASAGI TALIASGLAP QPHIFYGFLP
        msa324064.2{343_H36B}    SISDPGHDLV KAAIEGdIPV VSIPGASAGI TALIASGLAP QPHIFYGFLP
   msa324064.2{343_JM9130013}    SISDPGHDLV KAAIEGdIPV VSIPGASAGI TALIASGLAP QPHIFYGFLP
                    Consensus    ********** ******-*** ********** ********** **********

                                 151                                                200
      msa324064.2{343_18RS21}    RKkGQQITFF ETKqDYPETQ IFYESPFRVS DTLKHMKEIY GDRQVVLVRE
        msa324064.2{343_A909}    RKkGQQITFF ETKqDYPETQ IFYESPFRVS DTLKHMKEIY GDRQVVLVRE
        msa324064.2{343_M781}    RKkGQQITFF ETKqDYPETQ IFYESPFRVS DTLKHMKEIY GDRQVVLVRE
        msa324064.2{343_2603}    RKkGQQITFF ETKqDYPETQ IFYESPFRVS DTLKHMKEIY GDRQVVLVRE
        msa324064.2{343_COH1}    RKkGQQITFF ETKqDYPETQ IFYESPFRVS DTLKHMKEIY GDRQVVLVRE
        msa324064.2{343_M732}    RKkGQQITFF ETKqDYPETQ IFYESPFRVS DTLKHMKEIY GDRQVVLVRE
      msa324064.2{343_1169NT}    RKkGQQITFF ETKqDYPETQ IFYESPFRVS DTLKHMKEIY GDRQVVLVRE
         msa324064.2{343_090}    RKkGQQITFF ETKkDYPETQ IFYESPFRVS DTLKHMKEIY GDRQVVLVRE
      msa324064.2{343_CJB110}    RKkGQQITFF ETKkDYPETQ IFYESPFRVS DTLKHMKEIY GDRQVVLVRE
        msa324064.2{343_H36B}    RKqGQQITFF ETKkDYPETQ IFYESPFRVS DTLKHMKEIY GDRQVVLVRE
   msa324064.2{343_JM9130013}    RKqGQQITFF ETKkDYPETQ IFYESPFRVS DTLKHMKEIY GDRQVVLVRE
                    Consensus    **-******* ***-****** ********** ********** **********

                                 201                                                250
      msa324064.2{343_18RS21}    LTKLYEEYQR GTISQLLeHI EKVPLKGECL IIVDGKRDTE RVKDSSQQDP
        msa324064.2{343_A909}    LTKLYEEYQR GTISQLLeHI EKVPLKGECL IIVDGKRDTE RVKDSSQQDP
        msa324064.2{343_M781}    LTKLYEEYQR GTISQLLeHI EKVPLKGECL IIVDGKRDTE RVKDSSQQDP
        msa324064.2{343_2603}    LTKLYEEYQR GTISQLLeHI EKVPLKGECL IIVDGKRDTE RVKDSSQQDP
        msa324064.2{343_COH1}    LTKLYEEYQR GTISQLLeHI EKVPLKGECL IIVDGKRDTE RVKDSSQQDP
        msa324064.2{343_M732}    LTKLYEEYQR GTISQLLeHI EKVPLKGECL IIVDGKRDTE RVKDSSQQDP
      msa324064.2{343_1169NT}    LTKLYEEYQR GTISQLLeHI EKVPLKGECL IIVDGKRDTE RVKDSSQQDP
         msa324064.2{343_090}    LTKLYEEYQR GTISQLLgHI EKVPLKGECL IIVDGKRDTE RVKDSSQQDP
      msa324064.2{343_CJB110}    LTKLYEEYQR GTISQLLgHI EKVPLKGECL IIVDGKRDTE RVKDSSQQDP
        msa324064.2{343_H36B}    LTKLYEEYQR GTISQLLgHI EKVPLKGECL IIVDGKRDTE RVKDSSQQDP
   msa324064.2{343_JM9130013}    LTKLYEEYQR GTISQLLgHI EKVPLKGECL IIVDGKRDTE RVKDSSQQDP
                    Consensus    ********** *******-** ********** ********** **********

                                 251                                     289
      msa324064.2{343_18RS21}    lVLV~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~
        msa324064.2{343_A909}    lVLV~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~
        msa324064.2{343_M781}    lVLV~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~
        msa324064.2{343_2603}    lVLVkeyian gdktnqaikk vakefnlnrq elyasfhdl
        msa324064.2{343_COH1}    lVLV~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~
        msa324064.2{343_M732}    lVLV~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~
      msa324064.2{343_1169NT}    lVLV~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~
         msa324064.2{343_090}    lVLV~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~
      msa324064.2{343_CJB110}    lVLV~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~
        msa324064.2{343_H36B}    lVLV~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~
   msa324064.2{343_JM9130013}    vVLV~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~
                    Consensus    -********* ********** ********** *********
```

Table 75: Comparative Sequences relating to SAG0671

SEQ ID NO. 7501
STRAIN 2603
ATGAGCGTATATGTTAGTGGAATAGGAATTATT
TCTTCTTTGGGAAAGAATTATAGCGAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGA
ATTTCTAAACATTTATATAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCATA
ACTAGTGACCCAGAGGTTCCTGAGCAATACAAAGATGAGACACGTAATTTTAAATTTGCT
TTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTTAAAAGCTTATCATAAT
ATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAAAGAGTGCTGGTCAAAATGCCTTGTAT
CAATTTGAAGAAGGAGAGCGTCAAGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTAC
CATATTGCTGATGAATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCA
ACCGCCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAAGATGGC
GATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGATATTTCTTTAGCAGGC
TTCACATCACTAGGAGCTATTAATACAGAAATGGCATGTCAGCCCTATTCTTCTGGAAAA
GGAATCAATTTGGGTGAGGGCGCTGGTTTTGTTGTTCTTGTCAAAGATCAGTCCTTAGCT
AAATATGGAAAAATTATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCT
AAGCCAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCAGGTATT
GACTACAGTGAGATTGACTATATTAACGGTCACGGTACAGGTACTCAAGCTAATGATAAA
ATGGAAAAAAATATGTATGGTAAGTTTTTCCCGACAACGACATTGATCAGCAGTACCAAG
GGGCAAACGGGTCATACTCTAGGGGCTGCAGGTATTATCGAATTGATTAATTGTTTAGCG
GCAATAGAGGAACAGACTGTACCAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCA
GAAAATTTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAATTTTTCG
TTTGCTTTTGGTGGAAATAATAGTGGTGTCTTATTGTCATCTTTAGATTCACCTCTAGAA
ACATTACCTGCTAGAGAAAATCTTAAAATGGCTATCTTATCATCTGTTGCTTCCATTTCT
AAGAATGAATCACTTTCTATAACCTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAA
GCATTACGCTTTAAAGGGGCTAGACCACCCAAAACTGTCAACCCAGCACAATTTAGGAAA
ATGGATGATTTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAAAGCAAT
ATTAATCTAAAAAAACAAGATACTTCAAAAGTAGGAATTGTATTTACAACACTTTCTGGA
CCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAAATCACAACAGAAGGATATGCACATGTT
TCTGCTTCACGATTCCCGTTTACAGTAATGAATGCAGCAGCTGGTATGCTTTCTATCATT
TTTAAAATAACAGGTCCTTTATCTGTCATTTCGACAAATAGTGGAGCGCTTGATGGTATA
CAATATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGTTTCTGCT
AATCAGTGGACAGACATGAGTTTTATGTGGTGGCAACAATTAAACTATGATAGTCAAATG
TTTGTCGGTTCTGATTATTGTTCAGCACAAGTCCTCTCTCGTCAAGCATTGGATAATTCT
CCTATAATATTAGGTAGTAAACAATTAAAATATAGCCATAAAACATTCACAGATGTGATG
ACTATTTTTGATGCTGCGCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAAGAT
ATCAAAGGTTTCGTTTGGAATGAGCGGAAGAAGGCAGTTAGTTCAGATTATGATTTCTTA
GCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTGGTCAGTTTGGATTTTCA
TCTAATGGTGCTGGTGAAGAACTGGACTATACTGTTAATGAAAGTATAGAAAAGGGCTAT
TATTTAGTCCTATCTTATTCGATCTTCGGTGGTATCTCTTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7502
STRAIN 090
ATGTTAGTGGAATAGGAATTATTTCTTCTTTGGGAAAGaATTAT
AGCGAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACA
TTTATATAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCATAA
CTAGTGACCCAGAGGTTCCTGAGCAATACAAAGATGAGACACGTAATTTT
AAATTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAA
TTTAAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGG
GAAAGAGTGCTGGTCAAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGT
CAAGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGA
TGAATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAA
CCGCCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTT
CAAGATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAG
TGATATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAATACAGAAA
TGGCATGTCAGCCCTATTCTTCTGGAAAAGGAATCAATTTGGGTGAGGGC
GCTGGTTTTGTTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAAA
AATTATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTA
AGCCAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAA
GCAGGTATTGACTACAGTGAGATTGACTATATTAACGGTCACGGTACAGG
TACTCAAGCTAATGATAAAATGGAAAAAAATATGTATGGTAAGTTTTTCC
CGACAACGACATTGATCAGCAGTACCAAGGGGCAAACGGGTCATACTCTA
GGGGCTGCAGGTATTATCGAATTGATTAATTGTTTAGCGGCAATAGAGGA
ACAGACTGTACCAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCAG
AAAATTTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTA
AATTTTTCGTTTGCTTTTGGTGGAAATAATAGTGGTATCTTATTGTCATC
TTTAGATTCACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAAATGG
CTATCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATA
ACCTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTT
TAAAGGGGCTAGACCACCCAAAACTGTCAACCCAGCACAATTTAGGAAAA
TGGATGATTTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATA
GAAAGCAATATTAATCTAAAAAAACAAGATACTTCAAAAGTAGGAATTGT
ATTTACAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGC
AAATCACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCCGTTT
ACAGTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTAAAATAAC
AGGTCCTTTATCTGTCATTTCGACAAATAGTGGAGCGCTTGATGGTATAC
AATATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTT
GTTTCTGCTAATCAGTGGACAGACATGAGTTTTATGTGGTGGCAACAATT
AAACTATGATAGTCAAATGTTTGTCGGTTCTGATTATTGTTCAGCACAAG
TCCTCTCTCGTCAAGCATTGGATAATTCTCCTATAATATTAGGTAGTAAA
CAATTAAAATATAGCCATAAAACATTCACAGATGTGATGACTATTTTTGA
TGCTGCGCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAAGATA
TCAAAGGTTTCGTTTGGAATGAGCGGAAGAAGGCAGTTAGTTCAGATTAT
GATTTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGCTTC

Table 75: Comparative Sequences relating to SAG0671

TGGTCAGTTTGGATTTTCATCTAATGGTGCTGGTGAAGAACTGGACTATA
CTGTTAATGAAAGTATAGAAAAGGGCTATTATTTAGTCCTATCTTATTCG
ATCTTTGGTGGTATCTCTTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7503
STRAIN A909
ATGTTAGTGGAATAGGAATTATTTCTTCTTTGGGAAAGAATT
ATAGCGAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAA
CATTTATATAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCAT
AACTAGTGACCCAGAGGTTCCTGAGCAATACAAAGATGAGACACGTAATT
TTAAATTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTT
AATTTAAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGG
GGGAAAGAGTGCTGGTCAAAATGCCTTGTATCAATTTGAAGAAGGAGAGC
GTCAAGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCT
GATGAATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTC
AACCGCCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTAC
TTCAAGATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTA
AGTGATATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAATACAGA
AATGGCATGTCAGCCCTATTCTTCTGGAAAAGGAATCAATTTGGGTGAGG
GCGCTGGTTTTGTTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGA
AAAATTATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACC
TAAGCCAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTC
AAGCAGGTATTGACTACAGTGAGATTGACTATATTAACGGTCACGGTACA
GGTACTCAAGCTAATGATAAAATGGAAAAAAATATGTATGGTAAGTTTTT
CCCGACAACGACATTGATCAGCAGTACCAAGGGGCAAACGGGTCATACTC
TAGGGGCTGCAGGTATTATCGAATTGATTAATTGTTTAGCGGCAATAGAG
GAACAGACTGTACCAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCC
AGAAAATTTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTT
TAAATTTTTCGTTTGCTTTTGGTGGAAATAATAGTGGTGTCTTATTGTCA
TCTTTAGATTCACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAAAT
GGCTATCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTA
TAACCTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGC
TTTAAAGGGGCTAGACCACCCAAAACTGTCAACCCAGCACAATTTAGGAA
AATGGATGATTTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAA
TAGAAAGCAATATTAATCTAAAAAAACAAGATACTTCAAAAGTAGGAATT
GTATTTACAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAA
GCAAATCACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCCGT
TTACAGTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTAAAATA
ACAGGTCCTTTATCTGTCATTTCGACAAATAGTGGAGCGCTTGATGGTAT
ACAATATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTC
TTGTTTCTGCTAATCAGTGGACAGACATGAGTTTTATGTGGTGGCAACAA
TTAAACTATGATAGTCAAATGTTTGTCGGTTCTGATTATTGTTCAGCACA
AGTCCTCTCTCGTCAAGCATTGGATAATTCTCCTATAATATTAGGTAGTA
AACAATTAAAATATAGCCATAAAACATTCACAGATGTGATGACTATTTTT
GATGCTGCGCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAAGA
TATCAAAGGTTTCGTTTGGAATGAGCGGAAGAAGGCAGTTAGTTCAGATT
ATGATTTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGCT
TCTGGTCAGTTTGGATTTTCATCTAATGGTGCTGGTGAAGAACTGGACTA
TACTGTTAATGAAAGTATAGAAAAGGGCTATTATTTAGTCCTATCTTATT
CGATCTTCGGTGGTATCTCTTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7504
STRAIN H36B
ATGTTAGTGGAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGCGA
GCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATTTAT
ATAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCATAACTAGT
GACCCAGAGGTTCCTGAGCAATACAAAGATGAGACACGTAATTTTAAATT
TGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTTAA
AAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAAAG
AGTGCTGGTCAAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCAAGT
AGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATGAAT
TGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCGCC
TGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAAGA
TGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGATA
TTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAATACAGAAATGGCA
TGTCAGCCCTATTCTTCTGGAAAAGGAATCAATTTGGGTGAGGGCGCTGG
TTTTGTTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAAAAATTA
TCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAGCCA
ACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCAGG
TATTGACTACAGTGAGATTGACTATATTAACGGTCACGGTACAGGTACTC
AAGCTAATGATAAAATGGAAAAAAATATGTATGGTAAGTTTTTCCCGACA
ACGACATTGATCAGCAGTACCAAGGGGCAAACGGGTCATACTCTAGGGGC
TGCAGGTATTATCGAATTGATTAATTGTTTAGCGGCAATAGAGGAACAGA
CTGTACCAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCAGAAAAT
TTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAATTT
TTCGTTTGCTTTTGGTGGAAATAATAGTGGTGTCTTATTGTCATCTTTAG
ATTCACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAAATGGCTATC
TTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACCTA
TGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAAAG
GGGCTAGACCACCCAAAACTGTCAACCCAGCACAATTTAGGAAAATGGAT
GATTTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAAAG
CAATATTAATCTAAAAAAACAAGATACTTCAAAAGTAGGAATTGTATTTA
CAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAAATC

Table 75: Comparative Sequences relating to SAG0671

ACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCCGTTTACAGT
AATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTAAAATAACAGGTC
CTTTATCTGTCATTTCGACAAATAGTGGAGCGCTTGATGGTATACAATAT
GCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGTTTC
TGCTAATCAGTGGACAGACATGAGTTTTATGTGGTGGCAACAATTAAACT
ATGATAGTCAAATGTTTGTCGGTTCTGATTATTGTTCAGCACAAGTCCTC
TCTCGTCAAGCATTGGATAATTCTCCTATAATATTAGGTAGTAAACAATT
AAAATATAGCCATAAAACATTCACAGATGTGATGACTATTTTTGATGCTG
CGCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATCAAA
GGTTTCGTTTGGAATGAGCGGAAGAAGGCAGTTAGTTCAGATTATGATTT
CTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTGGTC
AGTTTGGATTTTCATCTAATGGTGCTGGTGAAGAACTGGACTATACTGTT
AATGAAAGTATAGAAAAGGGCTATTATTTAGTCCTATCTTATTCGATCTT
CGGTGGTATCTCTTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7505
STRAIN 18RS21
ATGTTAGTGGAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGC
GAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATTT
ATATAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCATAACTA
GTGACCCAGAGGTTCCTGAGCAATACAAAGATGAGACACGTAATTTTAAA
TTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTT
AAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAA
AGAGTGCTGGTCAAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCAA
GTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATGA
ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCG
CCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAA
GATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGA
TATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAATACAGAAATGG
CATGTCAGCCCTATTCTTCTGGAAAAGGAATCAATTTGGGTGAGGGCGCT
GGTTTTGTTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAAAAAT
TATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAGC
CAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCA
GGTATTGACTACAGTGAGATTGACTATATTAACGGTCACGGTACAGGTAC
TCAAGCTAATGATAAAATGGAAAAAAATATGTATGGTAAGTTTTTCCCGA
CAACGACATTGATCAGCAGTACCAAGGGGCAAACGGGTCATACTCTAGGG
GCTGCAGGTATTATCGAATTGATTAATTGTTTAGCGGCAATAGAGGAACA
GACTGTACCAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCAGAAA
ATTTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAAT
TTTTCGTTTGCTTTTGGTGGAAATAATAGTGGTGTCTTATTGTCATCTTT
AGATTCACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAAATGGCTA
TCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACC
TATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
AGGGGCTAGACCACCCAAAACTGTCAACCCAGCACAATTTAGGAAAATGG
ATGATTTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAA
AGCAATATTAATCTAAAAAAACAAGATACTTCAAAAGTAGGAATTGTATT
TACAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAAA
TCACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCCGTTTACA
GTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTAAAATAACAGG
TCCTTTATCTGTCATTTCGACAAATAGTGGAGCGCTTGATGGTATACAAT
ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGTT
TCTGCTAATCAGTGGACAGACATGAGTTTTATGTGGTGGCAACAATTAAA
CTATGATAGTCAAATGTTTGTCGGTTCTGATTATTGTTCAGCACAAGTCC
TCTCTCGTCAAGCATTGGATAATTCTCCTATAATATTAGGTAGTAAACAA
TTAAAATATAGCCATAAAACATTCACAGATGTGATGACTATTTTTGATGC
TGCGCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATCA
AAGGTTTCGTTTGGAATGAGCGGAAGAAGGCAGTTAGTTCAGATTATGAT
TTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTGG
TCAGTTTGGATTTTCATCTAATGGTGCTGGTGAAGAACTGGACTATACTG
TTAATGAAAGTATAGAAAAGGGCTATTATTTAGTCCTATCTTATTCGATC
TTCGGTGGTATCTCTTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7506
STRAIN M732
ATGTTAGTGGAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAG
CGAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATT
TATATAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCATAACT
AGTGACCCAGAGGTTCCTGAGCAATACAAAGATGAGACACGTAATTTTAA
ATTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATT
TAAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGA
AAGAGTGCTGGTCAAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCA
AGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATG
AATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACC
GCCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCA
AGATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTG
ATATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAATACAGAAATG
GCATGTCAGCCCTATTCTTCTGGAAAAGGAATCAATTTGGGTGAGGGCGC
TGGTTTTGTTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAAAAA
TTATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAG
CCAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGC
AGGTATTGACTACAGTGAGATTGACTATATTAACGGTCACGGTACAGGTA
CTCAAGCTAATGATAAAATGGAAAAAAATATGTATGGTAAGTTTTTCCCG
ACAACGACATTGATCAGCAGTACCAAGGGGCAAACGGGTCATACTCTAGG

Table 75: Comparative Sequences relating to SAG0671

GGCTGCAGGTATTATCGAATTGATTAATTGTTTAGCGGCAATAGAGGAAC
AGACTGTACCAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCAGAA
AATTTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAA
TTTTTCGTTTGCTTTTGGTGGAAATAATAGTGGTGTCTTATTGTCATCTT
TAGATTCACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAAATGGCT
ATCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAAC
CTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTA
AAGGGGCTAGACCACCCAAAACTGTCAACCCAGCACAATTTAGGAAAATG
GATGATTTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGA
AAGCAATATTAATCTAAAAAAACAAGATACTTCAAAAGTAGGAATTGTAT
TTACAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAA
ATCACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCCGTTTAC
AGTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTAAAATAACAG
GTCCTTTATCTGTCATTTCGACAAATAGTGGAGCGCTTGATGGTATACAA
TATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGT
TTCTGCTAATCAGTGGACAGACATGAGTTTTATGTGGTGGCAACAATTAA
ACTATGATAGTCAAATGTTTGTCGGTTCTGATTATTGTTCAGCACAAGTC
CTCTCTCGTCAAGCATTGGATAATTCTCCTATAATATTAGGTAGTAAACA
ATTAAAATATAGCCATAAAACATTCACAGATGTGATGACTATTTTTGATG
CTGCGCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATC
AAAGGTTTCGTTTGGAATGAGCGGAAGAAGGCAGTTAGTTCAGATTATGA
TTTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTG
GTCAGTTTGGATTTTCATCTAATGGTGCTGGTGAAGAACTGGACTAtaCT
GTTAATGAAAGTATAGAAAAGGGCTATTATTTAGTCCTATCTTATTCGAT
CTTCGGTGGTATCTCTTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7507
STRAIN COH1
ATGTTAGTGGAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGC
GAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATTT
ATATAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCATAACTA
GTGACCCAGAGGTTCCTGAGCAATACAAAGATGAGACACGTAATTTTAAA
TTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTT
AAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAA
AGAGTGCTGGTCAAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCAA
GTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATGA
ATTGATGGCTTATCATGATATTGTGGAGCTTCGTATGTTATTTCAACCG
CCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAA
GATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGA
TATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAATACAGAAATGG
CATGTCAGCCCTATTCTTCTGGAAAAGGAATCAATTTGGGTGAGGGCGCT
GGTTTTGTTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAAAAAT
TATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAGC
CAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCA
GGTATTGACTACAGTGAGATTGACTATATTAACGGTCACGGTACAGGTAC
TCAAGCTAATGATAAAATGGAAAAAAATATGTATGGTAAGTTTTTCCCGA
CAACGACATTGATCAGCAGTACCAAGGGGCAAACGGGTCATACTCTAGGG
GCTGCAGGTATTATCGAATTGATTAATTGTTTAGCGGCAATAGAGGAACA
GACTGTACCAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCAGAAA
ATTTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAAT
TTTTCGTTTGCTTTTGGTGGAAATAATAGTGGTGTCTTATTGTCATCTTT
AGATTCACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAAATGGCTA
TCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACC
TATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
AGGGGCTAGACCACCCAAAACTGTCAACCCAGCACAATTTAGGAAAATGG
ATGATTTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAA
AGCAATATTAATCTAAAAAAACAAGATACTTCAAAAGTAGGAATTGTATT
TACAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAAA
TCACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCCGTTTACA
GTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTAAAATAACAGG
TCCTTTATCTGTCATTTCGACAAATAGTGGAGCGCTTGATGGTATACAAT
ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGTT
TCTGCTAATCAGTGGACAGACATGAGTTTTATGTGGTGGCAACAATTAAA
CTATGATAGTCAAATGTTTGTCGGTTCTGATTATTGTTCAGCACAAGTCC
TCTCTCGTCAAGCATTGGATAATTCTCCTATAATATTAGGTAGTAAACAA
TTAAAATATAGCCATAAAACATTCACAGATGTGATGACTATTTTTGATGC
TGCGCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATCA
AAGGTTTCGTTTGGAATGAGCGGAAGAAGGCAGTTAGTTCAGATTATGAT
TTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTGG
TCAGTTTGGATTTTCATCTAATGGTGCTGGTGAAGAACTGGACTATACTG
TTAATGAAAGTATAGAAAAGGGCTATTATTTAGTCCTATCTTATTCGATC
TTCGGTGGTATCTCTTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7508
STRAIN M781
ATGTTAGTGGAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGC
GAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATTT
ATATAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCATAACTA
GTGACCCAGAGGTTCCTGAGCAATACAAAGATGAGACACGTAATTTTAAA
TTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTT
AAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAA
AGAGTGCTGGTCAAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCAA
GTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATGA

Table 75: Comparative Sequences relating to SAG0671

ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCG
CCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAA
GATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGA
TATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAATACAGAAATGG
CATGTCAGCCCTATTCTTCTGGAAAAGGAATCAATTTGGGTGAGGGCGCT
GGTTTTGTTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAAAAAT
TATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAGC
CAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCA
GGTATTGACTACAGTGAGATTGACTATATTAATGGTCACGGTACAGGTAC
TCAAGCTAATGATAAAATGGAAAAAAATATGTATGGTAAGTTTTTCCCGA
CAACGACATTGATCAGCAGTACCAAGGGGCAAACGGGTCATACTCTAGGG
GCTGCAGGTATTATCGAATTGATTAATTGTTTAGCGGCAATAGAGGAACA
GACTGTACCAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCAGAAA
ATTTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAAT
TTTTCGTTTGCTTTTGGTGGAAATAATAGTGGTATCTTATTGTCATCTTT
AGATTCACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAAATGGCTA
TCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACC
TATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
AGGGGCTAGACCACCCAAAACTGTCAACCCAGCACAATTTAGGAAAATGG
ATGATTTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAA
AGCAATATTAATCTAAAAAAACAAGATACTTCAAAAGTAGGAATTGTATT
TACAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAAA
TCACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCCGTTTACA
GTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTAAAATAACAGG
TCCTTTATCTGTCATTTCGACAAATAGTGGAGCGCTTGATGGTATACAAT
ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGTT
TCTGCTAATCAGTGGACAGACATGAGTTTTATGTGGTGGCAACAATTAAA
CTATGATAGTCAAATGTTTGTCGGTTCTGATTATTGTTCAGCACAAGTCC
TCTCTCGTCAAGCATTGGATAATTCTCCTATAATATTAGGTAGTAAACAA
TTAAAATATAGCCATAAAACATTCACAGATGTGATGACTATTTTTGATGC
TGCGCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATCA
AAGGTTTCGTTTGGAATGAGCGGAAGAAGGCAGTTAGTTCAGATTATGAT
TTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTGG
TCAGTTTGGATTTTCATCTAATGGTGCTGGTGAAGAACTGGACTATACTG
TTAATGAAAGTATAGAAAAGGGCTATTATTTAGTCCTATCTTATTCGATC
TTTGGTGGTATCTCTTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7509
STRAIN CJB110
ATGTTAGTGGAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGC
GAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATTT
ATATAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCATAACTA
GTGACCCAGAGGTTCCTGAGCAATACAAAGATGAGACACGTAATTTTAAA
TTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTT
AAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAA
AGAGTGCTGGTCAAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCAA
GTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATGA
ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCG
CCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAA
GATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGA
TATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAATACAGAAATGG
CATGTCAGCCCTATTCTTCTGGAAAAGGAATCAATTTGGGTGAGGGCGCT
GGTTTTGTTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAAAAAT
TATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAGC
CAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCA
GGTATTGACTACAGTGAGATTGACTATATTAATGGTCACGGTACAGGTAC
TCAAGCTAATGATAAAATGGAAAAAAATATGTATGGTAAGTTTTTCCCGA
CAACGACATTGATCAGCAGTACCAAGGGGCAAACGGGTCATACTCTAGGG
GCTGCAGGTATTATCGAATTGATTAATTGTTTAGCGGCAATAGAGGAACA
GACTGTACCAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCAGAAA
ATTTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAAT
TTTTCGTTTGCTTTTGGTGGAAATAATAGTGGTATCTTATTGTCATCTTT
AGATTCACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAAATGGCTA
TCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACC
TATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
AGGGGCTAGACCACCCAAAACTGTCAACCCAGCACAATTTAGGAAAATGG
ATGATTTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAA
AGCAATATTAATCTAAAAAAACAAGATACTTCAAAAGTAGGAATTGTATT
TACAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAAA
TCACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCCGTTTACA
GTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTAAAATAACAGG
TCCTTTATCTGTCATTTCGACAAATAGTGGAGCGCTTGATGGTATACAAT
ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGTT
TCTGCTAATCAGTGGACAGACATGAGTTTTATGTGGTGGCAACAATTAAA
CTATGATAGTCAAATGTTTGTCGGTTCTGATTATTGTTCAGCACAAGTCC
TCTCTCGTCAAGCATTGGATAATTCTCCTATAATATTAGGTAGTAAACAA
TTAAAATATAGCCATAAAACATTCACAGATGTGATGACTATTTTTGATGC
TGCGCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATCA
AAGGTTTCGTTTGGAATGAGCGGAAGAAGGCAGTTAGTTCAGATTATGAT
TTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTGG
TCAGTTTGGATTTTCATCTAATGGTGCTGGTGAAGAACTGGACTATACTG
TTAATGAAAGTATAGAAAAGGGCTATTATTTAGTCCTATCTTATTCGATC
TTTGGTGGTATCTCTTTTGCTATTATTGAAAAAAGG

Table 75: Comparative Sequences relating to SAG0671

SEQ ID NO. 7510
STRAIN 1169NT
ATGTTAGTGGAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAG
CGAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATT
TATATAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCATAACT
AGTGACCCAGAGGTTCCTGAGCAATACAAAGATGAGACACGTAATTTTAA
ATTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATT
TAAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGA
AAGAGTGCTGGTCAAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCA
AGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATG
AATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACC
GCCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCA
AGATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTG
ATATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAATACAGAAATG
GCATGTCAGCCCTATTCTTCTGGAAAAGGAATCAATTTGGGTGAGGGCGC
TGGTTTTGTTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAAAAA
TTATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAG
CCAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGC
AGGTATTGACTACAGTGAGATTGACTATATTAACGGTCACGGTACAGGTA
CTCAAGCTAATGATAAAATGGAAAAAAATATGTATGGTAAGTTTTTCCCG
ACAACGACATTGATCAGCAGTACCAAGGGGCAAACGGGTCATACTCTAGG
GGCTGCAGGTATTATCGAATTGATTAATTGTTTAGCGGCAATAGAGGAAC
AGACTGTACCAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCAGAA
AATTTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAA
TTTTTCGTTTGCTTTTGGTGGAAATAATAGTGGTATCTTATTGTCATCTT
TAGATTCACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAAATGGCT
ATCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAAC
CTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTA
AAGGGGCTAGACCACCCAAAACTGTCAACCCAGCACAATTTAGGAAAATG
GATGATTTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGA
AAGCAATATTAATCTAAAAAAACAAGATACTTCAAAAGTAGGAATTGTAT
TTACAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAA
ATCACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCCGTTTAC
AGTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTAAAATAACAG
GTCCTTTATCTGTCATTTCGACAAATAGTGGAGCGCTTGATGGTATACAA
TATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGT
TTCTGCTAATCAGTGGACAGACATGAGTTTTATGTGGTGGCAACAATTAA
ACTATGATAGTCAAATGTTTGTCGGTTCTGATTATTGTTCAGCACAAGTC
CTCTCTCGTCAAGCATTGGATAATTCTCCTATAATATTAGGTAGTAAACA
ATTAAAATATAGCCATAAAACATTCACAGATGTGATGACTATTTTTGATG
CTGCGCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATC
AAAGGTTTCGTTTGGAATGAGCGGAAGAAGGCAGTTAGTTCAGATTATGA
TTTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTG
GTCAGTTTGGATTTTCATCTAATGGTGCTGGTGAAGAACTGGACTATACT
GTTAATGAAAGTATAGAAAAGGGCTATTATTTAGTCCTATCTTATTCGAT
CTTTGGTGGTATCTCTTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7511
STRAIN JM9130013
ATGTTAGTGGAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGCGAG
CATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATTTATA
TAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCATAACTAGTG
ACCCAGAGGTTCCTGAGCAATACAAAGATGAGACACGTAATTTTAAATTT
GCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTTAAA
AGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAAAGA
GTGCTGGTCAAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCAAGTA
GATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATGAATT
GATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCGCCT
GTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAAGAT
GGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGATAT
TTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAATACAGAAATGGCAT
GTCAGCCCTATTCTTCTGGAAAAGGAATCAATTTGGGTGAGGGCGCTGGT
TTTGTTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAAAAATTAT
CGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAGCCAA
CAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCAGGT
ATTGACTACAGTGAGATTGACTATATTAACGGTCACGGTACAGGTACTCA
AGCTAATGATAAAATGGAAAAAAATATGTATGGTAAGTTTTTCCCGACAA
CGACATTGATCAGCAGTACCAAGGGGCAAACGGGTCATACTCTAGGGGCT
GCAGGTATTATCGAATTGATTAATTGTTTAGCGGCAATAGAGGAACAGAC
TGTACCAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCAGAAAATT
TTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAATTTT
TCGTTTGCTTTTGGTGGAAATAATAGTGGTGTCTTATTGTCATCTTTAGA
TTCACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAAATGGCTATCT
TATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACCTAT
GAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAAAGG
GGCTAGACCACCCAAAACTGTCAACCCAGCACAATTTAGGAAAATGGATG
ATTTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAAAGC
AATATTAATCTAAAAAAACAAGATACTTCAAAAGTAGGAATTGTATTTAC
AACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAAATCA
CAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCCGTTTACAGTA
ATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTAAAATAACAGGTCC
TTTATCTGTCATTTCGACAAATAGTGGAGCGCTTGATGGTATACAATATG

Table 75: Comparative Sequences relating to SAG0671

```
CCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGTTTCT
GCTAATCAGTGGACAGACATGAGTTTTATGTGGTGGCAACAATTAAACTA
TGATAGTCAAATGTTTGTCGGTTCTGATTATTGTTCAGCACAAGTCCTCT
CTCGTCAAGCATTGGATAATTCTCCTATAATATTAGGTAGTAAACAATTA
AAATATAGCCATAAAACATTCACAGATGTGATGACTATTTTTGATGCTGC
GCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATCAAAG
GTTTCGTTTGGAATGAGCGGAAGAAGGCAGTTAGTTCAGATTATGATTTC
TTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTGGTCA
GTTTGGATTTTCATCTAATGGTGCTGGTGAAGAACTGGACTATACTGTTA
ATGAAAGTATAGAAAAGGGCTATTATTTAGTCCTATCTTATTCGATCTTC
GGTGGTATCTCTTTTGCTATTATTGAAAAAAGG
```

```
PRETTY of: /biotmp/msa118688.2{*}   April 9, 2003 02:55  ..

                              1                                                      50
     msa118688.2{361_18RS21}  ~~~~~~~~~~ ATGTTAGTGG AATAGGAATT ATTTCTTCTT TGGGAAAGAA
       msa118688.2{361_A909}  ~~~~~~~~~~ ATGTTAGTGG AATAGGAATT ATTTCTTCTT TGGGAAAGAA
       msa118688.2{361_COH1}  ~~~~~~~~~~ ATGTTAGTGG AATAGGAATT ATTTCTTCTT TGGGAAAGAA
       msa118688.2{361_H36B}  ~~~~~~~~~~ ATGTTAGTGG AATAGGAATT ATTTCTTCTT TGGGAAAGAA
  msa118688.2{361_JM9130013}  ~~~~~~~~~~ ATGTTAGTGG AATAGGAATT ATTTCTTCTT TGGGAAAGAA
       msa118688.2{361_M732}  ~~~~~~~~~~ ATGTTAGTGG AATAGGAATT ATTTCTTCTT TGGGAAAGAA
    msa118688.2{GBS361_2603}  atgagcgtat ATGTTAGTGG AATAGGAATT ATTTCTTCTT TGGGAAAGAA
        msa118688.2{361_090}  ~~~~~~~~~~ ATGTTAGTGG AATAGGAATT ATTTCTTCTT TGGGAAAGAA
     msa118688.2{361_1169NT}  ~~~~~~~~~~ ATGTTAGTGG AATAGGAATT ATTTCTTCTT TGGGAAAGAA
     msa118688.2{361_CJB110}  ~~~~~~~~~~ ATGTTAGTGG AATAGGAATT ATTTCTTCTT TGGGAAAGAA
       msa118688.2{361_M781}  ~~~~~~~~~~ ATGTTAGTGG AATAGGAATT ATTTCTTCTT TGGGAAAGAA
                   Consensus  ********** ********** ********** ********** **********

                              51                                                    100
     msa118688.2{361_18RS21}  TTATAGCGAG CATAAACAGC ATCTCTTCGA CTTAAAAGAA GGAATTTCTA
       msa118688.2{361_A909}  TTATAGCGAG CATAAACAGC ATCTCTTCGA CTTAAAAGAA GGAATTTCTA
       msa118688.2{361_COH1}  TTATAGCGAG CATAAACAGC ATCTCTTCGA CTTAAAAGAA GGAATTTCTA
       msa118688.2{361_H36B}  TTATAGCGAG CATAAACAGC ATCTCTTCGA CTTAAAAGAA GGAATTTCTA
  msa118688.2{361_JM9130013}  TTATAGCGAG CATAAACAGC ATCTCTTCGA CTTAAAAGAA GGAATTTCTA
       msa118688.2{361_M732}  TTATAGCGAG CATAAACAGC ATCTCTTCGA CTTAAAAGAA GGAATTTCTA
    msa118688.2{GBS361_2603}  TTATAGCGAG CATAAACAGC ATCTCTTCGA CTTAAAAGAA GGAATTTCTA
        msa118688.2{361_090}  TTATAGCGAG CATAAACAGC ATCTCTTCGA CTTAAAAGAA GGAATTTCTA
     msa118688.2{361_1169NT}  TTATAGCGAG CATAAACAGC ATCTCTTCGA CTTAAAAGAA GGAATTTCTA
     msa118688.2{361_CJB110}  TTATAGCGAG CATAAACAGC ATCTCTTCGA CTTAAAAGAA GGAATTTCTA
       msa118688.2{361_M781}  TTATAGCGAG CATAAACAGC ATCTCTTCGA CTTAAAAGAA GGAATTTCTA
                   Consensus  ********** ********** ********** ********** **********

                              101                                                   150
     msa118688.2{361_18RS21}  AACATTTATA TAAAAATCAC GACTCTATTT TAGAATCTTA TACAGGAAGC
       msa118688.2{361_A909}  AACATTTATA TAAAAATCAC GACTCTATTT TAGAATCTTA TACAGGAAGC
       msa118688.2{361_COH1}  AACATTTATA TAAAAATCAC GACTCTATTT TAGAATCTTA TACAGGAAGC
       msa118688.2{361_H36B}  AACATTTATA TAAAAATCAC GACTCTATTT TAGAATCTTA TACAGGAAGC
  msa118688.2{361_JM9130013}  AACATTTATA TAAAAATCAC GACTCTATTT TAGAATCTTA TACAGGAAGC
       msa118688.2{361_M732}  AACATTTATA TAAAAATCAC GACTCTATTT TAGAATCTTA TACAGGAAGC
    msa118688.2{GBS361_2603}  AACATTTATA TAAAAATCAC GACTCTATTT TAGAATCTTA TACAGGAAGC
        msa118688.2{361_090}  AACATTTATA TAAAAATCAC GACTCTATTT TAGAATCTTA TACAGGAAGC
     msa118688.2{361_1169NT}  AACATTTATA TAAAAATCAC GACTCTATTT TAGAATCTTA TACAGGAAGC
     msa118688.2{361_CJB110}  AACATTTATA TAAAAATCAC GACTCTATTT TAGAATCTTA TACAGGAAGC
       msa118688.2{361_M781}  AACATTTATA TAAAAATCAC GACTCTATTT TAGAATCTTA TACAGGAAGC
                   Consensus  ********** ********** ********** ********** **********

                              151                                                   200
     msa118688.2{361_18RS21}  ATAACTAGTG ACCCAGAGGT TCCTGAGCAA TACAAAGATG AGACACGTAA
       msa118688.2{361_A909}  ATAACTAGTG ACCCAGAGGT TCCTGAGCAA TACAAAGATG AGACACGTAA
       msa118688.2{361_COH1}  ATAACTAGTG ACCCAGAGGT TCCTGAGCAA TACAAAGATG AGACACGTAA
       msa118688.2{361_H36B}  ATAACTAGTG ACCCAGAGGT TCCTGAGCAA TACAAAGATG AGACACGTAA
  msa118688.2{361_JM9130013}  ATAACTAGTG ACCCAGAGGT TCCTGAGCAA TACAAAGATG AGACACGTAA
       msa118688.2{361_M732}  ATAACTAGTG ACCCAGAGGT TCCTGAGCAA TACAAAGATG AGACACGTAA
    msa118688.2{GBS361_2603}  ATAACTAGTG ACCCAGAGGT TCCTGAGCAA TACAAAGATG AGACACGTAA
        msa118688.2{361_090}  ATAACTAGTG ACCCAGAGGT TCCTGAGCAA TACAAAGATG AGACACGTAA
     msa118688.2{361_1169NT}  ATAACTAGTG ACCCAGAGGT TCCTGAGCAA TACAAAGATG AGACACGTAA
     msa118688.2{361_CJB110}  ATAACTAGTG ACCCAGAGGT TCCTGAGCAA TACAAAGATG AGACACGTAA
       msa118688.2{361_M781}  ATAACTAGTG ACCCAGAGGT TCCTGAGCAA TACAAAGATG AGACACGTAA
                   Consensus  ********** ********** ********** ********** **********

                              201                                                   250
     msa118688.2{361_18RS21}  TTTTAAATTT GCTTTTACCG CTTTTGAAGA GGCTCTTGCT TCTTCAGGTG
       msa118688.2{361_A909}  TTTTAAATTT GCTTTTACCG CTTTTGAAGA GGCTCTTGCT TCTTCAGGTG
       msa118688.2{361_COH1}  TTTTAAATTT GCTTTTACCG CTTTTGAAGA GGCTCTTGCT TCTTCAGGTG
       msa118688.2{361_H36B}  TTTTAAATTT GCTTTTACCG CTTTTGAAGA GGCTCTTGCT TCTTCAGGTG
  msa118688.2{361_JM9130013}  TTTTAAATTT GCTTTTACCG CTTTTGAAGA GGCTCTTGCT TCTTCAGGTG
       msa118688.2{361_M732}  TTTTAAATTT GCTTTTACCG CTTTTGAAGA GGCTCTTGCT TCTTCAGGTG
    msa118688.2{GBS361_2603}  TTTTAAATTT GCTTTTACCG CTTTTGAAGA GGCTCTTGCT TCTTCAGGTG
        msa118688.2{361_090}  TTTTAAATTT GCTTTTACCG CTTTTGAAGA GGCTCTTGCT TCTTCAGGTG
     msa118688.2{361_1169NT}  TTTTAAATTT GCTTTTACCG CTTTTGAAGA GGCTCTTGCT TCTTCAGGTG
     msa118688.2{361_CJB110}  TTTTAAATTT GCTTTTACCG CTTTTGAAGA GGCTCTTGCT TCTTCAGGTG
       msa118688.2{361_M781}  TTTTAAATTT GCTTTTACCG CTTTTGAAGA GGCTCTTGCT TCTTCAGGTG
                   Consensus  ********** ********** ********** ********** **********
```

Table 75: Comparative Sequences relating to SAG0671

```
                                251                                                   300
   msa118688.2{361_18RS21}     TTAATTTAAA AGCTTATCAT AATATTGCTG TGTGTTTAGG GACCTCACTT
     msa118688.2{361_A909}     TTAATTTAAA AGCTTATCAT AATATTGCTG TGTGTTTAGG GACCTCACTT
     msa118688.2{361_COH1}     TTAATTTAAA AGCTTATCAT AATATTGCTG TGTGTTTAGG GACCTCACTT
     msa118688.2{361_H36B}     TTAATTTAAA AGCTTATCAT AATATTGCTG TGTGTTTAGG GACCTCACTT
msa118688.2{361_JM9130013}     TTAATTTAAA AGCTTATCAT AATATTGCTG TGTGTTTAGG GACCTCACTT
     msa118688.2{361_M732}     TTAATTTAAA AGCTTATCAT AATATTGCTG TGTGTTTAGG GACCTCACTT
  msa118688.2{GBS361_2603}     TTAATTTAAA AGCTTATCAT AATATTGCTG TGTGTTTAGG GACCTCACTT
      msa118688.2{361_090}     TTAATTTAAA AGCTTATCAT AATATTGCTG TGTGTTTAGG GACCTCACTT
   msa118688.2{361_1169NT}     TTAATTTAAA AGCTTATCAT AATATTGCTG TGTGTTTAGG GACCTCACTT
   msa118688.2{361_CJB110}     TTAATTTAAA AGCTTATCAT AATATTGCTG TGTGTTTAGG GACCTCACTT
     msa118688.2{361_M781}     TTAATTTAAA AGCTTATCAT AATATTGCTG TGTGTTTAGG GACCTCACTT
                 Consensus     ********** ********** ********** ********** **********

                                301                                                   350
   msa118688.2{361_18RS21}     GGGGGAAAGA GTGCTGGTCA AAATGCCTTG TATCAATTTG AAGAAGGAGA
     msa118688.2{361_A909}     GGGGGAAAGA GTGCTGGTCA AAATGCCTTG TATCAATTTG AAGAAGGAGA
     msa118688.2{361_COH1}     GGGGGAAAGA GTGCTGGTCA AAATGCCTTG TATCAATTTG AAGAAGGAGA
     msa118688.2{361_H36B}     GGGGGAAAGA GTGCTGGTCA AAATGCCTTG TATCAATTTG AAGAAGGAGA
msa118688.2{361_JM9130013}     GGGGGAAAGA GTGCTGGTCA AAATGCCTTG TATCAATTTG AAGAAGGAGA
     msa118688.2{361_M732}     GGGGGAAAGA GTGCTGGTCA AAATGCCTTG TATCAATTTG AAGAAGGAGA
  msa118688.2{GBS361_2603}     GGGGGAAAGA GTGCTGGTCA AAATGCCTTG TATCAATTTG AAGAAGGAGA
      msa118688.2{361_090}     GGGGGAAAGA GTGCTGGTCA AAATGCCTTG TATCAATTTG AAGAAGGAGA
   msa118688.2{361_1169NT}     GGGGGAAAGA GTGCTGGTCA AAATGCCTTG TATCAATTTG AAGAAGGAGA
   msa118688.2{361_CJB110}     GGGGGAAAGA GTGCTGGTCA AAATGCCTTG TATCAATTTG AAGAAGGAGA
     msa118688.2{361_M781}     GGGGGAAAGA GTGCTGGTCA AAATGCCTTG TATCAATTTG AAGAAGGAGA
                 Consensus     ********** ********** ********** ********** **********

                                351                                                   400
   msa118688.2{361_18RS21}     GCGTCAAGTA GATGCTAGTT TATTAGAAAA AGCATCTGTT TACCATATTG
     msa118688.2{361_A909}     GCGTCAAGTA GATGCTAGTT TATTAGAAAA AGCATCTGTT TACCATATTG
     msa118688.2{361_COH1}     GCGTCAAGTA GATGCTAGTT TATTAGAAAA AGCATCTGTT TACCATATTG
     msa118688.2{361_H36B}     GCGTCAAGTA GATGCTAGTT TATTAGAAAA AGCATCTGTT TACCATATTG
msa118688.2{361_JM9130013}     GCGTCAAGTA GATGCTAGTT TATTAGAAAA AGCATCTGTT TACCATATTG
     msa118688.2{361_M732}     GCGTCAAGTA GATGCTAGTT TATTAGAAAA AGCATCTGTT TACCATATTG
  msa118688.2{GBS361_2603}     GCGTCAAGTA GATGCTAGTT TATTAGAAAA AGCATCTGTT TACCATATTG
      msa118688.2{361_090}     GCGTCAAGTA GATGCTAGTT TATTAGAAAA AGCATCTGTT TACCATATTG
   msa118688.2{361_1169NT}     GCGTCAAGTA GATGCTAGTT TATTAGAAAA AGCATCTGTT TACCATATTG
   msa118688.2{361_CJB110}     GCGTCAAGTA GATGCTAGTT TATTAGAAAA AGCATCTGTT TACCATATTG
     msa118688.2{361_M781}     GCGTCAAGTA GATGCTAGTT TATTAGAAAA AGCATCTGTT TACCATATTG
                 Consensus     ********** ********** ********** ********** **********

                                401                                                   450
   msa118688.2{361_18RS21}     CTGATGAATT GATGGCTTAT CATGATATTG TGGGAGCTTC GTATGTTATT
     msa118688.2{361_A909}     CTGATGAATT GATGGCTTAT CATGATATTG TGGGAGCTTC GTATGTTATT
     msa118688.2{361_COH1}     CTGATGAATT GATGGCTTAT CATGATATTG TGGGAGCTTC GTATGTTATT
     msa118688.2{361_H36B}     CTGATGAATT GATGGCTTAT CATGATATTG TGGGAGCTTC GTATGTTATT
msa118688.2{361_JM9130013}     CTGATGAATT GATGGCTTAT CATGATATTG TGGGAGCTTC GTATGTTATT
     msa118688.2{361_M732}     CTGATGAATT GATGGCTTAT CATGATATTG TGGGAGCTTC GTATGTTATT
  msa118688.2{GBS361_2603}     CTGATGAATT GATGGCTTAT CATGATATTG TGGGAGCTTC GTATGTTATT
      msa118688.2{361_090}     CTGATGAATT GATGGCTTAT CATGATATTG TGGGAGCTTC GTATGTTATT
   msa118688.2{361_1169NT}     CTGATGAATT GATGGCTTAT CATGATATTG TGGGAGCTTC GTATGTTATT
   msa118688.2{361_CJB110}     CTGATGAATT GATGGCTTAT CATGATATTG TGGGAGCTTC GTATGTTATT
     msa118688.2{361_M781}     CTGATGAATT GATGGCTTAT CATGATATTG TGGGAGCTTC GTATGTTATT
                 Consensus     ********** ********** ********** ********** **********

                                451                                                   500
   msa118688.2{361_18RS21}     TCAACCGCCT GTTCTGCAAG TAATAATGCC GTAATATTAG GAACACAATT
     msa118688.2{361_A909}     TCAACCGCCT GTTCTGCAAG TAATAATGCC GTAATATTAG GAACACAATT
     msa118688.2{361_COH1}     TCAACCGCCT GTTCTGCAAG TAATAATGCC GTAATATTAG GAACACAATT
     msa118688.2{361_H36B}     TCAACCGCCT GTTCTGCAAG TAATAATGCC GTAATATTAG GAACACAATT
msa118688.2{361_JM9130013}     TCAACCGCCT GTTCTGCAAG TAATAATGCC GTAATATTAG GAACACAATT
     msa118688.2{361_M732}     TCAACCGCCT GTTCTGCAAG TAATAATGCC GTAATATTAG GAACACAATT
  msa118688.2{GBS361_2603}     TCAACCGCCT GTTCTGCAAG TAATAATGCC GTAATATTAG GAACACAATT
      msa118688.2{361_090}     TCAACCGCCT GTTCTGCAAG TAATAATGCC GTAATATTAG GAACACAATT
   msa118688.2{361_1169NT}     TCAACCGCCT GTTCTGCAAG TAATAATGCC GTAATATTAG GAACACAATT
   msa118688.2{361_CJB110}     TCAACCGCCT GTTCTGCAAG TAATAATGCC GTAATATTAG GAACACAATT
     msa118688.2{361_M781}     TCAACCGCCT GTTCTGCAAG TAATAATGCC GTAATATTAG GAACACAATT
                 Consensus     ********** ********** ********** ********** **********

                                501                                                   550
   msa118688.2{361_18RS21}     ACTTCAAGAT GGCGATTGTG ATTTAGCTAT TTGTGGTGGC TGTGATGAGT
     msa118688.2{361_A909}     ACTTCAAGAT GGCGATTGTG ATTTAGCTAT TTGTGGTGGC TGTGATGAGT
     msa118688.2{361_COH1}     ACTTCAAGAT GGCGATTGTG ATTTAGCTAT TTGTGGTGGC TGTGATGAGT
     msa118688.2{361_H36B}     ACTTCAAGAT GGCGATTGTG ATTTAGCTAT TTGTGGTGGC TGTGATGAGT
msa118688.2{361_JM9130013}     ACTTCAAGAT GGCGATTGTG ATTTAGCTAT TTGTGGTGGC TGTGATGAGT
     msa118688.2{361_M732}     ACTTCAAGAT GGCGATTGTG ATTTAGCTAT TTGTGGTGGC TGTGATGAGT
  msa118688.2{GBS361_2603}     ACTTCAAGAT GGCGATTGTG ATTTAGCTAT TTGTGGTGGC TGTGATGAGT
      msa118688.2{361_090}     ACTTCAAGAT GGCGATTGTG ATTTAGCTAT TTGTGGTGGC TGTGATGAGT
   msa118688.2{361_1169NT}     ACTTCAAGAT GGCGATTGTG ATTTAGCTAT TTGTGGTGGC TGTGATGAGT
   msa118688.2{361_CJB110}     ACTTCAAGAT GGCGATTGTG ATTTAGCTAT TTGTGGTGGC TGTGATGAGT
     msa118688.2{361_M781}     ACTTCAAGAT GGCGATTGTG ATTTAGCTAT TTGTGGTGGC TGTGATGAGT
```

Table 75: Comparative Sequences relating to SAG0671

```
                 Consensus  ********** ********** ********** ********** **********

                            551                                                600
   msa118688.2{361_18RS21}  TAAGTGATAT TTCTTTAGCA GGCTTCACAT CACTAGGAGC TATTAATACA
     msa118688.2{361_A909}  TAAGTGATAT TTCTTTAGCA GGCTTCACAT CACTAGGAGC TATTAATACA
     msa118688.2{361_COH1}  TAAGTGATAT TTCTTTAGCA GGCTTCACAT CACTAGGAGC TATTAATACA
     msa118688.2{361_H36B}  TAAGTGATAT TTCTTTAGCA GGCTTCACAT CACTAGGAGC TATTAATACA
msa118688.2{361_JM9130013}  TAAGTGATAT TTCTTTAGCA GGCTTCACAT CACTAGGAGC TATTAATACA
     msa118688.2{361_M732}  TAAGTGATAT TTCTTTAGCA GGCTTCACAT CACTAGGAGC TATTAATACA
  msa118688.2{GBS361_2603}  TAAGTGATAT TTCTTTAGCA GGCTTCACAT CACTAGGAGC TATTAATACA
      msa118688.2{361_090}  TAAGTGATAT TTCTTTAGCA GGCTTCACAT CACTAGGAGC TATTAATACA
   msa118688.2{361_1169NT}  TAAGTGATAT TTCTTTAGCA GGCTTCACAT CACTAGGAGC TATTAATACA
   msa118688.2{361_CJB110}  TAAGTGATAT TTCTTTAGCA GGCTTCACAT CACTAGGAGC TATTAATACA
     msa118688.2{361_M781}  TAAGTGATAT TTCTTTAGCA GGCTTCACAT CACTAGGAGC TATTAATACA
                 Consensus  ********** ********** ********** ********** **********

                            601                                                650
   msa118688.2{361_18RS21}  GAAATGGCAT GTCAGCCCTA TTCTTCTGGA AAAGGAATCA ATTTGGGTGA
     msa118688.2{361_A909}  GAAATGGCAT GTCAGCCCTA TTCTTCTGGA AAAGGAATCA ATTTGGGTGA
     msa118688.2{361_COH1}  GAAATGGCAT GTCAGCCCTA TTCTTCTGGA AAAGGAATCA ATTTGGGTGA
     msa118688.2{361_H36B}  GAAATGGCAT GTCAGCCCTA TTCTTCTGGA AAAGGAATCA ATTTGGGTGA
msa118688.2{361_JM9130013}  GAAATGGCAT GTCAGCCCTA TTCTTCTGGA AAAGGAATCA ATTTGGGTGA
     msa118688.2{361_M732}  GAAATGGCAT GTCAGCCCTA TTCTTCTGGA AAAGGAATCA ATTTGGGTGA
  msa118688.2{GBS361_2603}  GAAATGGCAT GTCAGCCCTA TTCTTCTGGA AAAGGAATCA ATTTGGGTGA
      msa118688.2{361_090}  GAAATGGCAT GTCAGCCCTA TTCTTCTGGA AAAGGAATCA ATTTGGGTGA
   msa118688.2{361_1169NT}  GAAATGGCAT GTCAGCCCTA TTCTTCTGGA AAAGGAATCA ATTTGGGTGA
   msa118688.2{361_CJB110}  GAAATGGCAT GTCAGCCCTA TTCTTCTGGA AAAGGAATCA ATTTGGGTGA
     msa118688.2{361_M781}  GAAATGGCAT GTCAGCCCTA TTCTTCTGGA AAAGGAATCA ATTTGGGTGA
                 Consensus  ********** ********** ********** ********** **********

                            651                                                700
   msa118688.2{361_18RS21}  GGGCGCTGGT TTTGTTGTTC TTGTCAAAGA TCAGTCCTTA GCTAAATATG
     msa118688.2{361_A909}  GGGCGCTGGT TTTGTTGTTC TTGTCAAAGA TCAGTCCTTA GCTAAATATG
     msa118688.2{361_COH1}  GGGCGCTGGT TTTGTTGTTC TTGTCAAAGA TCAGTCCTTA GCTAAATATG
     msa118688.2{361_H36B}  GGGCGCTGGT TTTGTTGTTC TTGTCAAAGA TCAGTCCTTA GCTAAATATG
msa118688.2{361_JM9130013}  GGGCGCTGGT TTTGTTGTTC TTGTCAAAGA TCAGTCCTTA GCTAAATATG
     msa118688.2{361_M732}  GGGCGCTGGT TTTGTTGTTC TTGTCAAAGA TCAGTCCTTA GCTAAATATG
  msa118688.2{GBS361_2603}  GGGCGCTGGT TTTGTTGTTC TTGTCAAAGA TCAGTCCTTA GCTAAATATG
      msa118688.2{361_090}  GGGCGCTGGT TTTGTTGTTC TTGTCAAAGA TCAGTCCTTA GCTAAATATG
   msa118688.2{361_1169NT}  GGGCGCTGGT TTTGTTGTTC TTGTCAAAGA TCAGTCCTTA GCTAAATATG
   msa118688.2{361_CJB110}  GGGCGCTGGT TTTGTTGTTC TTGTCAAAGA TCAGTCCTTA GCTAAATATG
     msa118688.2{361_M781}  GGGCGCTGGT TTTGTTGTTC TTGTCAAAGA TCAGTCCTTA GCTAAATATG
                 Consensus  ********** ********** ********** ********** **********

                            701                                                750
   msa118688.2{361_18RS21}  GAAAAATTAT CGGTGGTCTT ATTACTTCAG ATGGTTATCA TATAACAGCA
     msa118688.2{361_A909}  GAAAAATTAT CGGTGGTCTT ATTACTTCAG ATGGTTATCA TATAACAGCA
     msa118688.2{361_COH1}  GAAAAATTAT CGGTGGTCTT ATTACTTCAG ATGGTTATCA TATAACAGCA
     msa118688.2{361_H36B}  GAAAAATTAT CGGTGGTCTT ATTACTTCAG ATGGTTATCA TATAACAGCA
msa118688.2{361_JM9130013}  GAAAAATTAT CGGTGGTCTT ATTACTTCAG ATGGTTATCA TATAACAGCA
     msa118688.2{361_M732}  GAAAAATTAT CGGTGGTCTT ATTACTTCAG ATGGTTATCA TATAACAGCA
  msa118688.2{GBS361_2603}  GAAAAATTAT CGGTGGTCTT ATTACTTCAG ATGGTTATCA TATAACAGCA
      msa118688.2{361_090}  GAAAAATTAT CGGTGGTCTT ATTACTTCAG ATGGTTATCA TATAACAGCA
   msa118688.2{361_1169NT}  GAAAAATTAT CGGTGGTCTT ATTACTTCAG ATGGTTATCA TATAACAGCA
   msa118688.2{361_CJB110}  GAAAAATTAT CGGTGGTCTT ATTACTTCAG ATGGTTATCA TATAACAGCA
     msa118688.2{361_M781}  GAAAAATTAT CGGTGGTCTT ATTACTTCAG ATGGTTATCA TATAACAGCA
                 Consensus  ********** ********** ********** ********** **********

                            751                                                800
   msa118688.2{361_18RS21}  CCTAAGCCAA CAGGTGAAGG GGCGGCACAG ATTGCAAAGC AGCTAGTGAC
     msa118688.2{361_A909}  CCTAAGCCAA CAGGTGAAGG GGCGGCACAG ATTGCAAAGC AGCTAGTGAC
     msa118688.2{361_COH1}  CCTAAGCCAA CAGGTGAAGG GGCGGCACAG ATTGCAAAGC AGCTAGTGAC
     msa118688.2{361_H36B}  CCTAAGCCAA CAGGTGAAGG GGCGGCACAG ATTGCAAAGC AGCTAGTGAC
msa118688.2{361_JM9130013}  CCTAAGCCAA CAGGTGAAGG GGCGGCACAG ATTGCAAAGC AGCTAGTGAC
     msa118688.2{361_M732}  CCTAAGCCAA CAGGTGAAGG GGCGGCACAG ATTGCAAAGC AGCTAGTGAC
  msa118688.2{GBS361_2603}  CCTAAGCCAA CAGGTGAAGG GGCGGCACAG ATTGCAAAGC AGCTAGTGAC
      msa118688.2{361_090}  CCTAAGCCAA CAGGTGAAGG GGCGGCACAG ATTGCAAAGC AGCTAGTGAC
   msa118688.2{361_1169NT}  CCTAAGCCAA CAGGTGAAGG GGCGGCACAG ATTGCAAAGC AGCTAGTGAC
   msa118688.2{361_CJB110}  CCTAAGCCAA CAGGTGAAGG GGCGGCACAG ATTGCAAAGC AGCTAGTGAC
     msa118688.2{361_M781}  CCTAAGCCAA CAGGTGAAGG GGCGGCACAG ATTGCAAAGC AGCTAGTGAC
                 Consensus  ********** ********** ********** ********** **********

                            801                                                850
   msa118688.2{361_18RS21}  TCAAGCAGGT ATTGACTACA GTGAGATTGA CTATATTAAc GGTCACGGTA
     msa118688.2{361_A909}  TCAAGCAGGT ATTGACTACA GTGAGATTGA CTATATTAAc GGTCACGGTA
     msa118688.2{361_COH1}  TCAAGCAGGT ATTGACTACA GTGAGATTGA CTATATTAAc GGTCACGGTA
     msa118688.2{361_H36B}  TCAAGCAGGT ATTGACTACA GTGAGATTGA CTATATTAAc GGTCACGGTA
msa118688.2{361_JM9130013}  TCAAGCAGGT ATTGACTACA GTGAGATTGA CTATATTAAc GGTCACGGTA
     msa118688.2{361_M732}  TCAAGCAGGT ATTGACTACA GTGAGATTGA CTATATTAAc GGTCACGGTA
  msa118688.2{GBS361_2603}  TCAAGCAGGT ATTGACTACA GTGAGATTGA CTATATTAAc GGTCACGGTA
      msa118688.2{361_090}  TCAAGCAGGT ATTGACTACA GTGAGATTGA CTATATTAAc GGTCACGGTA
   msa118688.2{361_1169NT}  TCAAGCAGGT ATTGACTACA GTGAGATTGA CTATATTAAc GGTCACGGTA
   msa118688.2{361_CJB110}  TCAAGCAGGT ATTGACTACA GTGAGATTGA CTATATTAAt GGTCACGGTA
```

Table 75: Comparative Sequences relating to SAG0671

```
      msal18688.2{361_M781}  TCAAGCAGGT ATTGACTACA GTGAGATTGA CTATATTAAt GGTCACGGTA
                  Consensus  ********** ********** ********** *********_ **********

                             851                                              900
     msal18688.2{361_18RS21}  CAGGTACTCA AGCTAATGAT AAAATGGAAA AAAATATGTA TGGTAAGTTT
       msal18688.2{361_A909}  CAGGTACTCA AGCTAATGAT AAAATGGAAA AAAATATGTA TGGTAAGTTT
       msal18688.2{361_COH1}  CAGGTACTCA AGCTAATGAT AAAATGGAAA AAAATATGTA TGGTAAGTTT
       msal18688.2{361_H36B}  CAGGTACTCA AGCTAATGAT AAAATGGAAA AAAATATGTA TGGTAAGTTT
  msal18688.2{361_JM9130013}  CAGGTACTCA AGCTAATGAT AAAATGGAAA AAAATATGTA TGGTAAGTTT
       msal18688.2{361_M732}  CAGGTACTCA AGCTAATGAT AAAATGGAAA AAAATATGTA TGGTAAGTTT
    msal18688.2{GBS361_2603}  CAGGTACTCA AGCTAATGAT AAAATGGAAA AAAATATGTA TGGTAAGTTT
        msal18688.2{361_090}  CAGGTACTCA AGCTAATGAT AAAATGGAAA AAAATATGTA TGGTAAGTTT
     msal18688.2{361_1169NT}  CAGGTACTCA AGCTAATGAT AAAATGGAAA AAAATATGTA TGGTAAGTTT
     msal18688.2{361_CJB110}  CAGGTACTCA AGCTAATGAT AAAATGGAAA AAAATATGTA TGGTAAGTTT
       msal18688.2{361_M781}  CAGGTACTCA AGCTAATGAT AAAATGGAAA AAAATATGTA TGGTAAGTTT
                   Consensus  ********** ********** ********** ********** **********

                              901                                              950
     msal18688.2{361_18RS21}  TTCCCGACAA CGACATTGAT CAGCAGTACC AAGGGGCAAA CGGGTCATAC
       msal18688.2{361_A909}  TTCCCGACAA CGACATTGAT CAGCAGTACC AAGGGGCAAA CGGGTCATAC
       msal18688.2{361_COH1}  TTCCCGACAA CGACATTGAT CAGCAGTACC AAGGGGCAAA CGGGTCATAC
       msal18688.2{361_H36B}  TTCCCGACAA CGACATTGAT CAGCAGTACC AAGGGGCAAA CGGGTCATAC
  msal18688.2{361_JM9130013}  TTCCCGACAA CGACATTGAT CAGCAGTACC AAGGGGCAAA CGGGTCATAC
       msal18688.2{361_M732}  TTCCCGACAA CGACATTGAT CAGCAGTACC AAGGGGCAAA CGGGTCATAC
    msal18688.2{GBS361_2603}  TTCCCGACAA CGACATTGAT CAGCAGTACC AAGGGGCAAA CGGGTCATAC
        msal18688.2{361_090}  TTCCCGACAA CGACATTGAT CAGCAGTACC AAGGGGCAAA CGGGTCATAC
     msal18688.2{361_1169NT}  TTCCCGACAA CGACATTGAT CAGCAGTACC AAGGGGCAAA CGGGTCATAC
     msal18688.2{361_CJB110}  TTCCCGACAA CGACATTGAT CAGCAGTACC AAGGGGCAAA CGGGTCATAC
       msal18688.2{361_M781}  TTCCCGACAA CGACATTGAT CAGCAGTACC AAGGGGCAAA CGGGTCATAC
                   Consensus  ********** ********** ********** ********** **********

                              951                                             1000
     msal18688.2{361_18RS21}  TCTAGGGGCT GCAGGTATTA TCGAATTGAT TAATTGTTTA GCGGCAATAG
       msal18688.2{361_A909}  TCTAGGGGCT GCAGGTATTA TCGAATTGAT TAATTGTTTA GCGGCAATAG
       msal18688.2{361_COH1}  TCTAGGGGCT GCAGGTATTA TCGAATTGAT TAATTGTTTA GCGGCAATAG
       msal18688.2{361_H36B}  TCTAGGGGCT GCAGGTATTA TCGAATTGAT TAATTGTTTA GCGGCAATAG
  msal18688.2{361_JM9130013}  TCTAGGGGCT GCAGGTATTA TCGAATTGAT TAATTGTTTA GCGGCAATAG
       msal18688.2{361_M732}  TCTAGGGGCT GCAGGTATTA TCGAATTGAT TAATTGTTTA GCGGCAATAG
    msal18688.2{GBS361_2603}  TCTAGGGGCT GCAGGTATTA TCGAATTGAT TAATTGTTTA GCGGCAATAG
        msal18688.2{361_090}  TCTAGGGGCT GCAGGTATTA TCGAATTGAT TAATTGTTTA GCGGCAATAG
     msal18688.2{361_1169NT}  TCTAGGGGCT GCAGGTATTA TCGAATTGAT TAATTGTTTA GCGGCAATAG
     msal18688.2{361_CJB110}  TCTAGGGGCT GCAGGTATTA TCGAATTGAT TAATTGTTTA GCGGCAATAG
       msal18688.2{361_M781}  TCTAGGGGCT GCAGGTATTA TCGAATTGAT TAATTGTTTA GCGGCAATAG
                   Consensus  ********** ********** ********** ********** **********

                              1001                                            1050
     msal18688.2{361_18RS21}  AGGAACAGAC TGTACCAGCA ACTAAAAATG AGATTGGGAT AGAAGGTTTT
       msal18688.2{361_A909}  AGGAACAGAC TGTACCAGCA ACTAAAAATG AGATTGGGAT AGAAGGTTTT
       msal18688.2{361_COH1}  AGGAACAGAC TGTACCAGCA ACTAAAAATG AGATTGGGAT AGAAGGTTTT
       msal18688.2{361_H36B}  AGGAACAGAC TGTACCAGCA ACTAAAAATG AGATTGGGAT AGAAGGTTTT
  msal18688.2{361_JM9130013}  AGGAACAGAC TGTACCAGCA ACTAAAAATG AGATTGGGAT AGAAGGTTTT
       msal18688.2{361_M732}  AGGAACAGAC TGTACCAGCA ACTAAAAATG AGATTGGGAT AGAAGGTTTT
    msal18688.2{GBS361_2603}  AGGAACAGAC TGTACCAGCA ACTAAAAATG AGATTGGGAT AGAAGGTTTT
        msal18688.2{361_090}  AGGAACAGAC TGTACCAGCA ACTAAAAATG AGATTGGGAT AGAAGGTTTT
     msal18688.2{361_1169NT}  AGGAACAGAC TGTACCAGCA ACTAAAAATG AGATTGGGAT AGAAGGTTTT
     msal18688.2{361_CJB110}  AGGAACAGAC TGTACCAGCA ACTAAAAATG AGATTGGGAT AGAAGGTTTT
       msal18688.2{361_M781}  AGGAACAGAC TGTACCAGCA ACTAAAAATG AGATTGGGAT AGAAGGTTTT
                   Consensus  ********** ********** ********** ********** **********

                              1051                                            1100
     msal18688.2{361_18RS21}  CCAGAAAATT TTGTCTATCA TCAAAAGAGA GAATACCCAA TAAGAAATGC
       msal18688.2{361_A909}  CCAGAAAATT TTGTCTATCA TCAAAAGAGA GAATACCCAA TAAGAAATGC
       msal18688.2{361_COH1}  CCAGAAAATT TTGTCTATCA TCAAAAGAGA GAATACCCAA TAAGAAATGC
       msal18688.2{361_H36B}  CCAGAAAATT TTGTCTATCA TCAAAAGAGA GAATACCCAA TAAGAAATGC
  msal18688.2{361_JM9130013}  CCAGAAAATT TTGTCTATCA TCAAAAGAGA GAATACCCAA TAAGAAATGC
       msal18688.2{361_M732}  CCAGAAAATT TTGTCTATCA TCAAAAGAGA GAATACCCAA TAAGAAATGC
    msal18688.2{GBS361_2603}  CCAGAAAATT TTGTCTATCA TCAAAAGAGA GAATACCCAA TAAGAAATGC
        msal18688.2{361_090}  CCAGAAAATT TTGTCTATCA TCAAAAGAGA GAATACCCAA TAAGAAATGC
     msal18688.2{361_1169NT}  CCAGAAAATT TTGTCTATCA TCAAAAGAGA GAATACCCAA TAAGAAATGC
     msal18688.2{361_CJB110}  CCAGAAAATT TTGTCTATCA TCAAAAGAGA GAATACCCAA TAAGAAATGC
       msal18688.2{361_M781}  CCAGAAAATT TTGTCTATCA TCAAAAGAGA GAATACCCAA TAAGAAATGC
                   Consensus  ********** ********** ********** ********** **********

                              1101                                            1150
     msal18688.2{361_18RS21}  TTTAAATTTT TCGTTTGCTT TTGGTGGAAA TAATAGTGGT gTCTTATTGT
       msal18688.2{361_A909}  TTTAAATTTT TCGTTTGCTT TTGGTGGAAA TAATAGTGGT gTCTTATTGT
       msal18688.2{361_COH1}  TTTAAATTTT TCGTTTGCTT TTGGTGGAAA TAATAGTGGT gTCTTATTGT
       msal18688.2{361_H36B}  TTTAAATTTT TCGTTTGCTT TTGGTGGAAA TAATAGTGGT gTCTTATTGT
  msal18688.2{361_JM9130013}  TTTAAATTTT TCGTTTGCTT TTGGTGGAAA TAATAGTGGT gTCTTATTGT
       msal18688.2{361_M732}  TTTAAATTTT TCGTTTGCTT TTGGTGGAAA TAATAGTGGT gTCTTATTGT
    msal18688.2{GBS361_2603}  TTTAAATTTT TCGTTTGCTT TTGGTGGAAA TAATAGTGGT gTCTTATTGT
        msal18688.2{361_090}  TTTAAATTTT TCGTTTGCTT TTGGTGGAAA TAATAGTGGT aTCTTATTGT
     msal18688.2{361_1169NT}  TTTAAATTTT TCGTTTGCTT TTGGTGGAAA TAATAGTGGT aTCTTATTGT
```

Table 75: Comparative Sequences relating to SAG0671

```
   msa118688.2{361_CJB110}  TTTAAATTTT TCGTTTGCTT TTGGTGGAAA TAATAGTGGT aTCTTATTGT
    msa118688.2{361_M781}  TTTAAATTTT TCGTTTGCTT TTGGTGGAAA TAATAGTGGT aTCTTATTGT
                Consensus  ********** ********** ********** ********** -*********

                           1151                                              1200
   msa118688.2{361_18RS21}  CATCTTTAGA TTCACCTCTA GAAACATTAC CTGCTAGAGA AAATCTTAAA
    msa118688.2{361_A909}  CATCTTTAGA TTCACCTCTA GAAACATTAC CTGCTAGAGA AAATCTTAAA
    msa118688.2{361_COH1}  CATCTTTAGA TTCACCTCTA GAAACATTAC CTGCTAGAGA AAATCTTAAA
    msa118688.2{361_H36B}  CATCTTTAGA TTCACCTCTA GAAACATTAC CTGCTAGAGA AAATCTTAAA
msa118688.2{361_JM9130013}  CATCTTTAGA TTCACCTCTA GAAACATTAC CTGCTAGAGA AAATCTTAAA
    msa118688.2{361_M732}  CATCTTTAGA TTCACCTCTA GAAACATTAC CTGCTAGAGA AAATCTTAAA
  msa118688.2{GBS361_2603}  CATCTTTAGA TTCACCTCTA GAAACATTAC CTGCTAGAGA AAATCTTAAA
     msa118688.2{361_090}  CATCTTTAGA TTCACCTCTA GAAACATTAC CTGCTAGAGA AAATCTTAAA
   msa118688.2{361_1169NT}  CATCTTTAGA TTCACCTCTA GAAACATTAC CTGCTAGAGA AAATCTTAAA
   msa118688.2{361_CJB110}  CATCTTTAGA TTCACCTCTA GAAACATTAC CTGCTAGAGA AAATCTTAAA
    msa118688.2{361_M781}  CATCTTTAGA TTCACCTCTA GAAACATTAC CTGCTAGAGA AAATCTTAAA
                Consensus  ********** ********** ********** ********** **********

                           1201                                              1250
   msa118688.2{361_18RS21}  ATGGCTATCT TATCATCTGT TGCTTCCATT TCTAAGAATG AATCACTTTC
    msa118688.2{361_A909}  ATGGCTATCT TATCATCTGT TGCTTCCATT TCTAAGAATG AATCACTTTC
    msa118688.2{361_COH1}  ATGGCTATCT TATCATCTGT TGCTTCCATT TCTAAGAATG AATCACTTTC
    msa118688.2{361_H36B}  ATGGCTATCT TATCATCTGT TGCTTCCATT TCTAAGAATG AATCACTTTC
msa118688.2{361_JM9130013}  ATGGCTATCT TATCATCTGT TGCTTCCATT TCTAAGAATG AATCACTTTC
    msa118688.2{361_M732}  ATGGCTATCT TATCATCTGT TGCTTCCATT TCTAAGAATG AATCACTTTC
  msa118688.2{GBS361_2603}  ATGGCTATCT TATCATCTGT TGCTTCCATT TCTAAGAATG AATCACTTTC
     msa118688.2{361_090}  ATGGCTATCT TATCATCTGT TGCTTCCATT TCTAAGAATG AATCACTTTC
   msa118688.2{361_1169NT}  ATGGCTATCT TATCATCTGT TGCTTCCATT TCTAAGAATG AATCACTTTC
   msa118688.2{361_CJB110}  ATGGCTATCT TATCATCTGT TGCTTCCATT TCTAAGAATG AATCACTTTC
    msa118688.2{361_M781}  ATGGCTATCT TATCATCTGT TGCTTCCATT TCTAAGAATG AATCACTTTC
                Consensus  ********** ********** ********** ********** **********

                           1251                                              1300
   msa118688.2{361_18RS21}  TATAACCTAT GAAAAAGTTG CTAGTAATTT CAACGACTTT GAAGCATTAC
    msa118688.2{361_A909}  TATAACCTAT GAAAAAGTTG CTAGTAATTT CAACGACTTT GAAGCATTAC
    msa118688.2{361_COH1}  TATAACCTAT GAAAAAGTTG CTAGTAATTT CAACGACTTT GAAGCATTAC
    msa118688.2{361_H36B}  TATAACCTAT GAAAAAGTTG CTAGTAATTT CAACGACTTT GAAGCATTAC
msa118688.2{361_JM9130013}  TATAACCTAT GAAAAAGTTG CTAGTAATTT CAACGACTTT GAAGCATTAC
    msa118688.2{361_M732}  TATAACCTAT GAAAAAGTTG CTAGTAATTT CAACGACTTT GAAGCATTAC
  msa118688.2{GBS361_2603}  TATAACCTAT GAAAAAGTTG CTAGTAATTT CAACGACTTT GAAGCATTAC
     msa118688.2{361_090}  TATAACCTAT GAAAAAGTTG CTAGTAATTT CAACGACTTT GAAGCATTAC
   msa118688.2{361_1169NT}  TATAACCTAT GAAAAAGTTG CTAGTAATTT CAACGACTTT GAAGCATTAC
   msa118688.2{361_CJB110}  TATAACCTAT GAAAAAGTTG CTAGTAATTT CAACGACTTT GAAGCATTAC
    msa118688.2{361_M781}  TATAACCTAT GAAAAAGTTG CTAGTAATTT CAACGACTTT GAAGCATTAC
                Consensus  ********** ********** ********** ********** **********

                           1301                                              1350
   msa118688.2{361_18RS21}  GCTTTAAAGG GGCTAGACCA CCCAAAACTG TCAACCCAGC ACAATTTAGG
    msa118688.2{361_A909}  GCTTTAAAGG GGCTAGACCA CCCAAAACTG TCAACCCAGC ACAATTTAGG
    msa118688.2{361_COH1}  GCTTTAAAGG GGCTAGACCA CCCAAAACTG TCAACCCAGC ACAATTTAGG
    msa118688.2{361_H36B}  GCTTTAAAGG GGCTAGACCA CCCAAAACTG TCAACCCAGC ACAATTTAGG
msa118688.2{361_JM9130013}  GCTTTAAAGG GGCTAGACCA CCCAAAACTG TCAACCCAGC ACAATTTAGG
    msa118688.2{361_M732}  GCTTTAAAGG GGCTAGACCA CCCAAAACTG TCAACCCAGC ACAATTTAGG
  msa118688.2{GBS361_2603}  GCTTTAAAGG GGCTAGACCA CCCAAAACTG TCAACCCAGC ACAATTTAGG
     msa118688.2{361_090}  GCTTTAAAGG GGCTAGACCA CCCAAAACTG TCAACCCAGC ACAATTTAGG
   msa118688.2{361_1169NT}  GCTTTAAAGG GGCTAGACCA CCCAAAACTG TCAACCCAGC ACAATTTAGG
   msa118688.2{361_CJB110}  GCTTTAAAGG GGCTAGACCA CCCAAAACTG TCAACCCAGC ACAATTTAGG
    msa118688.2{361_M781}  GCTTTAAAGG GGCTAGACCA CCCAAAACTG TCAACCCAGC ACAATTTAGG
                Consensus  ********** ********** ********** ********** **********

                           1351                                              1400
   msa118688.2{361_18RS21}  AAAATGGATG ATTTTTCCAA AATGGTTGCC GTAACAACAG CTCAAGCACT
    msa118688.2{361_A909}  AAAATGGATG ATTTTTCCAA AATGGTTGCC GTAACAACAG CTCAAGCACT
    msa118688.2{361_COH1}  AAAATGGATG ATTTTTCCAA AATGGTTGCC GTAACAACAG CTCAAGCACT
    msa118688.2{361_H36B}  AAAATGGATG ATTTTTCCAA AATGGTTGCC GTAACAACAG CTCAAGCACT
msa118688.2{361_JM9130013}  AAAATGGATG ATTTTTCCAA AATGGTTGCC GTAACAACAG CTCAAGCACT
    msa118688.2{361_M732}  AAAATGGATG ATTTTTCCAA AATGGTTGCC GTAACAACAG CTCAAGCACT
  msa118688.2{GBS361_2603}  AAAATGGATG ATTTTTCCAA AATGGTTGCC GTAACAACAG CTCAAGCACT
     msa118688.2{361_090}  AAAATGGATG ATTTTTCCAA AATGGTTGCC GTAACAACAG CTCAAGCACT
   msa118688.2{361_1169NT}  AAAATGGATG ATTTTTCCAA AATGGTTGCC GTAACAACAG CTCAAGCACT
   msa118688.2{361_CJB110}  AAAATGGATG ATTTTTCCAA AATGGTTGCC GTAACAACAG CTCAAGCACT
    msa118688.2{361_M781}  AAAATGGATG ATTTTTCCAA AATGGTTGCC GTAACAACAG CTCAAGCACT
                Consensus  ********** ********** ********** ********** **********

                           1401                                              1450
   msa118688.2{361_18RS21}  AATAGAAAGC AATATTAATC TAAAAAAACA AGATACTTCA AAAGTAGGAA
    msa118688.2{361_A909}  AATAGAAAGC AATATTAATC TAAAAAAACA AGATACTTCA AAAGTAGGAA
    msa118688.2{361_COH1}  AATAGAAAGC AATATTAATC TAAAAAAACA AGATACTTCA AAAGTAGGAA
    msa118688.2{361_H36B}  AATAGAAAGC AATATTAATC TAAAAAAACA AGATACTTCA AAAGTAGGAA
msa118688.2{361_JM9130013}  AATAGAAAGC AATATTAATC TAAAAAAACA AGATACTTCA AAAGTAGGAA
    msa118688.2{361_M732}  AATAGAAAGC AATATTAATC TAAAAAAACA AGATACTTCA AAAGTAGGAA
  msa118688.2{GBS361_2603}  AATAGAAAGC AATATTAATC TAAAAAAACA AGATACTTCA AAAGTAGGAA
     msa118688.2{361_090}  AATAGAAAGC AATATTAATC TAAAAAAACA AGATACTTCA AAAGTAGGAA
```

Table 75: Comparative Sequences relating to SAG0671

```
    msa118688.2{361_1169NT}  AATAGAAAGC AATATTAATC TAAAAAAACA AGATACTTCA AAAGTAGGAA
    msa118688.2{361_CJB110}  AATAGAAAGC AATATTAATC TAAAAAAACA AGATACTTCA AAAGTAGGAA
      msa118688.2{361_M781}  AATAGAAAGC AATATTAATC TAAAAAAACA AGATACTTCA AAAGTAGGAA
                  Consensus  ********** ********** ********** ********** **********

                             1451                                              1500
    msa118688.2{361_18RS21}  TTGTATTTAC AACACTTTCT GGACCAGTTG AGGTTGTTGA AGGTATTGAA
      msa118688.2{361_A909}  TTGTATTTAC AACACTTTCT GGACCAGTTG AGGTTGTTGA AGGTATTGAA
      msa118688.2{361_COH1}  TTGTATTTAC AACACTTTCT GGACCAGTTG AGGTTGTTGA AGGTATTGAA
      msa118688.2{361_H36B}  TTGTATTTAC AACACTTTCT GGACCAGTTG AGGTTGTTGA AGGTATTGAA
msa118688.2{361_JM9130013}  TTGTATTTAC AACACTTTCT GGACCAGTTG AGGTTGTTGA AGGTATTGAA
      msa118688.2{361_M732}  TTGTATTTAC AACACTTTCT GGACCAGTTG AGGTTGTTGA AGGTATTGAA
   msa118688.2{GBS361_2603}  TTGTATTTAC AACACTTTCT GGACCAGTTG AGGTTGTTGA AGGTATTGAA
       msa118688.2{361_090}  TTGTATTTAC AACACTTTCT GGACCAGTTG AGGTTGTTGA AGGTATTGAA
    msa118688.2{361_1169NT}  TTGTATTTAC AACACTTTCT GGACCAGTTG AGGTTGTTGA AGGTATTGAA
    msa118688.2{361_CJB110}  TTGTATTTAC AACACTTTCT GGACCAGTTG AGGTTGTTGA AGGTATTGAA
      msa118688.2{361_M781}  TTGTATTTAC AACACTTTCT GGACCAGTTG AGGTTGTTGA AGGTATTGAA
                  Consensus  ********** ********** ********** ********** **********

                             1501                                              1550
    msa118688.2{361_18RS21}  AAGCAAATCA CAACAGAAGG ATATGCACAT GTTTCTGCTT CACGATTCCC
      msa118688.2{361_A909}  AAGCAAATCA CAACAGAAGG ATATGCACAT GTTTCTGCTT CACGATTCCC
      msa118688.2{361_COH1}  AAGCAAATCA CAACAGAAGG ATATGCACAT GTTTCTGCTT CACGATTCCC
      msa118688.2{361_H36B}  AAGCAAATCA CAACAGAAGG ATATGCACAT GTTTCTGCTT CACGATTCCC
msa118688.2{361_JM9130013}  AAGCAAATCA CAACAGAAGG ATATGCACAT GTTTCTGCTT CACGATTCCC
      msa118688.2{361_M732}  AAGCAAATCA CAACAGAAGG ATATGCACAT GTTTCTGCTT CACGATTCCC
   msa118688.2{GBS361_2603}  AAGCAAATCA CAACAGAAGG ATATGCACAT GTTTCTGCTT CACGATTCCC
       msa118688.2{361_090}  AAGCAAATCA CAACAGAAGG ATATGCACAT GTTTCTGCTT CACGATTCCC
    msa118688.2{361_1169NT}  AAGCAAATCA CAACAGAAGG ATATGCACAT GTTTCTGCTT CACGATTCCC
    msa118688.2{361_CJB110}  AAGCAAATCA CAACAGAAGG ATATGCACAT GTTTCTGCTT CACGATTCCC
      msa118688.2{361_M781}  AAGCAAATCA CAACAGAAGG ATATGCACAT GTTTCTGCTT CACGATTCCC
                  Consensus  ********** ********** ********** ********** **********

                             1551                                              1600
    msa118688.2{361_18RS21}  GTTTACAGTA ATGAATGCAG CAGCTGGTAT GCTTTCTATC ATTTTTAAAA
      msa118688.2{361_A909}  GTTTACAGTA ATGAATGCAG CAGCTGGTAT GCTTTCTATC ATTTTTAAAA
      msa118688.2{361_COH1}  GTTTACAGTA ATGAATGCAG CAGCTGGTAT GCTTTCTATC ATTTTTAAAA
      msa118688.2{361_H36B}  GTTTACAGTA ATGAATGCAG CAGCTGGTAT GCTTTCTATC ATTTTTAAAA
msa118688.2{361_JM9130013}  GTTTACAGTA ATGAATGCAG CAGCTGGTAT GCTTTCTATC ATTTTTAAAA
      msa118688.2{361_M732}  GTTTACAGTA ATGAATGCAG CAGCTGGTAT GCTTTCTATC ATTTTTAAAA
   msa118688.2{GBS361_2603}  GTTTACAGTA ATGAATGCAG CAGCTGGTAT GCTTTCTATC ATTTTTAAAA
       msa118688.2{361_090}  GTTTACAGTA ATGAATGCAG CAGCTGGTAT GCTTTCTATC ATTTTTAAAA
    msa118688.2{361_1169NT}  GTTTACAGTA ATGAATGCAG CAGCTGGTAT GCTTTCTATC ATTTTTAAAA
    msa118688.2{361_CJB110}  GTTTACAGTA ATGAATGCAG CAGCTGGTAT GCTTTCTATC ATTTTTAAAA
      msa118688.2{361_M781}  GTTTACAGTA ATGAATGCAG CAGCTGGTAT GCTTTCTATC ATTTTTAAAA
                  Consensus  ********** ********** ********** ********** **********

                             1601                                              1650
    msa118688.2{361_18RS21}  TAACAGGTCC TTTATCTGTC ATTTCGACAA ATAGTGGAGC GCTTGATGGT
      msa118688.2{361_A909}  TAACAGGTCC TTTATCTGTC ATTTCGACAA ATAGTGGAGC GCTTGATGGT
      msa118688.2{361_COH1}  TAACAGGTCC TTTATCTGTC ATTTCGACAA ATAGTGGAGC GCTTGATGGT
      msa118688.2{361_H36B}  TAACAGGTCC TTTATCTGTC ATTTCGACAA ATAGTGGAGC GCTTGATGGT
msa118688.2{361_JM9130013}  TAACAGGTCC TTTATCTGTC ATTTCGACAA ATAGTGGAGC GCTTGATGGT
      msa118688.2{361_M732}  TAACAGGTCC TTTATCTGTC ATTTCGACAA ATAGTGGAGC GCTTGATGGT
   msa118688.2{GBS361_2603}  TAACAGGTCC TTTATCTGTC ATTTCGACAA ATAGTGGAGC GCTTGATGGT
       msa118688.2{361_090}  TAACAGGTCC TTTATCTGTC ATTTCGACAA ATAGTGGAGC GCTTGATGGT
    msa118688.2{361_1169NT}  TAACAGGTCC TTTATCTGTC ATTTCGACAA ATAGTGGAGC GCTTGATGGT
    msa118688.2{361_CJB110}  TAACAGGTCC TTTATCTGTC ATTTCGACAA ATAGTGGAGC GCTTGATGGT
      msa118688.2{361_M781}  TAACAGGTCC TTTATCTGTC ATTTCGACAA ATAGTGGAGC GCTTGATGGT
                  Consensus  ********** ********** ********** ********** **********

                             1651                                              1700
    msa118688.2{361_18RS21}  ATACAATATG CCAAGGAAAT GATGCGTAAC GATAATCTAG ACTATGTGAT
      msa118688.2{361_A909}  ATACAATATG CCAAGGAAAT GATGCGTAAC GATAATCTAG ACTATGTGAT
      msa118688.2{361_COH1}  ATACAATATG CCAAGGAAAT GATGCGTAAC GATAATCTAG ACTATGTGAT
      msa118688.2{361_H36B}  ATACAATATG CCAAGGAAAT GATGCGTAAC GATAATCTAG ACTATGTGAT
msa118688.2{361_JM9130013}  ATACAATATG CCAAGGAAAT GATGCGTAAC GATAATCTAG ACTATGTGAT
      msa118688.2{361_M732}  ATACAATATG CCAAGGAAAT GATGCGTAAC GATAATCTAG ACTATGTGAT
   msa118688.2{GBS361_2603}  ATACAATATG CCAAGGAAAT GATGCGTAAC GATAATCTAG ACTATGTGAT
       msa118688.2{361_090}  ATACAATATG CCAAGGAAAT GATGCGTAAC GATAATCTAG ACTATGTGAT
    msa118688.2{361_1169NT}  ATACAATATG CCAAGGAAAT GATGCGTAAC GATAATCTAG ACTATGTGAT
    msa118688.2{361_CJB110}  ATACAATATG CCAAGGAAAT GATGCGTAAC GATAATCTAG ACTATGTGAT
      msa118688.2{361_M781}  ATACAATATG CCAAGGAAAT GATGCGTAAC GATAATCTAG ACTATGTGAT
                  Consensus  ********** ********** ********** ********** **********

                             1701                                              1750
    msa118688.2{361_18RS21}  TCTTGTTTCT GCTAATCAGT GGACAGACAT GAGTTTTATG TGGTGGCAAC
      msa118688.2{361_A909}  TCTTGTTTCT GCTAATCAGT GGACAGACAT GAGTTTTATG TGGTGGCAAC
      msa118688.2{361_COH1}  TCTTGTTTCT GCTAATCAGT GGACAGACAT GAGTTTTATG TGGTGGCAAC
      msa118688.2{361_H36B}  TCTTGTTTCT GCTAATCAGT GGACAGACAT GAGTTTTATG TGGTGGCAAC
msa118688.2{361_JM9130013}  TCTTGTTTCT GCTAATCAGT GGACAGACAT GAGTTTTATG TGGTGGCAAC
      msa118688.2{361_M732}  TCTTGTTTCT GCTAATCAGT GGACAGACAT GAGTTTTATG TGGTGGCAAC
   msa118688.2{GBS361_2603}  TCTTGTTTCT GCTAATCAGT GGACAGACAT GAGTTTTATG TGGTGGCAAC
```

Table 75: Comparative Sequences relating to SAG0671

```
       msa118688.2{361_090}   TCTTGTTTCT GCTAATCAGT GGACAGACAT GAGTTTTATG TGGTGGCAAC
    msa118688.2{361_1169NT}   TCTTGTTTCT GCTAATCAGT GGACAGACAT GAGTTTTATG TGGTGGCAAC
    msa118688.2{361_CJB110}   TCTTGTTTCT GCTAATCAGT GGACAGACAT GAGTTTTATG TGGTGGCAAC
      msa118688.2{361_M781}   TCTTGTTTCT GCTAATCAGT GGACAGACAT GAGTTTTATG TGGTGGCAAC
                  Consensus   ********** ********** ********** ********** **********

                              1751                                             1800
     msa118688.2{361_18RS21}  AATTAAACTA TGATAGTCAA ATGTTTGTCG GTTCTGATTA TTGTTCAGCA
       msa118688.2{361_A909}  AATTAAACTA TGATAGTCAA ATGTTTGTCG GTTCTGATTA TTGTTCAGCA
       msa118688.2{361_COH1}  AATTAAACTA TGATAGTCAA ATGTTTGTCG GTTCTGATTA TTGTTCAGCA
       msa118688.2{361_H36B}  AATTAAACTA TGATAGTCAA ATGTTTGTCG GTTCTGATTA TTGTTCAGCA
  msa118688.2{361_JM9130013}  AATTAAACTA TGATAGTCAA ATGTTTGTCG GTTCTGATTA TTGTTCAGCA
       msa118688.2{361_M732}  AATTAAACTA TGATAGTCAA ATGTTTGTCG GTTCTGATTA TTGTTCAGCA
    msa118688.2{GBS361_2603}  AATTAAACTA TGATAGTCAA ATGTTTGTCG GTTCTGATTA TTGTTCAGCA
        msa118688.2{361_090}  AATTAAACTA TGATAGTCAA ATGTTTGTCG GTTCTGATTA TTGTTCAGCA
     msa118688.2{361_1169NT}  AATTAAACTA TGATAGTCAA ATGTTTGTCG GTTCTGATTA TTGTTCAGCA
     msa118688.2{361_CJB110}  AATTAAACTA TGATAGTCAA ATGTTTGTCG GTTCTGATTA TTGTTCAGCA
       msa118688.2{361_M781}  AATTAAACTA TGATAGTCAA ATGTTTGTCG GTTCTGATTA TTGTTCAGCA
                   Consensus  ********** ********** ********** ********** **********

                              1801                                             1850
     msa118688.2{361_18RS21}  CAAGTCCTCT CTCGTCAAGC ATTGGATAAT TCTCCTATAA TATTAGGTAG
       msa118688.2{361_A909}  CAAGTCCTCT CTCGTCAAGC ATTGGATAAT TCTCCTATAA TATTAGGTAG
       msa118688.2{361_COH1}  CAAGTCCTCT CTCGTCAAGC ATTGGATAAT TCTCCTATAA TATTAGGTAG
       msa118688.2{361_H36B}  CAAGTCCTCT CTCGTCAAGC ATTGGATAAT TCTCCTATAA TATTAGGTAG
  msa118688.2{361_JM9130013}  CAAGTCCTCT CTCGTCAAGC ATTGGATAAT TCTCCTATAA TATTAGGTAG
       msa118688.2{361_M732}  CAAGTCCTCT CTCGTCAAGC ATTGGATAAT TCTCCTATAA TATTAGGTAG
    msa118688.2{GBS361_2603}  CAAGTCCTCT CTCGTCAAGC ATTGGATAAT TCTCCTATAA TATTAGGTAG
        msa118688.2{361_090}  CAAGTCCTCT CTCGTCAAGC ATTGGATAAT TCTCCTATAA TATTAGGTAG
     msa118688.2{361_1169NT}  CAAGTCCTCT CTCGTCAAGC ATTGGATAAT TCTCCTATAA TATTAGGTAG
     msa118688.2{361_CJB110}  CAAGTCCTCT CTCGTCAAGC ATTGGATAAT TCTCCTATAA TATTAGGTAG
       msa118688.2{361_M781}  CAAGTCCTCT CTCGTCAAGC ATTGGATAAT TCTCCTATAA TATTAGGTAG
                   Consensus  ********** ********** ********** ********** **********

                              1851                                             1900
     msa118688.2{361_18RS21}  TAAACAATTA AAATATAGCC ATAAAACATT CACAGATGTG ATGACTATTT
       msa118688.2{361_A909}  TAAACAATTA AAATATAGCC ATAAAACATT CACAGATGTG ATGACTATTT
       msa118688.2{361_COH1}  TAAACAATTA AAATATAGCC ATAAAACATT CACAGATGTG ATGACTATTT
       msa118688.2{361_H36B}  TAAACAATTA AAATATAGCC ATAAAACATT CACAGATGTG ATGACTATTT
  msa118688.2{361_JM9130013}  TAAACAATTA AAATATAGCC ATAAAACATT CACAGATGTG ATGACTATTT
       msa118688.2{361_M732}  TAAACAATTA AAATATAGCC ATAAAACATT CACAGATGTG ATGACTATTT
    msa118688.2{GBS361_2603}  TAAACAATTA AAATATAGCC ATAAAACATT CACAGATGTG ATGACTATTT
        msa118688.2{361_090}  TAAACAATTA AAATATAGCC ATAAAACATT CACAGATGTG ATGACTATTT
     msa118688.2{361_1169NT}  TAAACAATTA AAATATAGCC ATAAAACATT CACAGATGTG ATGACTATTT
     msa118688.2{361_CJB110}  TAAACAATTA AAATATAGCC ATAAAACATT CACAGATGTG ATGACTATTT
       msa118688.2{361_M781}  TAAACAATTA AAATATAGCC ATAAAACATT CACAGATGTG ATGACTATTT
                   Consensus  ********** ********** ********** ********** **********

                              1901                                             1950
     msa118688.2{361_18RS21}  TTGATGCTGC GCTTCAAAAT TTATTATCAG ACTTAGGACT AACCATAAAA
       msa118688.2{361_A909}  TTGATGCTGC GCTTCAAAAT TTATTATCAG ACTTAGGACT AACCATAAAA
       msa118688.2{361_COH1}  TTGATGCTGC GCTTCAAAAT TTATTATCAG ACTTAGGACT AACCATAAAA
       msa118688.2{361_H36B}  TTGATGCTGC GCTTCAAAAT TTATTATCAG ACTTAGGACT AACCATAAAA
  msa118688.2{361_JM9130013}  TTGATGCTGC GCTTCAAAAT TTATTATCAG ACTTAGGACT AACCATAAAA
       msa118688.2{361_M732}  TTGATGCTGC GCTTCAAAAT TTATTATCAG ACTTAGGACT AACCATAAAA
    msa118688.2{GBS361_2603}  TTGATGCTGC GCTTCAAAAT TTATTATCAG ACTTAGGACT AACCATAAAA
        msa118688.2{361_090}  TTGATGCTGC GCTTCAAAAT TTATTATCAG ACTTAGGACT AACCATAAAA
     msa118688.2{361_1169NT}  TTGATGCTGC GCTTCAAAAT TTATTATCAG ACTTAGGACT AACCATAAAA
     msa118688.2{361_CJB110}  TTGATGCTGC GCTTCAAAAT TTATTATCAG ACTTAGGACT AACCATAAAA
       msa118688.2{361_M781}  TTGATGCTGC GCTTCAAAAT TTATTATCAG ACTTAGGACT AACCATAAAA
                   Consensus  ********** ********** ********** ********** **********

                              1951                                             2000
     msa118688.2{361_18RS21}  GATATCAAAG GTTTCGTTTG GAATGAGCGG AAGAAGGCAG TTAGTTCAGA
       msa118688.2{361_A909}  GATATCAAAG GTTTCGTTTG GAATGAGCGG AAGAAGGCAG TTAGTTCAGA
       msa118688.2{361_COH1}  GATATCAAAG GTTTCGTTTG GAATGAGCGG AAGAAGGCAG TTAGTTCAGA
       msa118688.2{361_H36B}  GATATCAAAG GTTTCGTTTG GAATGAGCGG AAGAAGGCAG TTAGTTCAGA
  msa118688.2{361_JM9130013}  GATATCAAAG GTTTCGTTTG GAATGAGCGG AAGAAGGCAG TTAGTTCAGA
       msa118688.2{361_M732}  GATATCAAAG GTTTCGTTTG GAATGAGCGG AAGAAGGCAG TTAGTTCAGA
    msa118688.2{GBS361_2603}  GATATCAAAG GTTTCGTTTG GAATGAGCGG AAGAAGGCAG TTAGTTCAGA
        msa118688.2{361_090}  GATATCAAAG GTTTCGTTTG GAATGAGCGG AAGAAGGCAG TTAGTTCAGA
     msa118688.2{361_1169NT}  GATATCAAAG GTTTCGTTTG GAATGAGCGG AAGAAGGCAG TTAGTTCAGA
     msa118688.2{361_CJB110}  GATATCAAAG GTTTCGTTTG GAATGAGCGG AAGAAGGCAG TTAGTTCAGA
       msa118688.2{361_M781}  GATATCAAAG GTTTCGTTTG GAATGAGCGG AAGAAGGCAG TTAGTTCAGA
                   Consensus  ********** ********** ********** ********** **********

                              2001                                             2050
     msa118688.2{361_18RS21}  TTATGATTTC TTAGCGAACT TGTCTGAGTA TTATAATATG CCAAACCTTG
       msa118688.2{361_A909}  TTATGATTTC TTAGCGAACT TGTCTGAGTA TTATAATATG CCAAACCTTG
       msa118688.2{361_COH1}  TTATGATTTC TTAGCGAACT TGTCTGAGTA TTATAATATG CCAAACCTTG
       msa118688.2{361_H36B}  TTATGATTTC TTAGCGAACT TGTCTGAGTA TTATAATATG CCAAACCTTG
  msa118688.2{361_JM9130013}  TTATGATTTC TTAGCGAACT TGTCTGAGTA TTATAATATG CCAAACCTTG
       msa118688.2{361_M732}  TTATGATTTC TTAGCGAACT TGTCTGAGTA TTATAATATG CCAAACCTTG
```

Table 75: Comparative Sequences relating to SAG0671

```
  msa118688.2{GBS361_2603}  TTATGATTTC TTAGCGAACT TGTCTGAGTA TTATAATATG CCAAACCTTG
      msa118688.2{361_090}  TTATGATTTC TTAGCGAACT TGTCTGAGTA TTATAATATG CCAAACCTTG
   msa118688.2{361_1169NT}  TTATGATTTC TTAGCGAACT TGTCTGAGTA TTATAATATG CCAAACCTTG
   msa118688.2{361_CJB110}  TTATGATTTC TTAGCGAACT TGTCTGAGTA TTATAATATG CCAAACCTTG
     msa118688.2{361_M781}  TTATGATTTC TTAGCGAACT TGTCTGAGTA TTATAATATG CCAAACCTTG
                 Consensus  ********** ********** ********** ********** **********

                            2051                                              2100
    msa118688.2{361_18RS21}  CTTCTGGTCA GTTTGGATTT TCATCTAATG GTGCTGGTGA AGAACTGGAC
      msa118688.2{361_A909}  CTTCTGGTCA GTTTGGATTT TCATCTAATG GTGCTGGTGA AGAACTGGAC
      msa118688.2{361_COH1}  CTTCTGGTCA GTTTGGATTT TCATCTAATG GTGCTGGTGA AGAACTGGAC
      msa118688.2{361_H36B}  CTTCTGGTCA GTTTGGATTT TCATCTAATG GTGCTGGTGA AGAACTGGAC
 msa118688.2{361_JM9130013}  CTTCTGGTCA GTTTGGATTT TCATCTAATG GTGCTGGTGA AGAACTGGAC
      msa118688.2{361_M732}  CTTCTGGTCA GTTTGGATTT TCATCTAATG GTGCTGGTGA AGAACTGGAC
   msa118688.2{GBS361_2603}  CTTCTGGTCA GTTTGGATTT TCATCTAATG GTGCTGGTGA AGAACTGGAC
       msa118688.2{361_090}  CTTCTGGTCA GTTTGGATTT TCATCTAATG GTGCTGGTGA AGAACTGGAC
    msa118688.2{361_1169NT}  CTTCTGGTCA GTTTGGATTT TCATCTAATG GTGCTGGTGA AGAACTGGAC
    msa118688.2{361_CJB110}  CTTCTGGTCA GTTTGGATTT TCATCTAATG GTGCTGGTGA AGAACTGGAC
      msa118688.2{361_M781}  CTTCTGGTCA GTTTGGATTT TCATCTAATG GTGCTGGTGA AGAACTGGAC
                  Consensus  ********** ********** ********** ********** **********

                             2101                                              2150
    msa118688.2{361_18RS21}  TATACTGTTA ATGAAAGTAT AGAAAAGGGC TATTATTTAG TCCTATCTTA
      msa118688.2{361_A909}  TATACTGTTA ATGAAAGTAT AGAAAAGGGC TATTATTTAG TCCTATCTTA
      msa118688.2{361_COH1}  TATACTGTTA ATGAAAGTAT AGAAAAGGGC TATTATTTAG TCCTATCTTA
      msa118688.2{361_H36B}  TATACTGTTA ATGAAAGTAT AGAAAAGGGC TATTATTTAG TCCTATCTTA
 msa118688.2{361_JM9130013}  TATACTGTTA ATGAAAGTAT AGAAAAGGGC TATTATTTAG TCCTATCTTA
      msa118688.2{361_M732}  TATACTGTTA ATGAAAGTAT AGAAAAGGGC TATTATTTAG TCCTATCTTA
   msa118688.2{GBS361_2603}  TATACTGTTA ATGAAAGTAT AGAAAAGGGC TATTATTTAG TCCTATCTTA
       msa118688.2{361_090}  TATACTGTTA ATGAAAGTAT AGAAAAGGGC TATTATTTAG TCCTATCTTA
    msa118688.2{361_1169NT}  TATACTGTTA ATGAAAGTAT AGAAAAGGGC TATTATTTAG TCCTATCTTA
    msa118688.2{361_CJB110}  TATACTGTTA ATGAAAGTAT AGAAAAGGGC TATTATTTAG TCCTATCTTA
      msa118688.2{361_M781}  TATACTGTTA ATGAAAGTAT AGAAAAGGGC TATTATTTAG TCCTATCTTA
                  Consensus  ********** ********** ********** ********** **********

                             2151                                      2193
    msa118688.2{361_18RS21}  TTCGATCTTc GGTGGTATCT CTTTTGCTAT TATTGAAAAA AGG
      msa118688.2{361_A909}  TTCGATCTTc GGTGGTATCT CTTTTGCTAT TATTGAAAAA AGG
      msa118688.2{361_COH1}  TTCGATCTTc GGTGGTATCT CTTTTGCTAT TATTGAAAAA AGG
      msa118688.2{361_H36B}  TTCGATCTTc GGTGGTATCT CTTTTGCTAT TATTGAAAAA AGG
 msa118688.2{361_JM9130013}  TTCGATCTTc GGTGGTATCT CTTTTGCTAT TATTGAAAAA AGG
      msa118688.2{361_M732}  TTCGATCTTc GGTGGTATCT CTTTTGCTAT TATTGAAAAA AGG
   msa118688.2{GBS361_2603}  TTCGATCTTc GGTGGTATCT CTTTTGCTAT TATTGAAAAA AGG
       msa118688.2{361_090}  TTCGATCTTt GGTGGTATCT CTTTTGCTAT TATTGAAAAA AGG
    msa118688.2{361_1169NT}  TTCGATCTTt GGTGGTATCT CTTTTGCTAT TATTGAAAAA AGG
    msa118688.2{361_CJB110}  TTCGATCTTt GGTGGTATCT CTTTTGCTAT TATTGAAAAA AGG
      msa118688.2{361_M781}  TTCGATCTTt GGTGGTATCT CTTTTGCTAT TATTGAAAAA AGG
                  Consensus  *********- ********** ********** ********** ***
```

SEQ ID NO. 7512
STRAIN 2603 frame: 1
MSVYVSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPEVPEQ
YKDETRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGKSAGQNALYQFEEGERQV
DASLLEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLQDGDCDLAICGG
CDELSDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKIIGGL
ITSDGYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKF
FPTTTLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKR
EYPIRNALNFSFAFGGNNSGVLLSSLDSPLETLPARENLKMAILSSVASISKNESLSITY
EKVASNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTS
KVGIVFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSV
ISTNSGALDGIQYAKEMMRNDNLDYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSA
QVLSRQALDNSPIILGSKQLKYSHKTFTDVMTIFDAALQNLLSDLGLTIKDIKGFVWNER
KKAVSSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIF
GGISFAIIEKR

SEQ ID NO. 7513
STRAIN 090 frame: 3
VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLQDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
RNALNFSFAFGGNNSGILLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSAQVLS
RQALDNSPIILGSKQLKYSHKTFTDVMTIFDAALQNLLSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIFGGIS
FAIIEKR

SEQ ID NO. 7514
STRAIN A909 frame: 3

Table 75: Comparative Sequences relating to SAG0671

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLQDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
RNALNFSFAFGGNNSGVLLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSAQVLS
RQALDNSPIILGSKQLKYSHKTFTDVMTIFDAALQNLLSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIFGGIS
FAIIEKR

SEQ ID NO. 7515
STRAIN H36B frame: 3
VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLQDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
RNALNFSFAFGGNNSGVLLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSAQVLS
RQALDNSPIILGSKQLKYSHKTFTDVMTIFDAALQNLLSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIFGGIS
FAIIEKR

SEQ ID NO. 7516
STRAIN 18RS21 frame: 3
VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLQDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
RNALNFSFAFGGNNSGVLLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSAQVLS
RQALDNSPIILGSKQLKYSHKTFTDVMTIFDAALQNLLSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIFGGIS
FAIIEKR

SEQ ID NO. 7517
STRAIN M732 frame: 3
VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLQDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
RNALNFSFAFGGNNSGVLLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSAQVLS
RQALDNSPIILGSKQLKYSHKTFTDVMTIFDAALQNLLSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIFGGIS
FAIIEKR

SEQ ID NO. 7518
STRAIN COH1 frame: 3
VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLQDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
RNALNFSFAFGGNNSGVLLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSAQVLS
RQALDNSPIILGSKQLKYSHKTFTDVMTIFDAALQNLLSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIFGGIS
FAIIEKR

SEQ ID NO. 7519
STRAIN M781 frame: 3
VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGKSAGQNALYQFEEGERQVDASL

Table 75: Comparative Sequences relating to SAG0671

LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLQDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
RNALNFSFAFGGNNSGILLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSAQVLS
RQALDNSPIILGSKQLKYSHKTFTDVMTIFDAALQNLLSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIFGGIS
FAIIEKR

SEQ ID NO. 7520
STRAIN CJB110 frame: 3
VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLQDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
RNALNFSFAFGGNNSGILLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSAQVLS
RQALDNSPIILGSKQLKYSHKTFTDVMTIFDAALQNLLSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIFGGIS
FAIIEKR

SEQ ID NO. 7521
STRAIN 1169NT frame: 3
VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLQDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
RNALNFSFAFGGNNSGILLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSAQVLS
RQALDNSPIILGSKQLKYSHKTFTDVMTIFDAALQNLLSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIFGGIS
FAIIEKR

SEQ ID NO. 7522
STRAIN JM9130013 frame: 3
VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDIVGASYVISTACSASNNAVILGTQLLQDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
RNALNFSFAFGGNNSGVLLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSANQWTDMSFMWWQQLNYDSQMFVGSDYCSAQVLS
RQALDNSPIILGSKQLKYSHKTFTDVMTIFDAALQNLLSDLGLTIKDIKGFVWNERKKAV
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYYLVLSYSIFGGIS
FAIIEKR

```
PRETTY of: /biotmp/msa118713.2{*}   April 9, 2003 02:54  ..

                                  1                                                  50
        msa118713.2{361_090}  ----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESYTGS
      msa118713.2{361_1169NT}  ----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESYTGS
      msa118713.2{361_CJB110}  ----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESYTGS
        msa118713.2{361_M781}  ----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESYTGS
      msa118713.2{361_18RS21}  ----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESYTGS
        msa118713.2{361_A909}  ----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESYTGS
        msa118713.2{361_COH1}  ----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESYTGS
        msa118713.2{361_H36B}  ----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESYTGS
   msa118713.2{361_JM9130013}  ----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESYTGS
        msa118713.2{361_M732}  ----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESYTGS
    msa118713.2{GBS361_2603}  msvyVSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESYTGS
                   Consensus  ********** ********** ********** ********** **********

                              51                                                100
        msa118713.2{361_090}  ITSDPEVPEQ YKDETRNFKF AFTAFEEALA SSGVNLKAYH NIAVCLGTSL
      msa118713.2{361_1169NT}  ITSDPEVPEQ YKDETRNFKF AFTAFEEALA SSGVNLKAYH NIAVCLGTSL
      msa118713.2{361_CJB110}  ITSDPEVPEQ YKDETRNFKF AFTAFEEALA SSGVNLKAYH NIAVCLGTSL
        msa118713.2{361_M781}  ITSDPEVPEQ YKDETRNFKF AFTAFEEALA SSGVNLKAYH NIAVCLGTSL
      msa118713.2{361_18RS21}  ITSDPEVPEQ YKDETRNFKF AFTAFEEALA SSGVNLKAYH NIAVCLGTSL
```

Table 75: Comparative Sequences relating to SAG0671

```
     msa118713.2{361_A909}  ITSDPEVPEQ YKDETRNFKF AFTAFEEALA SSGVNLKAYH NIAVCLGTSL
     msa118713.2{361_COH1}  ITSDPEVPEQ YKDETRNFKF AFTAFEEALA SSGVNLKAYH NIAVCLGTSL
     msa118713.2{361_H36B}  ITSDPEVPEQ YKDETRNFKF AFTAFEEALA SSGVNLKAYH NIAVCLGTSL
msa118713.2{361_JM9130013}  ITSDPEVPEQ YKDETRNFKF AFTAFEEALA SSGVNLKAYH NIAVCLGTSL
     msa118713.2{361_M732}  ITSDPEVPEQ YKDETRNFKF AFTAFEEALA SSGVNLKAYH NIAVCLGTSL
  msa118713.2{GBS361_2603}  ITSDPEVPEQ YKDETRNFKF AFTAFEEALA SSGVNLKAYH NIAVCLGTSL
                 Consensus  ********** ********** ********** ********** **********

                            101                                              150
      msa118713.2{361_090}  GGKSAGQNAL YQFEEGERQV DASLLEKASV YHIADELMAY HDIVGASYVI
    msa118713.2{361_1169NT}  GGKSAGQNAL YQFEEGERQV DASLLEKASV YHIADELMAY HDIVGASYVI
    msa118713.2{361_CJB110}  GGKSAGQNAL YQFEEGERQV DASLLEKASV YHIADELMAY HDIVGASYVI
     msa118713.2{361_M781}  GGKSAGQNAL YQFEEGERQV DASLLEKASV YHIADELMAY HDIVGASYVI
    msa118713.2{361_18RS21}  GGKSAGQNAL YQFEEGERQV DASLLEKASV YHIADELMAY HDIVGASYVI
     msa118713.2{361_A909}  GGKSAGQNAL YQFEEGERQV DASLLEKASV YHIADELMAY HDIVGASYVI
     msa118713.2{361_COH1}  GGKSAGQNAL YQFEEGERQV DASLLEKASV YHIADELMAY HDIVGASYVI
     msa118713.2{361_H36B}  GGKSAGQNAL YQFEEGERQV DASLLEKASV YHIADELMAY HDIVGASYVI
msa118713.2{361_JM9130013}  GGKSAGQNAL YQFEEGERQV DASLLEKASV YHIADELMAY HDIVGASYVI
     msa118713.2{361_M732}  GGKSAGQNAL YQFEEGERQV DASLLEKASV YHIADELMAY HDIVGASYVI
  msa118713.2{GBS361_2603}  GGKSAGQNAL YQFEEGERQV DASLLEKASV YHIADELMAY HDIVGASYVI
                 Consensus  ********** ********** ********** ********** **********

                            151                                              200
      msa118713.2{361_090}  STACSASNNA VILGTQLLQD GDCDLAICGG CDELSDISLA GFTSLGAINT
    msa118713.2{361_1169NT}  STACSASNNA VILGTQLLQD GDCDLAICGG CDELSDISLA GFTSLGAINT
    msa118713.2{361_CJB110}  STACSASNNA VILGTQLLQD GDCDLAICGG CDELSDISLA GFTSLGAINT
     msa118713.2{361_M781}  STACSASNNA VILGTQLLQD GDCDLAICGG CDELSDISLA GFTSLGAINT
    msa118713.2{361_18RS21}  STACSASNNA VILGTQLLQD GDCDLAICGG CDELSDISLA GFTSLGAINT
     msa118713.2{361_A909}  STACSASNNA VILGTQLLQD GDCDLAICGG CDELSDISLA GFTSLGAINT
     msa118713.2{361_COH1}  STACSASNNA VILGTQLLQD GDCDLAICGG CDELSDISLA GFTSLGAINT
     msa118713.2{361_H36B}  STACSASNNA VILGTQLLQD GDCDLAICGG CDELSDISLA GFTSLGAINT
msa118713.2{361_JM9130013}  STACSASNNA VILGTQLLQD GDCDLAICGG CDELSDISLA GFTSLGAINT
     msa118713.2{361_M732}  STACSASNNA VILGTQLLQD GDCDLAICGG CDELSDISLA GFTSLGAINT
  msa118713.2{GBS361_2603}  STACSASNNA VILGTQLLQD GDCDLAICGG CDELSDISLA GFTSLGAINT
                 Consensus  ********** ********** ********** ********** **********

                            201                                              250
      msa118713.2{361_090}  EMACQPYSSG KGINLGEGAG FVVLVKDQSL AKYGKIIGGL ITSDGYHITA
    msa118713.2{361_1169NT}  EMACQPYSSG KGINLGEGAG FVVLVKDQSL AKYGKIIGGL ITSDGYHITA
    msa118713.2{361_CJB110}  EMACQPYSSG KGINLGEGAG FVVLVKDQSL AKYGKIIGGL ITSDGYHITA
     msa118713.2{361_M781}  EMACQPYSSG KGINLGEGAG FVVLVKDQSL AKYGKIIGGL ITSDGYHITA
    msa118713.2{361_18RS21}  EMACQPYSSG KGINLGEGAG FVVLVKDQSL AKYGKIIGGL ITSDGYHITA
     msa118713.2{361_A909}  EMACQPYSSG KGINLGEGAG FVVLVKDQSL AKYGKIIGGL ITSDGYHITA
     msa118713.2{361_COH1}  EMACQPYSSG KGINLGEGAG FVVLVKDQSL AKYGKIIGGL ITSDGYHITA
     msa118713.2{361_H36B}  EMACQPYSSG KGINLGEGAG FVVLVKDQSL AKYGKIIGGL ITSDGYHITA
msa118713.2{361_JM9130013}  EMACQPYSSG KGINLGEGAG FVVLVKDQSL AKYGKIIGGL ITSDGYHITA
     msa118713.2{361_M732}  EMACQPYSSG KGINLGEGAG FVVLVKDQSL AKYGKIIGGL ITSDGYHITA
  msa118713.2{GBS361_2603}  EMACQPYSSG KGINLGEGAG FVVLVKDQSL AKYGKIIGGL ITSDGYHITA
                 Consensus  ********** ********** ********** ********** **********

                            251                                              300
      msa118713.2{361_090}  PKPTGEGAAQ IAKQLVTQAG IDYSEIDYIN GHGTGTQAND KMEKNMYGKF
    msa118713.2{361_1169NT}  PKPTGEGAAQ IAKQLVTQAG IDYSEIDYIN GHGTGTQAND KMEKNMYGKF
    msa118713.2{361_CJB110}  PKPTGEGAAQ IAKQLVTQAG IDYSEIDYIN GHGTGTQAND KMEKNMYGKF
     msa118713.2{361_M781}  PKPTGEGAAQ IAKQLVTQAG IDYSEIDYIN GHGTGTQAND KMEKNMYGKF
    msa118713.2{361_18RS21}  PKPTGEGAAQ IAKQLVTQAG IDYSEIDYIN GHGTGTQAND KMEKNMYGKF
     msa118713.2{361_A909}  PKPTGEGAAQ IAKQLVTQAG IDYSEIDYIN GHGTGTQAND KMEKNMYGKF
     msa118713.2{361_COH1}  PKPTGEGAAQ IAKQLVTQAG IDYSEIDYIN GHGTGTQAND KMEKNMYGKF
     msa118713.2{361_H36B}  PKPTGEGAAQ IAKQLVTQAG IDYSEIDYIN GHGTGTQAND KMEKNMYGKF
msa118713.2{361_JM9130013}  PKPTGEGAAQ IAKQLVTQAG IDYSEIDYIN GHGTGTQAND KMEKNMYGKF
     msa118713.2{361_M732}  PKPTGEGAAQ IAKQLVTQAG IDYSEIDYIN GHGTGTQAND KMEKNMYGKF
  msa118713.2{GBS361_2603}  PKPTGEGAAQ IAKQLVTQAG IDYSEIDYIN GHGTGTQAND KMEKNMYGKF
                 Consensus  ********** ********** ********** ********** **********

                            301                                              350
      msa118713.2{361_090}  FPTTTLISST KGQTGHTLGA AGIIELINCL AAIEEQTVPA TKNEIGIEGF
    msa118713.2{361_1169NT}  FPTTTLISST KGQTGHTLGA AGIIELINCL AAIEEQTVPA TKNEIGIEGF
    msa118713.2{361_CJB110}  FPTTTLISST KGQTGHTLGA AGIIELINCL AAIEEQTVPA TKNEIGIEGF
     msa118713.2{361_M781}  FPTTTLISST KGQTGHTLGA AGIIELINCL AAIEEQTVPA TKNEIGIEGF
    msa118713.2{361_18RS21}  FPTTTLISST KGQTGHTLGA AGIIELINCL AAIEEQTVPA TKNEIGIEGF
     msa118713.2{361_A909}  FPTTTLISST KGQTGHTLGA AGIIELINCL AAIEEQTVPA TKNEIGIEGF
     msa118713.2{361_COH1}  FPTTTLISST KGQTGHTLGA AGIIELINCL AAIEEQTVPA TKNEIGIEGF
     msa118713.2{361_H36B}  FPTTTLISST KGQTGHTLGA AGIIELINCL AAIEEQTVPA TKNEIGIEGF
msa118713.2{361_JM9130013}  FPTTTLISST KGQTGHTLGA AGIIELINCL AAIEEQTVPA TKNEIGIEGF
     msa118713.2{361_M732}  FPTTTLISST KGQTGHTLGA AGIIELINCL AAIEEQTVPA TKNEIGIEGF
  msa118713.2{GBS361_2603}  FPTTTLISST KGQTGHTLGA AGIIELINCL AAIEEQTVPA TKNEIGIEGF
                 Consensus  ********** ********** ********** ********** **********

                            351                                              400
      msa118713.2{361_090}  PENFVYHQKR EYPIRNALNF SFAFGGNNSG iLLSSLDSPL ETLPARENLK
    msa118713.2{361_1169NT}  PENFVYHQKR EYPIRNALNF SFAFGGNNSG iLLSSLDSPL ETLPARENLK
    msa118713.2{361_CJB110}  PENFVYHQKR EYPIRNALNF SFAFGGNNSG iLLSSLDSPL ETLPARENLK
     msa118713.2{361_M781}  PENFVYHQKR EYPIRNALNF SFAFGGNNSG iLLSSLDSPL ETLPARENLK
```

Table 75: Comparative Sequences relating to SAG0671

```
  msa118713.2{361_18RS21}   PENFVYHQKR EYPIRNALNF SFAFGGNNSG vLLSSLDSPL ETLPARENLK
    msa118713.2{361_A909}   PENFVYHQKR EYPIRNALNF SFAFGGNNSG vLLSSLDSPL ETLPARENLK
    msa118713.2{361_COH1}   PENFVYHQKR EYPIRNALNF SFAFGGNNSG vLLSSLDSPL ETLPARENLK
    msa118713.2{361_H36B}   PENFVYHQKR EYPIRNALNF SFAFGGNNSG vLLSSLDSPL ETLPARENLK
msa118713.2{361_JM9130013}  PENFVYHQKR EYPIRNALNF SFAFGGNNSG vLLSSLDSPL ETLPARENLK
    msa118713.2{361_M732}   PENFVYHQKR EYPIRNALNF SFAFGGNNSG vLLSSLDSPL ETLPARENLK
 msa118713.2{GBS361_2603}   PENFVYHQKR EYPIRNALNF SFAFGGNNSG vLLSSLDSPL ETLPARENLK
                Consensus   ********** ********** ********** -********* **********

                            401                                               450
     msa118713.2{361_090}   MAILSSVASI SKNESLSITY EKVASNFNDF EALRFKGARP PKTVNPAQFR
  msa118713.2{361_1169NT}   MAILSSVASI SKNESLSITY EKVASNFNDF EALRFKGARP PKTVNPAQFR
  msa118713.2{361_CJB110}   MAILSSVASI SKNESLSITY EKVASNFNDF EALRFKGARP PKTVNPAQFR
    msa118713.2{361_M781}   MAILSSVASI SKNESLSITY EKVASNFNDF EALRFKGARP PKTVNPAQFR
  msa118713.2{361_18RS21}   MAILSSVASI SKNESLSITY EKVASNFNDF EALRFKGARP PKTVNPAQFR
    msa118713.2{361_A909}   MAILSSVASI SKNESLSITY EKVASNFNDF EALRFKGARP PKTVNPAQFR
    msa118713.2{361_COH1}   MAILSSVASI SKNESLSITY EKVASNFNDF EALRFKGARP PKTVNPAQFR
    msa118713.2{361_H36B}   MAILSSVASI SKNESLSITY EKVASNFNDF EALRFKGARP PKTVNPAQFR
msa118713.2{361_JM9130013}  MAILSSVASI SKNESLSITY EKVASNFNDF EALRFKGARP PKTVNPAQFR
    msa118713.2{361_M732}   MAILSSVASI SKNESLSITY EKVASNFNDF EALRFKGARP PKTVNPAQFR
 msa118713.2{GBS361_2603}   MAILSSVASI SKNESLSITY EKVASNFNDF EALRFKGARP PKTVNPAQFR
                Consensus   ********** ********** ********** ********** **********

                            451                                               500
     msa118713.2{361_090}   KMDDFSKMVA VTTAQALIES NINLKKQDTS KVGIVFTTLS GPVEVVEGIE
  msa118713.2{361_1169NT}   KMDDFSKMVA VTTAQALIES NINLKKQDTS KVGIVFTTLS GPVEVVEGIE
  msa118713.2{361_CJB110}   KMDDFSKMVA VTTAQALIES NINLKKQDTS KVGIVFTTLS GPVEVVEGIE
    msa118713.2{361_M781}   KMDDFSKMVA VTTAQALIES NINLKKQDTS KVGIVFTTLS GPVEVVEGIE
  msa118713.2{361_18RS21}   KMDDFSKMVA VTTAQALIES NINLKKQDTS KVGIVFTTLS GPVEVVEGIE
    msa118713.2{361_A909}   KMDDFSKMVA VTTAQALIES NINLKKQDTS KVGIVFTTLS GPVEVVEGIE
    msa118713.2{361_COH1}   KMDDFSKMVA VTTAQALIES NINLKKQDTS KVGIVFTTLS GPVEVVEGIE
    msa118713.2{361_H36B}   KMDDFSKMVA VTTAQALIES NINLKKQDTS KVGIVFTTLS GPVEVVEGIE
msa118713.2{361_JM9130013}  KMDDFSKMVA VTTAQALIES NINLKKQDTS KVGIVFTTLS GPVEVVEGIE
    msa118713.2{361_M732}   KMDDFSKMVA VTTAQALIES NINLKKQDTS KVGIVFTTLS GPVEVVEGIE
 msa118713.2{GBS361_2603}   KMDDFSKMVA VTTAQALIES NINLKKQDTS KVGIVFTTLS GPVEVVEGIE
                Consensus   ********** ********** ********** ********** **********

                            501                                               550
     msa118713.2{361_090}   KQITTEGYAH VSASRFPFTV MNAAAGMLSI IFKITGPLSV ISTNSGALDG
  msa118713.2{361_1169NT}   KQITTEGYAH VSASRFPFTV MNAAAGMLSI IFKITGPLSV ISTNSGALDG
  msa118713.2{361_CJB110}   KQITTEGYAH VSASRFPFTV MNAAAGMLSI IFKITGPLSV ISTNSGALDG
    msa118713.2{361_M781}   KQITTEGYAH VSASRFPFTV MNAAAGMLSI IFKITGPLSV ISTNSGALDG
  msa118713.2{361_18RS21}   KQITTEGYAH VSASRFPFTV MNAAAGMLSI IFKITGPLSV ISTNSGALDG
    msa118713.2{361_A909}   KQITTEGYAH VSASRFPFTV MNAAAGMLSI IFKITGPLSV ISTNSGALDG
    msa118713.2{361_COH1}   KQITTEGYAH VSASRFPFTV MNAAAGMLSI IFKITGPLSV ISTNSGALDG
    msa118713.2{361_H36B}   KQITTEGYAH VSASRFPFTV MNAAAGMLSI IFKITGPLSV ISTNSGALDG
msa118713.2{361_JM9130013}  KQITTEGYAH VSASRFPFTV MNAAAGMLSI IFKITGPLSV ISTNSGALDG
    msa118713.2{361_M732}   KQITTEGYAH VSASRFPFTV MNAAAGMLSI IFKITGPLSV ISTNSGALDG
 msa118713.2{GBS361_2603}   KQITTEGYAH VSASRFPFTV MNAAAGMLSI IFKITGPLSV ISTNSGALDG
                Consensus   ********** ********** ********** ********** **********

                            551                                               600
     msa118713.2{361_090}   IQYAKEMMRN DNLDYVILVS ANQWTDMSFM WWQQLNYDSQ MFVGSDYCSA
  msa118713.2{361_1169NT}   IQYAKEMMRN DNLDYVILVS ANQWTDMSFM WWQQLNYDSQ MFVGSDYCSA
  msa118713.2{361_CJB110}   IQYAKEMMRN DNLDYVILVS ANQWTDMSFM WWQQLNYDSQ MFVGSDYCSA
    msa118713.2{361_M781}   IQYAKEMMRN DNLDYVILVS ANQWTDMSFM WWQQLNYDSQ MFVGSDYCSA
  msa118713.2{361_18RS21}   IQYAKEMMRN DNLDYVILVS ANQWTDMSFM WWQQLNYDSQ MFVGSDYCSA
    msa118713.2{361_A909}   IQYAKEMMRN DNLDYVILVS ANQWTDMSFM WWQQLNYDSQ MFVGSDYCSA
    msa118713.2{361_COH1}   IQYAKEMMRN DNLDYVILVS ANQWTDMSFM WWQQLNYDSQ MFVGSDYCSA
    msa118713.2{361_H36B}   IQYAKEMMRN DNLDYVILVS ANQWTDMSFM WWQQLNYDSQ MFVGSDYCSA
msa118713.2{361_JM9130013}  IQYAKEMMRN DNLDYVILVS ANQWTDMSFM WWQQLNYDSQ MFVGSDYCSA
    msa118713.2{361_M732}   IQYAKEMMRN DNLDYVILVS ANQWTDMSFM WWQQLNYDSQ MFVGSDYCSA
 msa118713.2{GBS361_2603}   IQYAKEMMRN DNLDYVILVS ANQWTDMSFM WWQQLNYDSQ MFVGSDYCSA
                Consensus   ********** ********** ********** ********** **********

                            601                                               650
     msa118713.2{361_090}   QVLSRQALDN SPIILGSKQL KYSHKTFTDV MTIFDAALQN LLSDLGLTIK
  msa118713.2{361_1169NT}   QVLSRQALDN SPIILGSKQL KYSHKTFTDV MTIFDAALQN LLSDLGLTIK
  msa118713.2{361_CJB110}   QVLSRQALDN SPIILGSKQL KYSHKTFTDV MTIFDAALQN LLSDLGLTIK
    msa118713.2{361_M781}   QVLSRQALDN SPIILGSKQL KYSHKTFTDV MTIFDAALQN LLSDLGLTIK
  msa118713.2{361_18RS21}   QVLSRQALDN SPIILGSKQL KYSHKTFTDV MTIFDAALQN LLSDLGLTIK
    msa118713.2{361_A909}   QVLSRQALDN SPIILGSKQL KYSHKTFTDV MTIFDAALQN LLSDLGLTIK
    msa118713.2{361_COH1}   QVLSRQALDN SPIILGSKQL KYSHKTFTDV MTIFDAALQN LLSDLGLTIK
    msa118713.2{361_H36B}   QVLSRQALDN SPIILGSKQL KYSHKTFTDV MTIFDAALQN LLSDLGLTIK
msa118713.2{361_JM9130013}  QVLSRQALDN SPIILGSKQL KYSHKTFTDV MTIFDAALQN LLSDLGLTIK
    msa118713.2{361_M732}   QVLSRQALDN SPIILGSKQL KYSHKTFTDV MTIFDAALQN LLSDLGLTIK
 msa118713.2{GBS361_2603}   QVLSRQALDN SPIILGSKQL KYSHKTFTDV MTIFDAALQN LLSDLGLTIK
                Consensus   ********** ********** ********** ********** **********

                            651                                               700
     msa118713.2{361_090}   DIKGFVWNER KKAVSSDYDF LANLSEYYNM PNLASGQFGF SSNGAGEELD
  msa118713.2{361_1169NT}   DIKGFVWNER KKAVSSDYDF LANLSEYYNM PNLASGQFGF SSNGAGEELD
  msa118713.2{361_CJB110}   DIKGFVWNER KKAVSSDYDF LANLSEYYNM PNLASGQFGF SSNGAGEELD
```

Table 75: Comparative Sequences relating to SAG0671

```
      msa118713.2{361_M781}  DIKGFVWNER KKAVSSDYDF LANLSEYYNM PNLASGQFGF SSNGAGEELD
     msa118713.2{361_18RS21}  DIKGFVWNER KKAVSSDYDF LANLSEYYNM PNLASGQFGF SSNGAGEELD
      msa118713.2{361_A909}  DIKGFVWNER KKAVSSDYDF LANLSEYYNM PNLASGQFGF SSNGAGEELD
      msa118713.2{361_COH1}  DIKGFVWNER KKAVSSDYDF LANLSEYYNM PNLASGQFGF SSNGAGEELD
      msa118713.2{361_H36B}  DIKGFVWNER KKAVSSDYDF LANLSEYYNM PNLASGQFGF SSNGAGEELD
  msa118713.2{361_JM9130013}  DIKGFVWNER KKAVSSDYDF LANLSEYYNM PNLASGQFGF SSNGAGEELD
      msa118713.2{361_M732}  DIKGFVWNER KKAVSSDYDF LANLSEYYNM PNLASGQFGF SSNGAGEELD
   msa118713.2{GBS361_2603}  DIKGFVWNER KKAVSSDYDF LANLSEYYNM PNLASGQFGF SSNGAGEELD
                  Consensus  ********** ********** ********** ********** **********

                             701                            731
       msa118713.2{361_090}  YTVNESIEKG YYLVLSYSIF GGISFAIIEK R
    msa118713.2{361_1169NT}  YTVNESIEKG YYLVLSYSIF GGISFAIIEK R
    msa118713.2{361_CJB110}  YTVNESIEKG YYLVLSYSIF GGISFAIIEK R
      msa118713.2{361_M781}  YTVNESIEKG YYLVLSYSIF GGISFAIIEK R
     msa118713.2{361_18RS21}  YTVNESIEKG YYLVLSYSIF GGISFAIIEK R
      msa118713.2{361_A909}  YTVNESIEKG YYLVLSYSIF GGISFAIIEK R
      msa118713.2{361_COH1}  YTVNESIEKG YYLVLSYSIF GGISFAIIEK R
      msa118713.2{361_H36B}  YTVNESIEKG YYLVLSYSIF GGISFAIIEK R
  msa118713.2{361_JM9130013}  YTVNESIEKG YYLVLSYSIF GGISFAIIEK R
      msa118713.2{361_M732}  YTVNESIEKG YYLVLSYSIF GGISFAIIEK R
   msa118713.2{GBS361_2603}  YTVNESIEKG YYLVLSYSIF GGISFAIIEK R
                  Consensus  ********** ********** ********** *
```

Table 76: Comparative Sequences relating to SAG0260

SEQ ID NO. 7601
STRAIN 2603
ATGAAAAAAGTCATCGATTTAAAAAAACTACAAAAAGCATATGCCTCAGAAACCGTTTTA
AATAATATTAATTTGGAGGTGTTTAAAGGCGAAATAATTGGATTAATAGGACCCTCTGGA
GCAGGGAAATCTACCTTGATTAAAACTATGCTTGGCATGGAAAAAGCAGATAAGGGAACA
GCTCTTGTTCTTGATACTCAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATG
GCTCAATCTGATGCCTTATACGAGTCTTTAACTGGCTTAGAAAATTTATTATTCTTTGGA
AAAATGAAAGGTATTCAAAAAACTGAATTAAAACAGCAGATAACTCATATTTCTAAAGTA
GTAGATCTAGAAAACCAACTTGATAAATTTGTCTCAGGTTACTCAGGAGGTATGAAAAGA
CGGCTTTCTCTAGCCATCGCCCTACTTGGAAACCCCACAGTTTTAATCCTAGATGAACCT
ACCGTTGGAATTGATCCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAG
GATGAAGGACATTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTAACAAGT
AAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGATACTCCATTACATTTAAAA
AAACAATTTAATGTGAGTACTATTGAGGAAGTTTTCTTAAAAGCTGAAGGAGAA

SEQ ID NO. 7602
STRAIN 090
ATTTAAAAAAACTACAAAAAGCATATGCCTCAGAAACTGTTTTAAATAAT
ATTAATTTGGAGGTGTTTAAAGGCGAAATAATTGGATTAATAGGACCCTC
TGGAGCAGGGAAATCTACCTTGATTAAAACTATGCTTGGCATGGAAAAAG
CAGATAAGGGAACAGCTCTTGTTCTTGATACTCAAATGCCAGATCGTAAT
ATTTTAAATCAAATTGGCTATATGGCTCAATCTGATGCCTTATACGAATC
TTTAACTGCCTTAGAAaATTTATTATTCTTTGGAAAAATGAAAGGTATTC
AAAAAACTGAATTAAAACAGCAGATAACTCATATTTcTAAAGTAGTAGAT
CTAGAAAACCAACTTGATAAATTTGTCTCAGGTTACTCAGGAGGTATGAA
AAGACGGCTTTCTCTAGCCATCGCCCTACTTGGAAACCCCACAGTTTTAA
TCCTAGATGAACCTACCGTTGGAATTGATCCATCCTTGAGGAGAAAAATC
TGGCAAGAGCTAATTAATATTAaGGATGAAGGACGTTCTATCTTTATTAC
AACCCACGTTATGGATGAAGCAGAATTAACAAGTAAGGTTGCACTACTAT
TACGTGGAAACATTATTGCCTTTGATACTCCATTACATTTAAAAAAACAA
TTTAATGTGAGTACTATtGAGGAAGTTTTCTTAAAAGCTGAAGGAGAA

SEQ ID NO. 7603
STRAIN A909
AAAAAAGTCATCGATTTAAAAAAACTACAAAAAGCATATGCCTCA
GAAACCGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGCGAAATAAT
TGGATTAATAGGACCCTCTGGAGCAGGGAAATCTACCTTGATTAAAACTA
TGCTTGGCATGGAAAAAGCAGATAAGGGAACAGCTCTTGTTCTTGATACT
CAAATGCCAGATCATAATATTTTAAATCAAATTGGCTATATGGCTCAATC
TGATGCCTTATACGAGTCTTTAACTGGCTTAGAAAATTTATTATTCTTTG
GAAAAATGAAAGGTATTCAAAAAACTGAATTAAAACAGCAGATAACTCAT
ATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTCTCAGG
TTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTACTTG
GAAACCCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTGATCCA
TCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAGGATGAAGG
ACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTAACAA
GTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGATACTCCA
TTACATTTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAGTTTTCTT
AAAAGCTGAAGGAGAA

SEQ ID NO. 7604
STRAIN H36B
AAAAAAGTCATTGATTTAAAAAAACTACAAAAAGCATATGCC
TCAGAAACCGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGCGAAAT
AATTGGATTAATAGGACCCTCTGGAGCAGGGAAATCTACCTTGATTAAAA
CTATGCTTGGCATGGAAAAAGCAGATAAGGGAaCAGCTCTTGTTCTTGAT
ACTCAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGCTCA
ATCTGATGCCTTATACGAGTCTTTAACTGGCTTAGAAAATTTATTATTCT
TTGGAAAAATGAAAGGTATTCAAAAAACTGAATTAAAACAGCAGATAACT
CATATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTCTC
AGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTAC
TTGGAAACCCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTGAT
CCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAGGATGA
AGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTAA
CAAGTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGATACT
CCATTACATTTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAGTTTT
CTTAAAAGCTGAAGGAGAA

SEQ ID NO. 7605
STRAIN 18RS21
GATTTAAAAAAACTACAAAAAGCATATGCCTCAGAAACCGTTTTAAATAA
TATTAATTTGGAGGTGTTTAAAGGCGAAATAATTGGATTAATAGGACCCT
CTGGAGCAGGGAAATCTACcTTGATTAAAACTATGCTTGGCATGGAAAAA
GCAGATAAGGGAACAGCTCTTGTTCTTGATACTCAAATGCCAGATCGTAA
TATTTTAAATCAAATTGGCTATATGGCTCAATcTGATGCCTTATACGAGT
CTTTAACTGGCTTAGAAAATTTATTATTCTTTGGAAAAATGAAAGGTATT
CAAAAAACTGAATTAAAACAGCAGATAACTCATATTTCTAAAGTAGTAGA
TCTAGAAAACCAACTTGATAAATTTGTCTCAGGTTACTCAGGAGGTATGA
AAAGACGGCTTTCTcTAGCCATCGCCCTACTTGGAAACCCCACAGTTTTA
ATCCTAGATGAACCTACCGTTGGAATTGATCCATCCTTGAGGAGAAAAAT
CTGGCAAGAGCTAATTAATATTAaGGATGAAGGACATTCTATCTTTATTA
CAACCCACGTTATGGATGAAGCAGAATTAACAAGTAAGGTTGCACTACTA

Table 76: Comparative Sequences relating to SAG0260

TTACGTGGAAACATTATTGCCTTTGATACTCCATTACATTTAAAAAAACA
ATTTAATGTGAGTACTATTGAGGAAGTTTTCTTAAAAGCTGAAGGAGAA

SEQ ID NO. 7606
STRAIN M732
AAAAAAGTCATCGATTTAAAAAAACTACAAAAAGCATACGCCTCA
GAAACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGAGAAATAAT
TGGATTAATAGGACCCTCTGGAGCAGGGAAATCTACCTTGATTAAAACTA
TGCTTGGCATGGAAAAAGCAGATAAGGGAACAGCTCTTGTTCTTGATACT
CAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGCTCAATC
TGATGCCTTACACGAGTCTTTAACTGGCTTAGAAAATTTATTATTCTTTG
GAAAAATGAAAGGTATTCAAAAAACTGAATTAAAACAGCAGATAACTCAT
ATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTCTCAGG
TTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTACTTG
GAAACCCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTGATCCA
TCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAGGATGAAGG
ACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTAACAA
GTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGATACTCCA
TTACATTTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAGTTTTCTT
AAAAGCTGAAGGAGAA

SEQ ID NO. 7607
STRAIN COH1
AAAAAAGTCATCGATTTAAAAAAACTACAAAAAGCATACGCCTCAGAA
ACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGAGAAATAATTGG
ATTAATAGGACCCTCTGGAGCAGGGAAATCTACCTTGATTAAAACTATGC
TTGGCATGGAAAAAGCAGATAAGGGAACAGCTCTTGTTCTTGATACTCAA
ATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGCTCAATCTGA
TGCCTTACACGAGTCTTTAACTGGCTTAGAAAATTTATTATTCTTTGGAA
AAATGAAAGGTATTCAAAAAACTGAATTAAAACAGCAGATAACTCATATT
TCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTCTCAGGTTA
CTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTACTTGGAA
ACCCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTGATCCATCC
TTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAGGATGAAGGACG
TTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTAACAAGTA
AGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGATACTCCATTA
CATTTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAG

SEQ ID NO. 7608
STRAIN M781
AAAAAAGTCATCGATTTAAAAAAACTACAAAAAGCATAC
GCCTCAGAAACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGAGA
AATAATTGGATTAATAGGACCCTCTGGAGCAGGGAAATCTACCTTGATTA
AAACTATGCTTGGCATGGAAAAAGCAGATAAGGGAACAGCTCTTGTTCTT
GATACTCAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGC
TCAATCTGATGCCTTACACGAGTCTTTAACTGGCTTAGAAAATTTATTAT
TCTTTGGAAAAATGAAAGGTATTCAAAAAACTGAATTAAAACAGCAGATA
ACTCATATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGT
CTCAGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCC
TACTTGGAAACCCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATT
GATCCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAGGA
TGAAGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAT
TAACAAGTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGAT
ACTCCATTACATTTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAGT
TTTCTTAAAAGCTGAAGGAGAA

SEQ ID NO. 7609
STRAIN CJB110
AAAAAAGTCATCGATTTAAAAAAACTACAAAAAGCATATG
CCTCAGAAACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGCGAA
ATAATTGGATTAATAGGACCCTCTGGAGCAGGGAAATCTACCTTGATTAA
AACTATGCTTGGCATGGAAAAAGCAGATAAGGGAACAGCTCTTGTTCTTG
ATACTCAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGCT
CAATCTGATGCCTTATACGAATCTTTAACTGCCTTAGAAAATTTATTATT
CTTTGGAAAAATGAAAGGTATTCAAAAAACTGAATTAAAACAGCAGATAA
CTCATATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTC
TCAGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCT
ACTTGGAAACCCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTG
ATCCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAGGAT
GAAGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATT
AACAAGTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGATA
CTCCATTACATTTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAGTT
TTCTTAAAAGCTGAAGGAGAA

SEQ ID NO. 7610
STRAIN 1169NT
AAAAAAGTCATCGATTTAAAAAAACTACAAAAAGCATAC
GCCTCAGAAACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGCGA
AATAATTGGATTAATAGGACCCTCTGGAGCAGGGAAATCTACCTTGATTA
AAACTATGCTTGGCATGGAAAAAGCAGATAAGGGAACAGCTCTTGTTCTT
GATACTCAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGC
TCAATCTGATGCCTTATACGAATCTTTAACTGCCTTAGAAAATTTATTAT

Table 76: Comparative Sequences relating to SAG0260

TCTTTGGAAAAATGAAAGGTATTCAAAAAACTGAATTAAAACAGCAGATA
ACTCATATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGT
CTCAGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCC
TACTTGGAAACCCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATT
GATCCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAGGA
TGAAGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAT
TAACAAGTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGAT
ACTCCATTACATTTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAGT
TTTCTTAAAAGCTGAAGGAGAA

SEQ ID NO. 7611
STRAIN JM9130013
AAAAAAGTCATCGATTTAAAAAAACTACAAAAAGCATATGCC
TCAGAAACCGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGCGAAAT
AATTGGATTAATAGGACCCTCTGGAGCAGGGAAATCTACCTTGATTAAAA
CTATGCTTGGCATGGAAAAAGCAGATAAGGGAACAGCTCTTGTTCTTGAT
ACTCAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGCTCA
ATCTGATGCCTTATACGAGTCTTTAACTGGCTTAGAAAATTTATTATTCT
TTGGAAAAATGAAAGGTATTCAAAAAACTGAATTAAAACAGCAGATAACT
CATATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTCTC
AGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTAC
TTGGAAACCCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTGAT
CCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAGGATGA
AGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTAA
CAAGTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGATACT
CCATTACATTTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAGTTTT
CTTAAAAGCTGAAGGAGAA

```
PRETTY of: /biotmp/msa134270.2{*}   April 10, 2003 02:14  ..

                            1                                                   50
     msa134270.2{391_COH1}  ---aaaaaag tcatcgATTT AAAAAAACTA CAAAAAGCAT AcGCCTCAGA
     msa134270.2{391_M732}  ---aaaaaag tcatcgATTT AAAAAAACTA CAAAAAGCAT AcGCCTCAGA
     msa134270.2{391_M781}  ---aaaaaag tcatcgATTT AAAAAAACTA CAAAAAGCAT AcGCCTCAGA
      msa134270.2{391_090}  ---------- ------ATTT AAAAAAACTA CAAAAAGCAT AtGCCTCAGA
   msa134270.2{391_CJB110}  ---aaaaaag tcatcgATTT AAAAAAACTA CAAAAAGCAT AtGCCTCAGA
   msa134270.2{391_1169NT}  ---aaaaaag tcatcgATTT AAAAAAACTA CAAAAAGCAT AcGCCTCAGA
   msa134270.2{391_18RS21}  ---------- -----gATTT AAAAAAACTA CAAAAAGCAT AtGCCTCAGA
     msa134270.2{391_2603}  atgaaaaaag tcatcgATTT AAAAAAACTA CAAAAAGCAT AtGCCTCAGA
     msa134270.2{391_A909}  ---aaaaaag tcatcgATTT AAAAAAACTA CAAAAAGCAT AtGCCTCAGA
msa134270.2{391_JM9130013}  ---aaaaaag tcatcgATTT AAAAAAACTA CAAAAAGCAT AtGCCTCAGA
     msa134270.2{391_H36B}  ---aaaaaag tcattgATTT AAAAAAACTA CAAAAAGCAT AtGCCTCAGA
                 Consensus  ***------- ------**** ********** ********** *-********

                            51                                                 100
     msa134270.2{391_COH1}  AACtGTTTTA AATAATATTA ATTTGGAGGT GTTTAAAGGa GAAATAATTG
     msa134270.2{391_M732}  AACtGTTTTA AATAATATTA ATTTGGAGGT GTTTAAAGGa GAAATAATTG
     msa134270.2{391_M781}  AACtGTTTTA AATAATATTA ATTTGGAGGT GTTTAAAGGa GAAATAATTG
      msa134270.2{391_090}  AACtGTTTTA AATAATATTA ATTTGGAGGT GTTTAAAGGc GAAATAATTG
   msa134270.2{391_CJB110}  AACtGTTTTA AATAATATTA ATTTGGAGGT GTTTAAAGGc GAAATAATTG
   msa134270.2{391_1169NT}  AACtGTTTTA AATAATATTA ATTTGGAGGT GTTTAAAGGc GAAATAATTG
   msa134270.2{391_18RS21}  AACcGTTTTA AATAATATTA ATTTGGAGGT GTTTAAAGGc GAAATAATTG
     msa134270.2{391_2603}  AACcGTTTTA AATAATATTA ATTTGGAGGT GTTTAAAGGc GAAATAATTG
     msa134270.2{391_A909}  AACcGTTTTA AATAATATTA ATTTGGAGGT GTTTAAAGGc GAAATAATTG
msa134270.2{391_JM9130013}  AACcGTTTTA AATAATATTA ATTTGGAGGT GTTTAAAGGc GAAATAATTG
     msa134270.2{391_H36B}  AACcGTTTTA AATAATATTA ATTTGGAGGT GTTTAAAGGc GAAATAATTG
                 Consensus  ***-****** ********** ********** *********- **********

                            101                                                150
     msa134270.2{391_COH1}  GATTAATAGG ACCCTCTGGA GCAGGGAAAT CTACCTTGAT TAAAACTATG
     msa134270.2{391_M732}  GATTAATAGG ACCCTCTGGA GCAGGGAAAT CTACCTTGAT TAAAACTATG
     msa134270.2{391_M781}  GATTAATAGG ACCCTCTGGA GCAGGGAAAT CTACCTTGAT TAAAACTATG
      msa134270.2{391_090}  GATTAATAGG ACCCTCTGGA GCAGGGAAAT CTACCTTGAT TAAAACTATG
   msa134270.2{391_CJB110}  GATTAATAGG ACCCTCTGGA GCAGGGAAAT CTACCTTGAT TAAAACTATG
   msa134270.2{391_1169NT}  GATTAATAGG ACCCTCTGGA GCAGGGAAAT CTACCTTGAT TAAAACTATG
   msa134270.2{391_18RS21}  GATTAATAGG ACCCTCTGGA GCAGGGAAAT CTACCTTGAT TAAAACTATG
     msa134270.2{391_2603}  GATTAATAGG ACCCTCTGGA GCAGGGAAAT CTACCTTGAT TAAAACTATG
     msa134270.2{391_A909}  GATTAATAGG ACCCTCTGGA GCAGGGAAAT CTACCTTGAT TAAAACTATG
msa134270.2{391_JM9130013}  GATTAATAGG ACCCTCTGGA GCAGGGAAAT CTACCTTGAT TAAAACTATG
     msa134270.2{391_H36B}  GATTAATAGG ACCCTCTGGA GCAGGGAAAT CTACCTTGAT TAAAACTATG
                 Consensus  ********** ********** ********** ********** **********

                            151                                                200
     msa134270.2{391_COH1}  CTTGGCATGG AAAAAGCAGA TAAGGGAACA GCTCTTGTTC TTGATACTCA
     msa134270.2{391_M732}  CTTGGCATGG AAAAAGCAGA TAAGGGAACA GCTCTTGTTC TTGATACTCA
     msa134270.2{391_M781}  CTTGGCATGG AAAAAGCAGA TAAGGGAACA GCTCTTGTTC TTGATACTCA
      msa134270.2{391_090}  CTTGGCATGG AAAAAGCAGA TAAGGGAACA GCTCTTGTTC TTGATACTCA
   msa134270.2{391_CJB110}  CTTGGCATGG AAAAAGCAGA TAAGGGAACA GCTCTTGTTC TTGATACTCA
   msa134270.2{391_1169NT}  CTTGGCATGG AAAAAGCAGA TAAGGGAACA GCTCTTGTTC TTGATACTCA
   msa134270.2{391_18RS21}  CTTGGCATGG AAAAAGCAGA TAAGGGAACA GCTCTTGTTC TTGATACTCA
     msa134270.2{391_2603}  CTTGGCATGG AAAAAGCAGA TAAGGGAACA GCTCTTGTTC TTGATACTCA
     msa134270.2{391_A909}  CTTGGCATGG AAAAAGCAGA TAAGGGAACA GCTCTTGTTC TTGATACTCA
```

Table 76: Comparative Sequences relating to SAG0260

```
msa134270.2{391_JM9130013}  CTTGGCATGG AAAAAGCAGA TAAGGGAACA GCTCTTGTTC TTGATACTCA
     msa134270.2{391_H36B}  CTTGGCATGG AAAAAGCAGA TAAGGGAACA GCTCTTGTTC TTGATACTCA
                 Consensus  ********** ********** ********** ********** **********

                            201                                                250
     msa134270.2{391_COH1}  AATGCCAGAT CgTAATATTT TAAATCAAAT TGGCTATATG GCTCAATCTG
     msa134270.2{391_M732}  AATGCCAGAT CgTAATATTT TAAATCAAAT TGGCTATATG GCTCAATCTG
     msa134270.2{391_M781}  AATGCCAGAT CgTAATATTT TAAATCAAAT TGGCTATATG GCTCAATCTG
      msa134270.2{391_090}  AATGCCAGAT CgTAATATTT TAAATCAAAT TGGCTATATG GCTCAATCTG
   msa134270.2{391_CJB110}  AATGCCAGAT CgTAATATTT TAAATCAAAT TGGCTATATG GCTCAATCTG
   msa134270.2{391_1169NT}  AATGCCAGAT CgTAATATTT TAAATCAAAT TGGCTATATG GCTCAATCTG
   msa134270.2{391_18RS21}  AATGCCAGAT CgTAATATTT TAAATCAAAT TGGCTATATG GCTCAATCTG
     msa134270.2{391_2603}  AATGCCAGAT CgTAATATTT TAAATCAAAT TGGCTATATG GCTCAATCTG
     msa134270.2{391_A909}  AATGCCAGAT CaTAATATTT TAAATCAAAT TGGCTATATG GCTCAATCTG
msa134270.2{391_JM9130013}  AATGCCAGAT CgTAATATTT TAAATCAAAT TGGCTATATG GCTCAATCTG
     msa134270.2{391_H36B}  AATGCCAGAT CgTAATATTT TAAATCAAAT TGGCTATATG GCTCAATCTG
                 Consensus  ********** *_******** ********** ********** **********

                            251                                                300
     msa134270.2{391_COH1}  ATGCCTTAcA CGAgTCTTTA ACTGgCTTAG AAAATTTATT ATTCTTTGGA
     msa134270.2{391_M732}  ATGCCTTAcA CGAgTCTTTA ACTGgCTTAG AAAATTTATT ATTCTTTGGA
     msa134270.2{391_M781}  ATGCCTTAcA CGAgTCTTTA ACTGgCTTAG AAAATTTATT ATTCTTTGGA
      msa134270.2{391_090}  ATGCCTTAtA CGAaTCTTTA ACTGcCTTAG AAAATTTATT ATTCTTTGGA
   msa134270.2{391_CJB110}  ATGCCTTAtA CGAaTCTTTA ACTGcCTTAG AAAATTTATT ATTCTTTGGA
   msa134270.2{391_1169NT}  ATGCCTTAtA CGAaTCTTTA ACTGcCTTAG AAAATTTATT ATTCTTTGGA
   msa134270.2{391_18RS21}  ATGCCTTAtA CGAgTCTTTA ACTGgCTTAG AAAATTTATT ATTCTTTGGA
     msa134270.2{391_2603}  ATGCCTTAtA CGAgTCTTTA ACTGgCTTAG AAAATTTATT ATTCTTTGGA
     msa134270.2{391_A909}  ATGCCTTAtA CGAgTCTTTA ACTGgCTTAG AAAATTTATT ATTCTTTGGA
msa134270.2{391_JM9130013}  ATGCCTTAtA CGAgTCTTTA ACTGgCTTAG AAAATTTATT ATTCTTTGGA
     msa134270.2{391_H36B}  ATGCCTTAtA CGAgTCTTTA ACTGgCTTAG AAAATTTATT ATTCTTTGGA
                 Consensus  ********_* ***_****** ****_***** ********** **********

                            301                                                350
     msa134270.2{391_COH1}  AAAATGAAAG GTATTCAAAA AACTGAATTA AAACAGCAGA TAACTCATAT
     msa134270.2{391_M732}  AAAATGAAAG GTATTCAAAA AACTGAATTA AAACAGCAGA TAACTCATAT
     msa134270.2{391_M781}  AAAATGAAAG GTATTCAAAA AACTGAATTA AAACAGCAGA TAACTCATAT
      msa134270.2{391_090}  AAAATGAAAG GTATTCAAAA AACTGAATTA AAACAGCAGA TAACTCATAT
   msa134270.2{391_CJB110}  AAAATGAAAG GTATTCAAAA AACTGAATTA AAACAGCAGA TAACTCATAT
   msa134270.2{391_1169NT}  AAAATGAAAG GTATTCAAAA AACTGAATTA AAACAGCAGA TAACTCATAT
   msa134270.2{391_18RS21}  AAAATGAAAG GTATTCAAAA AACTGAATTA AAACAGCAGA TAACTCATAT
     msa134270.2{391_2603}  AAAATGAAAG GTATTCAAAA AACTGAATTA AAACAGCAGA TAACTCATAT
     msa134270.2{391_A909}  AAAATGAAAG GTATTCAAAA AACTGAATTA AAACAGCAGA TAACTCATAT
msa134270.2{391_JM9130013}  AAAATGAAAG GTATTCAAAA AACTGAATTA AAACAGCAGA TAACTCATAT
     msa134270.2{391_H36B}  AAAATGAAAG GTATTCAAAA AACTGAATTA AAACAGCAGA TAACTCATAT
                 Consensus  ********** ********** ********** ********** **********

                            351                                                400
     msa134270.2{391_COH1}  TTCTAAAGTA GTAGATCTAG AAAACCAACT TGATAAATTT GTCTCAGGTT
     msa134270.2{391_M732}  TTCTAAAGTA GTAGATCTAG AAAACCAACT TGATAAATTT GTCTCAGGTT
     msa134270.2{391_M781}  TTCTAAAGTA GTAGATCTAG AAAACCAACT TGATAAATTT GTCTCAGGTT
      msa134270.2{391_090}  TTCTAAAGTA GTAGATCTAG AAAACCAACT TGATAAATTT GTCTCAGGTT
   msa134270.2{391_CJB110}  TTCTAAAGTA GTAGATCTAG AAAACCAACT TGATAAATTT GTCTCAGGTT
   msa134270.2{391_1169NT}  TTCTAAAGTA GTAGATCTAG AAAACCAACT TGATAAATTT GTCTCAGGTT
   msa134270.2{391_18RS21}  TTCTAAAGTA GTAGATCTAG AAAACCAACT TGATAAATTT GTCTCAGGTT
     msa134270.2{391_2603}  TTCTAAAGTA GTAGATCTAG AAAACCAACT TGATAAATTT GTCTCAGGTT
     msa134270.2{391_A909}  TTCTAAAGTA GTAGATCTAG AAAACCAACT TGATAAATTT GTCTCAGGTT
msa134270.2{391_JM9130013}  TTCTAAAGTA GTAGATCTAG AAAACCAACT TGATAAATTT GTCTCAGGTT
     msa134270.2{391_H36B}  TTCTAAAGTA GTAGATCTAG AAAACCAACT TGATAAATTT GTCTCAGGTT
                 Consensus  ********** ********** ********** ********** **********

                            401                                                450
     msa134270.2{391_COH1}  ACTCAGGAGG TATGAAAAGA CGGCTTTCTC TAGCCATCGC CCTACTTGGA
     msa134270.2{391_M732}  ACTCAGGAGG TATGAAAAGA CGGCTTTCTC TAGCCATCGC CCTACTTGGA
     msa134270.2{391_M781}  ACTCAGGAGG TATGAAAAGA CGGCTTTCTC TAGCCATCGC CCTACTTGGA
      msa134270.2{391_090}  ACTCAGGAGG TATGAAAAGA CGGCTTTCTC TAGCCATCGC CCTACTTGGA
   msa134270.2{391_CJB110}  ACTCAGGAGG TATGAAAAGA CGGCTTTCTC TAGCCATCGC CCTACTTGGA
   msa134270.2{391_1169NT}  ACTCAGGAGG TATGAAAAGA CGGCTTTCTC TAGCCATCGC CCTACTTGGA
   msa134270.2{391_18RS21}  ACTCAGGAGG TATGAAAAGA CGGCTTTCTC TAGCCATCGC CCTACTTGGA
     msa134270.2{391_2603}  ACTCAGGAGG TATGAAAAGA CGGCTTTCTC TAGCCATCGC CCTACTTGGA
     msa134270.2{391_A909}  ACTCAGGAGG TATGAAAAGA CGGCTTTCTC TAGCCATCGC CCTACTTGGA
msa134270.2{391_JM9130013}  ACTCAGGAGG TATGAAAAGA CGGCTTTCTC TAGCCATCGC CCTACTTGGA
     msa134270.2{391_H36B}  ACTCAGGAGG TATGAAAAGA CGGCTTTCTC TAGCCATCGC CCTACTTGGA
                 Consensus  ********** ********** ********** ********** **********

                            451                                                500
     msa134270.2{391_COH1}  AACCCCACAG TTTTAATCCT AGATGAACCT ACCGTTGGAA TTGATCCATC
     msa134270.2{391_M732}  AACCCCACAG TTTTAATCCT AGATGAACCT ACCGTTGGAA TTGATCCATC
     msa134270.2{391_M781}  AACCCCACAG TTTTAATCCT AGATGAACCT ACCGTTGGAA TTGATCCATC
      msa134270.2{391_090}  AACCCCACAG TTTTAATCCT AGATGAACCT ACCGTTGGAA TTGATCCATC
   msa134270.2{391_CJB110}  AACCCCACAG TTTTAATCCT AGATGAACCT ACCGTTGGAA TTGATCCATC
   msa134270.2{391_1169NT}  AACCCCACAG TTTTAATCCT AGATGAACCT ACCGTTGGAA TTGATCCATC
   msa134270.2{391_18RS21}  AACCCCACAG TTTTAATCCT AGATGAACCT ACCGTTGGAA TTGATCCATC
     msa134270.2{391_2603}  AACCCCACAG TTTTAATCCT AGATGAACCT ACCGTTGGAA TTGATCCATC
```

Table 76: Comparative Sequences relating to SAG0260

```
     msa134270.2{391_A909} AACCCCACAG TTTTAATCCT AGATGAACCT ACCGTTGGAA TTGATCCATC
msa134270.2{391_JM9130013} AACCCCACAG TTTTAATCCT AGATGAACCT ACCGTTGGAA TTGATCCATC
     msa134270.2{391_H36B} AACCCCACAG TTTTAATCCT AGATGAACCT ACCGTTGGAA TTGATCCATC
                 Consensus ********** ********** ********** ********** **********

                           501                                                550
     msa134270.2{391_COH1} CTTGAGGAGA AAAATCTGGC AAGAGCTAAT TAATATTAAG GATGAAGGAC
     msa134270.2{391_M732} CTTGAGGAGA AAAATCTGGC AAGAGCTAAT TAATATTAAG GATGAAGGAC
     msa134270.2{391_M781} CTTGAGGAGA AAAATCTGGC AAGAGCTAAT TAATATTAAG GATGAAGGAC
      msa134270.2{391_090} CTTGAGGAGA AAAATCTGGC AAGAGCTAAT TAATATTAAG GATGAAGGAC
   msa134270.2{391_CJB110} CTTGAGGAGA AAAATCTGGC AAGAGCTAAT TAATATTAAG GATGAAGGAC
  msa134270.2{391_1169NT} CTTGAGGAGA AAAATCTGGC AAGAGCTAAT TAATATTAAG GATGAAGGAC
   msa134270.2{391_18RS21} CTTGAGGAGA AAAATCTGGC AAGAGCTAAT TAATATTAAG GATGAAGGAC
     msa134270.2{391_2603} CTTGAGGAGA AAAATCTGGC AAGAGCTAAT TAATATTAAG GATGAAGGAC
     msa134270.2{391_A909} CTTGAGGAGA AAAATCTGGC AAGAGCTAAT TAATATTAAG GATGAAGGAC
msa134270.2{391_JM9130013} CTTGAGGAGA AAAATCTGGC AAGAGCTAAT TAATATTAAG GATGAAGGAC
     msa134270.2{391_H36B} CTTGAGGAGA AAAATCTGGC AAGAGCTAAT TAATATTAAG GATGAAGGAC
                 Consensus ********** ********** ********** ********** **********

                           551                                                600
     msa134270.2{391_COH1} gTTCTATCTT TATTACAACC CACGTTATGG ATGAAGCAGA ATTAACAAGT
     msa134270.2{391_M732} gTTCTATCTT TATTACAACC CACGTTATGG ATGAAGCAGA ATTAACAAGT
     msa134270.2{391_M781} gTTCTATCTT TATTACAACC CACGTTATGG ATGAAGCAGA ATTAACAAGT
      msa134270.2{391_090} gTTCTATCTT TATTACAACC CACGTTATGG ATGAAGCAGA ATTAACAAGT
   msa134270.2{391_CJB110} gTTCTATCTT TATTACAACC CACGTTATGG ATGAAGCAGA ATTAACAAGT
   msa134270.2{391_1169NT} gTTCTATCTT TATTACAACC CACGTTATGG ATGAAGCAGA ATTAACAAGT
   msa134270.2{391_18RS21} aTTCTATCTT TATTACAACC CACGTTATGG ATGAAGCAGA ATTAACAAGT
     msa134270.2{391_2603} aTTCTATCTT TATTACAACC CACGTTATGG ATGAAGCAGA ATTAACAAGT
     msa134270.2{391_A909} gTTCTATCTT TATTACAACC CACGTTATGG ATGAAGCAGA ATTAACAAGT
msa134270.2{391_JM9130013} gTTCTATCTT TATTACAACC CACGTTATGG ATGAAGCAGA ATTAACAAGT
     msa134270.2{391_H36B} gTTCTATCTT TATTACAACC CACGTTATGG ATGAAGCAGA ATTAACAAGT
                 Consensus -********* ********** ********** ********** **********

                           601                                                650
     msa134270.2{391_COH1} AAGGTTGCAC TACTATTACG TGGAAACATT ATTGCCTTTG ATACTCCATT
     msa134270.2{391_M732} AAGGTTGCAC TACTATTACG TGGAAACATT ATTGCCTTTG ATACTCCATT
     msa134270.2{391_M781} AAGGTTGCAC TACTATTACG TGGAAACATT ATTGCCTTTG ATACTCCATT
      msa134270.2{391_090} AAGGTTGCAC TACTATTACG TGGAAACATT ATTGCCTTTG ATACTCCATT
   msa134270.2{391_CJB110} AAGGTTGCAC TACTATTACG TGGAAACATT ATTGCCTTTG ATACTCCATT
   msa134270.2{391_1169NT} AAGGTTGCAC TACTATTACG TGGAAACATT ATTGCCTTTG ATACTCCATT
   msa134270.2{391_18RS21} AAGGTTGCAC TACTATTACG TGGAAACATT ATTGCCTTTG ATACTCCATT
     msa134270.2{391_2603} AAGGTTGCAC TACTATTACG TGGAAACATT ATTGCCTTTG ATACTCCATT
     msa134270.2{391_A909} AAGGTTGCAC TACTATTACG TGGAAACATT ATTGCCTTTG ATACTCCATT
msa134270.2{391_JM9130013} AAGGTTGCAC TACTATTACG TGGAAACATT ATTGCCTTTG ATACTCCATT
     msa134270.2{391_H36B} AAGGTTGCAC TACTATTACG TGGAAACATT ATTGCCTTTG ATACTCCATT
                 Consensus ********** ********** ********** ********** **********

                           651                                                700
     msa134270.2{391_COH1} ACATTTAAAA AAACAATTTA ATGTGAGTAC TATTGAGGAA G~~~~~~~~~
     msa134270.2{391_M732} ACATTTAAAA AAACAATTTA ATGTGAGTAC TATTGAGGAA GTTTTCTTAA
     msa134270.2{391_M781} ACATTTAAAA AAACAATTTA ATGTGAGTAC TATTGAGGAA GTTTTCTTAA
      msa134270.2{391_090} ACATTTAAAA AAACAATTTA ATGTGAGTAC TATTGAGGAA GTTTTCTTAA
   msa134270.2{391_CJB110} ACATTTAAAA AAACAATTTA ATGTGAGTAC TATTGAGGAA GTTTTCTTAA
   msa134270.2{391_1169NT} ACATTTAAAA AAACAATTTA ATGTGAGTAC TATTGAGGAA GTTTTCTTAA
   msa134270.2{391_18RS21} ACATTTAAAA AAACAATTTA ATGTGAGTAC TATTGAGGAA GTTTTCTTAA
     msa134270.2{391_2603} ACATTTAAAA AAACAATTTA ATGTGAGTAC TATTGAGGAA GTTTTCTTAA
     msa134270.2{391_A909} ACATTTAAAA AAACAATTTA ATGTGAGTAC TATTGAGGAA GTTTTCTTAA
msa134270.2{391_JM9130013} ACATTTAAAA AAACAATTTA ATGTGAGTAC TATTGAGGAA GTTTTCTTAA
     msa134270.2{391_H36B} ACATTTAAAA AAACAATTTA ATGTGAGTAC TATTGAGGAA GTTTTCTTAA
                 Consensus ********** ********** ********** ********** **********

                           701          714
     msa134270.2{391_COH1} ~~~~~~~~~~ ~~~~
     msa134270.2{391_M732} AAGCTGAAGG AGAA
     msa134270.2{391_M781} AAGCTGAAGG AGAA
      msa134270.2{391_090} AAGCTGAAGG AGAA
   msa134270.2{391_CJB110} AAGCTGAAGG AGAA
   msa134270.2{391_1169NT} AAGCTGAAGG AGAA
   msa134270.2{391_18RS21} AAGCTGAAGG AGAA
     msa134270.2{391_2603} AAGCTGAAGG AGAA
     msa134270.2{391_A909} AAGCTGAAGG AGAA
msa134270.2{391_JM9130013} AAGCTGAAGG AGAA
     msa134270.2{391_H36B} AAGCTGAAGG AGAA
                 Consensus ********** ****
```

SEQ ID NO. 7612

STRAIN 2603 frame: 1

KKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
LVLDTQMPDRNILNQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQQITHISKVV
DLENQLDKFVSGYSGGMKRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
EGHSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7613

Table 76: Comparative Sequences relating to SAG0260

STRAIN 090 frame: 3
LKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGMEKADKGTALVLDT
QMPDRNILNQIGYMAQSDALYESLTALENLLFFGKMKGIQKTELKQQITHISKVVDLENQ
LDKFVSGYSGGMKRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKDEGRSI
FITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7614
STRAIN A909 frame: 1
KKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
LVLDTQMPDHNILNQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQQITHISKVV
DLENQLDKFVSGYSGGMKRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7615
STRAIN H36B frame: 1
KKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
LVLDTQMPDRNILNQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQQITHISKVV
DLENQLDKFVSGYSGGMKRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7616
STRAIN 18RS21 frame: 1
DLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGMEKADKGTALVLD
TQMPDRNILNQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQQITHISKVVDLEN
QLDKFVSGYSGGMKRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKDEGHS
IFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7617
STRAIN M732 frame: 1
KKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
LVLDTQMPDRNILNQIGYMAQSDALHESLTGLENLLFFGKMKGIQKTELKQQITHISKVV
DLENQLDKFVSGYSGGMKRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7618
STRAIN COH1 frame: 1
KKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
LVLDTQMPDRNILNQIGYMAQSDALHESLTGLENLLFFGKMKGIQKTELKQQITHISKVV
DLENQLDKFVSGYSGGMKRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7619
STRAIN M781 frame: 1
KKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
LVLDTQMPDRNILNQIGYMAQSDALHESLTGLENLLFFGKMKGIQKTELKQQITHISKVV
DLENQLDKFVSGYSGGMKRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7620
STRAIN CJB110 frame: 1
KKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
LVLDTQMPDRNILNQIGYMAQSDALYESLTALENLLFFGKMKGIQKTELKQQITHISKVV
DLENQLDKFVSGYSGGMKRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7621
STRAIN 1169NT frame: 1
KKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
LVLDTQMPDRNILNQIGYMAQSDALYESLTALENLLFFGKMKGIQKTELKQQITHISKVV
DLENQLDKFVSGYSGGMKRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7622
STRAIN JM9130013 frame: 1
KKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGMEKADKGTA
LVLDTQMPDRNILNQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQQITHISKVV
DLENQLDKFVSGYSGGMKRRLSLAIALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKD
EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

```
PRETTY of: /biotmp/msa134470.2{*}   April 10, 2003 02:16  ..

                                  1                                                50
      msa134470.2{391_090}    -----LKKLQ KAYASETVLN NINLEVFKGE IIGLIGPSGA GKSTLIKTML
   msa134470.2{391_1169NT}    KKVIDLKKLQ KAYASETVLN NINLEVFKGE IIGLIGPSGA GKSTLIKTML
   msa134470.2{391_CJB110}    KKVIDLKKLQ KAYASETVLN NINLEVFKGE IIGLIGPSGA GKSTLIKTML
     msa134470.2{391_COH1}    KKVIDLKKLQ KAYASETVLN NINLEVFKGE IIGLIGPSGA GKSTLIKTML
     msa134470.2{391_M732}    KKVIDLKKLQ KAYASETVLN NINLEVFKGE IIGLIGPSGA GKSTLIKTML
     msa134470.2{391_M781}    KKVIDLKKLQ KAYASETVLN NINLEVFKGE IIGLIGPSGA GKSTLIKTML
   msa134470.2{391_18RS21}    ----DLKKLQ KAYASETVLN NINLEVFKGE IIGLIGPSGA GKSTLIKTML
     msa134470.2{391_2603}    KKVIDLKKLQ KAYASETVLN NINLEVFKGE IIGLIGPSGA GKSTLIKTML
     msa134470.2{391_H36B}    KKVIDLKKLQ KAYASETVLN NINLEVFKGE IIGLIGPSGA GKSTLIKTML
msa134470.2{391_JM9130013}    KKVIDLKKLQ KAYASETVLN NINLEVFKGE IIGLIGPSGA GKSTLIKTML
```

Table 76: Comparative Sequences relating to SAG0260

```
     msa134470.2{391_A909}  KKVIDLKKLQ KAYASETVLN NINLEVFKGE IIGLIGPSGA GKSTLIKTML
                 Consensus  ********** ********** ********** ********** **********

                            51                                                 100
      msa134470.2{391_090}  GMEKADKGTA LVLDTQMPDr NILNQIGYMA QSDALyESLT aLENLLFFGK
   msa134470.2{391_1169NT}  GMEKADKGTA LVLDTQMPDr NILNQIGYMA QSDALyESLT aLENLLFFGK
   msa134470.2{391_CJB110}  GMEKADKGTA LVLDTQMPDr NILNQIGYMA QSDALyESLT aLENLLFFGK
     msa134470.2{391_COH1}  GMEKADKGTA LVLDTQMPDr NILNQIGYMA QSDALhESLT gLENLLFFGK
     msa134470.2{391_M732}  GMEKADKGTA LVLDTQMPDr NILNQIGYMA QSDALhESLT gLENLLFFGK
     msa134470.2{391_M781}  GMEKADKGTA LVLDTQMPDr NILNQIGYMA QSDALhESLT gLENLLFFGK
   msa134470.2{391_18RS21}  GMEKADKGTA LVLDTQMPDr NILNQIGYMA QSDALyESLT gLENLLFFGK
     msa134470.2{391_2603}  GMEKADKGTA LVLDTQMPDr NILNQIGYMA QSDALyESLT gLENLLFFGK
     msa134470.2{391_H36B}  GMEKADKGTA LVLDTQMPDr NILNQIGYMA QSDALyESLT gLENLLFFGK
msa134470.2{391_JM9130013}  GMEKADKGTA LVLDTQMPDr NILNQIGYMA QSDALyESLT gLENLLFFGK
     msa134470.2{391_A909}  GMEKADKGTA LVLDTQMPDh NILNQIGYMA QSDALyESLT gLENLLFFGK
                 Consensus  ********** *********_ ********** *****_**** _*********

                            101                                                150
      msa134470.2{391_090}  MKGIQKTELK QQITHISKVV DLENQLDKFV SGYSGGMKRR LSLAIALLGN
   msa134470.2{391_1169NT}  MKGIQKTELK QQITHISKVV DLENQLDKFV SGYSGGMKRR LSLAIALLGN
   msa134470.2{391_CJB110}  MKGIQKTELK QQITHISKVV DLENQLDKFV SGYSGGMKRR LSLAIALLGN
     msa134470.2{391_COH1}  MKGIQKTELK QQITHISKVV DLENQLDKFV SGYSGGMKRR LSLAIALLGN
     msa134470.2{391_M732}  MKGIQKTELK QQITHISKVV DLENQLDKFV SGYSGGMKRR LSLAIALLGN
     msa134470.2{391_M781}  MKGIQKTELK QQITHISKVV DLENQLDKFV SGYSGGMKRR LSLAIALLGN
   msa134470.2{391_18RS21}  MKGIQKTELK QQITHISKVV DLENQLDKFV SGYSGGMKRR LSLAIALLGN
     msa134470.2{391_2603}  MKGIQKTELK QQITHISKVV DLENQLDKFV SGYSGGMKRR LSLAIALLGN
     msa134470.2{391_H36B}  MKGIQKTELK QQITHISKVV DLENQLDKFV SGYSGGMKRR LSLAIALLGN
msa134470.2{391_JM9130013}  MKGIQKTELK QQITHISKVV DLENQLDKFV SGYSGGMKRR LSLAIALLGN
     msa134470.2{391_A909}  MKGIQKTELK QQITHISKVV DLENQLDKFV SGYSGGMKRR LSLAIALLGN
                 Consensus  ********** ********** ********** ********** **********

                            151                                                200
      msa134470.2{391_090}  PTVLILDEPT VGIDPSLRRK IWQELINIKD EGrSIFITTH VMDEAELTSK
   msa134470.2{391_1169NT}  PTVLILDEPT VGIDPSLRRK IWQELINIKD EGrSIFITTH VMDEAELTSK
   msa134470.2{391_CJB110}  PTVLILDEPT VGIDPSLRRK IWQELINIKD EGrSIFITTH VMDEAELTSK
     msa134470.2{391_COH1}  PTVLILDEPT VGIDPSLRRK IWQELINIKD EGrSIFITTH VMDEAELTSK
     msa134470.2{391_M732}  PTVLILDEPT VGIDPSLRRK IWQELINIKD EGrSIFITTH VMDEAELTSK
     msa134470.2{391_M781}  PTVLILDEPT VGIDPSLRRK IWQELINIKD EGrSIFITTH VMDEAELTSK
   msa134470.2{391_18RS21}  PTVLILDEPT VGIDPSLRRK IWQELINIKD EGhSIFITTH VMDEAELTSK
     msa134470.2{391_2603}  PTVLILDEPT VGIDPSLRRK IWQELINIKD EGhSIFITTH VMDEAELTSK
     msa134470.2{391_H36B}  PTVLILDEPT VGIDPSLRRK IWQELINIKD EGrSIFITTH VMDEAELTSK
msa134470.2{391_JM9130013}  PTVLILDEPT VGIDPSLRRK IWQELINIKD EGrSIFITTH VMDEAELTSK
     msa134470.2{391_A909}  PTVLILDEPT VGIDPSLRRK IWQELINIKD EGrSIFITTH VMDEAELTSK
                 Consensus  ********** ********** ********** **_******* **********

                            201                   224
      msa134470.2{391_090}  VALLLRGNII AFDTPLHLKK QFNV
   msa134470.2{391_1169NT}  VALLLRGNII AFDTPLHLKK QFNV
   msa134470.2{391_CJB110}  VALLLRGNII AFDTPLHLKK QFNV
     msa134470.2{391_COH1}  VALLLRGNII AFDTPLHLKK QFNV
     msa134470.2{391_M732}  VALLLRGNII AFDTPLHLKK QFNV
     msa134470.2{391_M781}  VALLLRGNII AFDTPLHLKK QFNV
   msa134470.2{391_18RS21}  VALLLRGNII AFDTPLHLKK QFNV
     msa134470.2{391_2603}  VALLLRGNII AFDTPLHLKK QFNV
     msa134470.2{391_H36B}  VALLLRGNII AFDTPLHLKK QFNV
msa134470.2{391_JM9130013}  VALLLRGNII AFDTPLHLKK QFNV
     msa134470.2{391_A909}  VALLLRGNII AFDTPLHLKK QFNV
                 Consensus  ********** ********** ****
```

Table 77: Comparative Sequences relating toSAG2059

SEQ ID NO. 7701
STRAIN 2603
TTGCCTATGTTGTCTGTTGGTTTAGTTTTAGAGGGTGGCGGAATGAGAGGTCTTTATACT
GCTGGAGTTTTAGATGCTTTTCTAGATGCAGGAATAAAAATAGATGGTATCGTATCTGTC
TCTGCTGGTGCATTGTTTGGTGTTAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGA
TACAATAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGGTTTCGAACA
GGGAATTTTGTTAATAAAGATTTCACCTATTATGAAGTTCCTATGAAATTGGATGTATTT
GACGATGAAGCATTTAAAAAATCAAGTATTGATTTTTACGTAGTTGCTACAGAGATGACA
TCTGGTAAACCTGAATATTTTAAAATTGATAGTGTTTTTGAACAAATGGAAATTTTACGT
GCTAGTTCAGCATTACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTA
GATGGTGGTTTATCTGATAGTATTCCCGTTGATTTTGCCCGTGGTTTAGGATTTGACAAG
TTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGCCTTCAAGTGGACGATTG
TATAAAACTCTGTATAGGAAATATCCTAATTTTGTAAAGACAGCCTCGAATCGGTACCAA
CAGTATAATAATAGTCTTGAAAAGGTCATGAGCCTTGAAAAAACAGGCGATCTATTTGCA
ATTAGACCGAGTAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGAT
AGTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCTGAATAGTTAT
CTAATGAAA

SEQ ID NO. 7702
STRAIN 090
CCTATGTTGTCTGTTGGTTTAGTTTTAG
AGGGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTTT
CTAGATGCAGGAATAAAAATAGATGGTATCGTATCTGTCTCTGCTGGTGC
ATTGTTTGGTGTTAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGAT
ACAATAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGG
TTTCGAACAGGGAATTTTGTTAATAAAGATTTCACCTATTATGAAGTTCC
TATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTG
ATTTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTT
AAAATTGATAGTGTTTTTGAACAAATGGAAATTTTACGTGCTAGTTCAGC
ATTACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAG
ATGGTGGTTTATCTGATAGTATTCCCGTTGATTTTGCCCGTGGTTTAGGA
TTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAA
GCCTTCAAGTGGACGATTGTATAAAACTCTGTATAGGAAATATCCTAATT
TTGTAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAA
AAGGTCATGAGCCTTGAAAAAACAGGCGATCTATTTGCAATTAGACCGAG
TAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATA
GTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCTG
AATAGTTATCTAATGAAA

SEQ ID NO. 7703
STRAIN A909
CCTATGTTGTCTGTTGGTTTAGTTTTAGAG
GGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTTTCT
AGATGCAGGAATAAAAGTAGATGGTATCATATCTGTCTCTGCTGGTGCAT
TGTTTGGTGTTAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATAC
AATAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGGCT
TCGAACAGGGAATTTTGTTAATAAAGATTTCACCTATTATGAAGTTCCTA
TGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGAT
TTTTACGCAGTTGCTACAGAGATGACATCTGGTAAACCTGAGTATTTTAA
AATTGATAGTGTTTTTGAACAAATGGAAATTTTACGTGCTAGTTCAGCAT
TACCAGTAGTCTCAAAGATGGTTGTTTGGCAGGGGAAAAAGTACTTAGAT
GGTGGTTTATCTGATAGTATTCCCGTTGATTTTGCCCGTGGTTTAGGATT
TGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGC
CTTCAAGTGGACGATTGTATAAAACTCTGTATAGGAAATATCCTAATTTT
GTAAAGACAGCCTCGAACCGGTACCAACAGTATAATAATAGCCTTGAAAA
GGTCATGAGCCTTGAAAAAACAGGCGATCTATTTGCAATTAGACCAAGTA
AGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAGT
ATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGGGATGCCTGAGCTGAA
TAGTTATCTAATGAAA

SEQ ID NO. 7704
STRAIN H36B
CCTATGTTGTCTGTTGGTTTAGTTTTAG
AGGGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTTT
CTAGATGCAGGAATAAAAGTAGATGGTATCATATCTGTCTCTGCTGGTGC
ATTGTTTGGTGTTAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGAT
ACAATAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGG
CTTCGAACAGGGAATTTTGTTAATAAAGATTTCACCTATTATGAAGTTCC
TATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTG
ATTTTTACGCAGTTGCTACAGAGATGACATCTGGTAAACCTGAGTATTTT
AAAATTGATAGTGTTTTTGAACAAATGGAAATTTTACGTGCTAGTTCAGC
ATTACCAGTAGTCTCAAAGATGGTTGTTTGGCAGGGGAAAAAGTACTTAG
ATGGTGGTTTATCTGATAGTATTCCCGTTGATTTTGCCCGTGGTTTAGGA
TTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAA
GCCTTCAAGTGGACGATTGTATAAAACTCTGTATAGGAAATATCCTAATT
TTGTAAAGACAGCCTCGAACCGGTACCAACAGTATAATAATAGCCTTGAA
AAGGTCATGAGCCTTGAAAAAACAGGCGATCTATTTGCAATTAGACCAAG
TAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATA
GTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGGGATGCCTGAGCTG
AATAGTTATCTAATGAAA

SEQ ID NO. 7705

Table 77: Comparative Sequences relating toSAG2059

STRAIN 18RS21
CCTATGTTGTCTGTTGGTTTAGTTTTAGAGG
GTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTTTCTA
GATGCAGGAATAAAAATAGATGGTATCGTATCTGTCTCTGCTGGTGCATT
GTTTGGTGTTAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATACA
ATAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGGTTT
CGAACAGGGAATTTTGTTAATAAAGATTTCACCTATTATGAAGTTCCTAT
GAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGATT
TTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTTAAA
ATTGATAGTGTTTTTGAACAAATGGAAATTTTACGTGCTAGTTCAGCATT
ACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAGATG
GTGGTTTATCTGATAGTATTCCCGTTGATTTTGCCCGTGGTTTAGGATTT
GACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGCC
TTCAAGTGGACGATTGTATAAAACTCTGTATAGGAAATATCCTAATTTTG
TAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAAAAG
GTCATGAGCCTTGAAAAAACAGGCGATCTATTTGCAATTAGACCGAGTAA
GAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAGTA
TTTATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCTGAAT
AGTTATCTAATGAAA

SEQ ID NO. 7706
STRAIN M732
CCTATGTTGTCTGTTGGTTTAGTTTTAGA
GGGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTTTC
TAGATGCAGGAATAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTGCA
TTGTTTGGTGTTAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATA
CAATAAAAAGTATTTATCCCACCCTGAATATATGAGTCTAAGATCATGGC
TTCGAACAGGGAATTTTGTTAATAAAGATTTCACCTATTATGAAGTTCCT
ATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGA
TTTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTTA
AAATTGATAGTGTTTTTGAACAAATGGAAATTTTACGTGCTAGTTCAGCA
TTACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAGA
TGGTGGTTTATCTGATAGTATTCCCGTTGATTTTGCCCGTGGTTTAGGAT
TTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAG
CCTTCAAGTGGACGATTGTATAAAACTCTGTATAGGAAATATCCTAATTT
TGTAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAAA
AGGTCATGAGCCTTGAAAAAACAGGCGATCTATTTGCAATTAGACCGAGT
AAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAG
TATTTATCAGCTTGGTATGAAATATGCTAAAAGTGTGATGCCTGAGCTGA
ATAGTTATCTAATGAAA

SEQ ID NO. 7707
STRAIN COH1
CCTATGTTGTCTGTTGGTTTAGTTTTA
GAGGGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTT
TCTAGATGCAGGAATAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTG
CATTGTTTGGTGTTAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGA
TACAATAAAAAGTATTTATCCCACCCTGAATATATGAGTCTAAGATCATG
GCTTCGAACAGGGAATTTTGTTAATAAAGATTTCACCTATTATGAAGTTC
CTATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATT
GATTTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTT
TAAAATTGATAGTGTTTTTGAACAAATGGAAATTTTACGTGCTAGTTCAG
CATTACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTA
GATGGTGGTTTATCTGATAGTATTCCCGTTGATTTTGCCCGTGGTTTAGG
ATTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAA
AGCCTTCAAGTGGACGATTGTATAAAACTCTGTATAGGAAATATCCTAAT
TTTGTAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGA
AAAGGTCATGAGCCTTGAAAAAACAGGCGATCTATTTGCAATTAGACCGA
GTAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGAT
AGTATTTATCAGCTTGGTATGAAATATGCTAAAAGTGTGATGCCTGAGCT
GAATAGTTATCTAATGAAA

SEQ ID NO. 7708
STRAIN M781
CCTATGTTGTCTGTTGGTTTAGTTTTAG
AGGGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTTT
CTAGATGCAGGAATAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTGC
ATTGTTTGGTGTTAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGAT
ACAATAAAAAGTATTTATCCCACCCTGAATATATGAGTCTAAGATCATGG
CTTCGAACAGGGAATTTTGTTAATAAAGATTTCACCTATTATGAAGTTCC
TATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTG
ATTTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTT
AAAATTGATAGTGTTTTTGAACAAATGGAAATTTTACGTGCTAGTTCAGC
ATTACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAG
ATGGTGGTTTATCTGATAGTATTCCCGTTGATTTTGCCCGTGGTTTAGGA
TTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAA
GCCTTCAAGTGGACGATTGTATAAAACTCTGTATAGGAAATATCCTAATT
TTGTAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAA
AAGGTCATGAGCCTTGAAAAAACAGGCGATCTATTTGCAATTAGACCGAG
TAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATA
GTATTTATCAGCTTGGTATGAAATATGCTAAAAGTGTGATGCCTGAGCTG
AATAGTTATCTAATGAAA

Table 77: Comparative Sequences relating toSAG2059

SEQ ID NO. 7709
STRAIN CJB110
CCTATGTTGTCTGTTGGTTTAGTTTTA
GAGGGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTT
TCTAGATGCAGGAATAAAAATAGATGGTATCGTATCTGTCTCTGCTGGTG
CATTGTTTGGTGTTAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGA
TACAATAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATG
GTTTCGAACAGGGAATTTTGTTAATAAAGATTTCACCTATTATGAAGTTC
CTATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATT
GATTTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTT
TAAAATTGATAGTGTTTTTGAACAAATGGAAATTTTACGTGCTAGTTCAG
CATTACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTA
GATGGTGGTTTATCTGATAGTATTCCCGTTGATTTTGCCCGTGGTTTAGG
ATTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAA
AGCCTTCAAGTGGACGATTGTATAAAACTCTGTATAGGAAATATCCTAAT
TTTGTAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGA
AAAGGTCATGAGCCTTGAAAAAACAGGCGATCTATTTGCAATTAGACCGA
GTAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGAT
AGTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCT
GAATAGTTATCTAATGAAA

SEQ ID NO. 7710
STRAIN 1169NT
CCTATGTTGTCTGTTGGTTTAGTTTTAGAGGGTG
GCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTTTCTAGAT
GCAGGAATAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTGCATTGTT
TGGTGTTAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATACAATA
AAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGATCATGGCTTCGA
ACAGGGAATTTTGTTAATAAAGATTTCACCTATTATGAAGTTCCTATGAA
ATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGATTTTT
ACGCAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTTAAAATT
GATAGTGTCTTTGAACAAATGGAAATTTTACGTGCTAGTTCAGCATTACC
AGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAGATGGTG
GTTTATCTGATAGTATCCCCGTTGATTTTGCCCGTGGTTTAGGATTTGAC
AAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGCCTTC
AAGTGGACGATTGTATAAAACTCTGTATAGGAAATATCCTAATTTTGTAA
AGACAGCCTCGAATCGGTACCAACAGTATAATAATAGCCTTGAAAAGGTC
ATGAGCCTTGAAAAAACAGGCGATCTATTTGCAATTAGGCCGAGTAAAAG
CTTGGTTATTGTCCGCTTAGAGAAGAATCCGGATAAACTTGATAGTATTT
ATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCTGAATAGT
TATCTAATGAAA

SEQ ID NO. 7711
STRAIN JM9130013
CCTATGTTGTCTGTTGGTTTAGTTTTAGAG
GGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTTTCT
AGATGCAGGAATAAAAGTAGATGGTATCATATCTGTCTCTGCTGGTGCAT
TGTTTGGTGTTAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATAC
AATAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGGCT
TCGAACAGGGAATTTTGTTAATAAAGATTTCACCTATTATGAAGTTCCTA
TGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGAT
TTTTACGCAGTTGCTACAGAGATGACATCTGGTAAACCTGAGTATTTTAA
AATTGATAGTGTTTTTGAACAAATGGAAATTTTACGTGCTAGTTCAGCAT
TACCAGTAGTCTCAAAGATGGTTGTTTGGCAGGGGAAAAAGTACTTAGAT
GGTGGTTTATCTGATAGTATTCCCGTTGATTTTGCCCGTGGTTTAGGATT
TGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGC
CTTCAAGTGGACGATTGTATAAAACTCTGTATAGGAAATATCCTAATTTT
GTAAAGACAGCCTCGAACCGGTACCAACAGTATAATAATAGCCTTGAAAA
GGTCATGAGCCTTGAAAAAACAGGCGATCTATTTGCAATTAGACCAAGTA
AGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAGT
ATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGGGATGCCTGAGCTGAA
TAGTTATCTAATGAAA

```
PRETTY of: /biotmp/msa47199.2{*}   February 19, 2003 05:51  ..

                           1                                                 50
      msa47199.2{394_A909}  ~~~CCTATGT TGTCTGTTGG TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
      msa47199.2{394_H36B}  ~~~CCTATGT TGTCTGTTGG TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
  msa47199.2{394_JM9130013}  ~~~CCTATGT TGTCTGTTGG TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
       msa47199.2{394_090}  ~~~CCTATGT TGTCTGTTGG TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
     msa47199.2{394_18RS21}  ~~~CCTATGT TGTCTGTTGG TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
      msa47199.2{394_2603}  ttgCCTATGT TGTCTGTTGG TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
     msa47199.2{394_CJB110}  ~~~CCTATGT TGTCTGTTGG TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
      msa47199.2{394_COH1}  ~~~CCTATGT TGTCTGTTGG TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
      msa47199.2{394_M732}  ~~~CCTATGT TGTCTGTTGG TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
      msa47199.2{394_M781}  ~~~CCTATGT TGTCTGTTGG TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
     msa47199.2{394_1169NT}  ~~~CCTATGT TGTCTGTTGG TTTAGTTTTA GAGGGTGGCG GAATGAGAGG
                Consensus  ********** ********** ********** ********** **********

                           51                                               100
      msa47199.2{394_A909}  TCTTTATACT GCTGGAGTTT TAGATGCTTT TCTAGATGCA GGAATAAAAg
      msa47199.2{394_H36B}  TCTTTATACT GCTGGAGTTT TAGATGCTTT TCTAGATGCA GGAATAAAAg
  msa47199.2{394_JM9130013}  TCTTTATACT GCTGGAGTTT TAGATGCTTT TCTAGATGCA GGAATAAAAg
```

Table 77: Comparative Sequences relating toSAG2059

```
       msa47199.2{394_090}  TCTTTATACT GCTGGAGTTT TAGATGCTTT TCTAGATGCA GGAATAAAAa
     msa47199.2{394_18RS21}  TCTTTATACT GCTGGAGTTT TAGATGCTTT TCTAGATGCA GGAATAAAAa
      msa47199.2{394_2603}  TCTTTATACT GCTGGAGTTT TAGATGCTTT TCTAGATGCA GGAATAAAAa
     msa47199.2{394_CJB110}  TCTTTATACT GCTGGAGTTT TAGATGCTTT TCTAGATGCA GGAATAAAAa
      msa47199.2{394_COH1}  TCTTTATACT GCTGGAGTTT TAGATGCTTT TCTAGATGCA GGAATAAAAa
      msa47199.2{394_M732}  TCTTTATACT GCTGGAGTTT TAGATGCTTT TCTAGATGCA GGAATAAAAa
      msa47199.2{394_M781}  TCTTTATACT GCTGGAGTTT TAGATGCTTT TCTAGATGCA GGAATAAAAa
     msa47199.2{394_1169NT}  TCTTTATACT GCTGGAGTTT TAGATGCTTT TCTAGATGCA GGAATAAAAa
               Consensus  ********** ********** ********** ********** *********_

                          101                                                150
      msa47199.2{394_A909}  TAGATGGTAT CaTATCTGTC TCTGCtGGTG CATTGTTTGG TGTTAATTTT
      msa47199.2{394_H36B}  TAGATGGTAT CaTATCTGTC TCTGCtGGTG CATTGTTTGG TGTTAATTTT
  msa47199.2{394_JM9130013}  TAGATGGTAT CaTATCTGTC TCTGCtGGTG CATTGTTTGG TGTTAATTTT
       msa47199.2{394_090}  TAGATGGTAT CgTATCTGTC TCTGCtGGTG CATTGTTTGG TGTTAATTTT
     msa47199.2{394_18RS21}  TAGATGGTAT CgTATCTGTC TCTGCtGGTG CATTGTTTGG TGTTAATTTT
      msa47199.2{394_2603}  TAGATGGTAT CgTATCTGTC TCTGCtGGTG CATTGTTTGG TGTTAATTTT
     msa47199.2{394_CJB110}  TAGATGGTAT CgTATCTGTC TCTGCtGGTG CATTGTTTGG TGTTAATTTT
      msa47199.2{394_COH1}  TAGATGGTAT CgTATCTGTC TCTGCgGGTG CATTGTTTGG TGTTAATTTT
      msa47199.2{394_M732}  TAGATGGTAT CgTATCTGTC TCTGCgGGTG CATTGTTTGG TGTTAATTTT
      msa47199.2{394_M781}  TAGATGGTAT CgTATCTGTC TCTGCgGGTG CATTGTTTGG TGTTAATTTT
     msa47199.2{394_1169NT}  TAGATGGTAT CgTATCTGTC TCTGCgGGTG CATTGTTTGG TGTTAATTTT
               Consensus  ********** *_******** *****_**** ********** **********

                          151                                                200
      msa47199.2{394_A909}  GTATCTAGAC AACGAGAGAG GGCTTTGCGA TACAATAAAA AGTATTTATC
      msa47199.2{394_H36B}  GTATCTAGAC AACGAGAGAG GGCTTTGCGA TACAATAAAA AGTATTTATC
  msa47199.2{394_JM9130013}  GTATCTAGAC AACGAGAGAG GGCTTTGCGA TACAATAAAA AGTATTTATC
       msa47199.2{394_090}  GTATCTAGAC AACGAGAGAG GGCTTTGCGA TACAATAAAA AGTATTTATC
     msa47199.2{394_18RS21}  GTATCTAGAC AACGAGAGAG GGCTTTGCGA TACAATAAAA AGTATTTATC
      msa47199.2{394_2603}  GTATCTAGAC AACGAGAGAG GGCTTTGCGA TACAATAAAA AGTATTTATC
     msa47199.2{394_CJB110}  GTATCTAGAC AACGAGAGAG GGCTTTGCGA TACAATAAAA AGTATTTATC
      msa47199.2{394_COH1}  GTATCTAGAC AACGAGAGAG GGCTTTGCGA TACAATAAAA AGTATTTATC
      msa47199.2{394_M732}  GTATCTAGAC AACGAGAGAG GGCTTTGCGA TACAATAAAA AGTATTTATC
      msa47199.2{394_M781}  GTATCTAGAC AACGAGAGAG GGCTTTGCGA TACAATAAAA AGTATTTATC
     msa47199.2{394_1169NT}  GTATCTAGAC AACGAGAGAG GGCTTTGCGA TACAATAAAA AGTATTTATC
               Consensus  ********** ********** ********** ********** **********

                          201                                                250
      msa47199.2{394_A909}  CCACCCTaAA TATATGAGTC TAAGgTCATG GcTTCGAACA GGGAATTTTG
      msa47199.2{394_H36B}  CCACCCTaAA TATATGAGTC TAAGgTCATG GcTTCGAACA GGGAATTTTG
  msa47199.2{394_JM9130013}  CCACCCTaAA TATATGAGTC TAAGgTCATG GcTTCGAACA GGGAATTTTG
       msa47199.2{394_090}  CCACCCTaAA TATATGAGTC TAAGgTCATG GtTTCGAACA GGGAATTTTG
     msa47199.2{394_18RS21}  CCACCCTaAA TATATGAGTC TAAGgTCATG GtTTCGAACA GGGAATTTTG
      msa47199.2{394_2603}  CCACCCTaAA TATATGAGTC TAAGgTCATG GtTTCGAACA GGGAATTTTG
     msa47199.2{394_CJB110}  CCACCCTaAA TATATGAGTC TAAGgTCATG GtTTCGAACA GGGAATTTTG
      msa47199.2{394_COH1}  CCACCCTgAA TATATGAGTC TAAGaTCATG GcTTCGAACA GGGAATTTTG
      msa47199.2{394_M732}  CCACCCTgAA TATATGAGTC TAAGaTCATG GcTTCGAACA GGGAATTTTG
      msa47199.2{394_M781}  CCACCCTgAA TATATGAGTC TAAGaTCATG GcTTCGAACA GGGAATTTTG
     msa47199.2{394_1169NT}  CCACCCTaAA TATATGAGTC TAAGaTCATG GcTTCGAACA GGGAATTTTG
               Consensus  *******_** ********** ****_***** *_******** **********

                          251                                                300
      msa47199.2{394_A909}  TTAATAAAGA TTTCACCTAT TATGAAGTTC CTATGAAATT GGATGTATTT
      msa47199.2{394_H36B}  TTAATAAAGA TTTCACCTAT TATGAAGTTC CTATGAAATT GGATGTATTT
  msa47199.2{394_JM9130013}  TTAATAAAGA TTTCACCTAT TATGAAGTTC CTATGAAATT GGATGTATTT
       msa47199.2{394_090}  TTAATAAAGA TTTCACCTAT TATGAAGTTC CTATGAAATT GGATGTATTT
     msa47199.2{394_18RS21}  TTAATAAAGA TTTCACCTAT TATGAAGTTC CTATGAAATT GGATGTATTT
      msa47199.2{394_2603}  TTAATAAAGA TTTCACCTAT TATGAAGTTC CTATGAAATT GGATGTATTT
     msa47199.2{394_CJB110}  TTAATAAAGA TTTCACCTAT TATGAAGTTC CTATGAAATT GGATGTATTT
      msa47199.2{394_COH1}  TTAATAAAGA TTTCACCTAT TATGAAGTTC CTATGAAATT GGATGTATTT
      msa47199.2{394_M732}  TTAATAAAGA TTTCACCTAT TATGAAGTTC CTATGAAATT GGATGTATTT
      msa47199.2{394_M781}  TTAATAAAGA TTTCACCTAT TATGAAGTTC CTATGAAATT GGATGTATTT
     msa47199.2{394_1169NT}  TTAATAAAGA TTTCACCTAT TATGAAGTTC CTATGAAATT GGATGTATTT
               Consensus  ********** ********** ********** ********** **********

                          301                                                350
      msa47199.2{394_A909}  GACGATGAAG CATTTAAAAA ATCAAGTATT GATTTTTACG cAGTTGCTAC
      msa47199.2{394_H36B}  GACGATGAAG CATTTAAAAA ATCAAGTATT GATTTTTACG cAGTTGCTAC
  msa47199.2{394_JM9130013}  GACGATGAAG CATTTAAAAA ATCAAGTATT GATTTTTACG cAGTTGCTAC
       msa47199.2{394_090}  GACGATGAAG CATTTAAAAA ATCAAGTATT GATTTTTACG tAGTTGCTAC
     msa47199.2{394_18RS21}  GACGATGAAG CATTTAAAAA ATCAAGTATT GATTTTTACG tAGTTGCTAC
      msa47199.2{394_2603}  GACGATGAAG CATTTAAAAA ATCAAGTATT GATTTTTACG tAGTTGCTAC
     msa47199.2{394_CJB110}  GACGATGAAG CATTTAAAAA ATCAAGTATT GATTTTTACG tAGTTGCTAC
      msa47199.2{394_COH1}  GACGATGAAG CATTTAAAAA ATCAAGTATT GATTTTTACG tAGTTGCTAC
      msa47199.2{394_M732}  GACGATGAAG CATTTAAAAA ATCAAGTATT GATTTTTACG tAGTTGCTAC
      msa47199.2{394_M781}  GACGATGAAG CATTTAAAAA ATCAAGTATT GATTTTTACG tAGTTGCTAC
     msa47199.2{394_1169NT}  GACGATGAAG CATTTAAAAA ATCAAGTATT GATTTTTACG cAGTTGCTAC
               Consensus  ********** ********** ********** ********** _*********

                          351                                                400
      msa47199.2{394_A909}  AGAGATGACA TCTGGTAAAC CTGAgTATTT TAAAATTGAT AGTGTtTTTG
      msa47199.2{394_H36B}  AGAGATGACA TCTGGTAAAC CTGAgTATTT TAAAATTGAT AGTGTtTTTG
```

Table 77: Comparative Sequences relating toSAG2059

```
msa47199.2{394_JM9130013}  AGAGATGACA TCTGGTAAAC CTGAgTATTT TAAAATTGAT AGTGTtTTTG
      msa47199.2{394_090}  AGAGATGACA TCTGGTAAAC CTGAaTATTT TAAAATTGAT AGTGTtTTTG
    msa47199.2{394_18RS21}  AGAGATGACA TCTGGTAAAC CTGAaTATTT TAAAATTGAT AGTGTtTTTG
     msa47199.2{394_2603}  AGAGATGACA TCTGGTAAAC CTGAaTATTT TAAAATTGAT AGTGTtTTTG
   msa47199.2{394_CJB110}  AGAGATGACA TCTGGTAAAC CTGAaTATTT TAAAATTGAT AGTGTtTTTG
     msa47199.2{394_COH1}  AGAGATGACA TCTGGTAAAC CTGAaTATTT TAAAATTGAT AGTGTtTTTG
     msa47199.2{394_M732}  AGAGATGACA TCTGGTAAAC CTGAaTATTT TAAAATTGAT AGTGTtTTTG
     msa47199.2{394_M781}  AGAGATGACA TCTGGTAAAC CTGAaTATTT TAAAATTGAT AGTGTtTTTG
   msa47199.2{394_1169NT}  AGAGATGACA TCTGGTAAAC CTGAaTATTT TAAAATTGAT AGTGTcTTTG
                Consensus  ********** ********** ****_***** ********** *****_****

                           401                                               450
     msa47199.2{394_A909}  AACAAATGGA AATTTTACGT GCTAGTTCAG CATTACCAGT AGTCTCAAAG
     msa47199.2{394_H36B}  AACAAATGGA AATTTTACGT GCTAGTTCAG CATTACCAGT AGTCTCAAAG
msa47199.2{394_JM9130013}  AACAAATGGA AATTTTACGT GCTAGTTCAG CATTACCAGT AGTCTCAAAG
      msa47199.2{394_090}  AACAAATGGA AATTTTACGT GCTAGTTCAG CATTACCAGT AGTCTCAAAG
   msa47199.2{394_18RS21}  AACAAATGGA AATTTTACGT GCTAGTTCAG CATTACCAGT AGTCTCAAAG
     msa47199.2{394_2603}  AACAAATGGA AATTTTACGT GCTAGTTCAG CATTACCAGT AGTCTCAAAG
   msa47199.2{394_CJB110}  AACAAATGGA AATTTTACGT GCTAGTTCAG CATTACCAGT AGTCTCAAAG
     msa47199.2{394_COH1}  AACAAATGGA AATTTTACGT GCTAGTTCAG CATTACCAGT AGTCTCAAAG
     msa47199.2{394_M732}  AACAAATGGA AATTTTACGT GCTAGTTCAG CATTACCAGT AGTCTCAAAG
     msa47199.2{394_M781}  AACAAATGGA AATTTTACGT GCTAGTTCAG CATTACCAGT AGTCTCAAAG
   msa47199.2{394_1169NT}  AACAAATGGA AATTTTACGT GCTAGTTCAG CATTACCAGT AGTCTCAAAG
                Consensus  ********** ********** ********** ********** **********

                           451                                               500
     msa47199.2{394_A909}  ATGGTTGtTT GGCAGGGGAA AAAGTACTTA GATGGTGGTT TATCTGATAG
     msa47199.2{394_H36B}  ATGGTTGtTT GGCAGGGGAA AAAGTACTTA GATGGTGGTT TATCTGATAG
msa47199.2{394_JM9130013}  ATGGTTGtTT GGCAGGGGAA AAAGTACTTA GATGGTGGTT TATCTGATAG
      msa47199.2{394_090}  ATGGTTGaTT GGCAGGGGAA AAAGTACTTA GATGGTGGTT TATCTGATAG
   msa47199.2{394_18RS21}  ATGGTTGaTT GGCAGGGGAA AAAGTACTTA GATGGTGGTT TATCTGATAG
     msa47199.2{394_2603}  ATGGTTGaTT GGCAGGGGAA AAAGTACTTA GATGGTGGTT TATCTGATAG
   msa47199.2{394_CJB110}  ATGGTTGaTT GGCAGGGGAA AAAGTACTTA GATGGTGGTT TATCTGATAG
     msa47199.2{394_COH1}  ATGGTTGaTT GGCAGGGGAA AAAGTACTTA GATGGTGGTT TATCTGATAG
     msa47199.2{394_M732}  ATGGTTGaTT GGCAGGGGAA AAAGTACTTA GATGGTGGTT TATCTGATAG
     msa47199.2{394_M781}  ATGGTTGaTT GGCAGGGGAA AAAGTACTTA GATGGTGGTT TATCTGATAG
   msa47199.2{394_1169NT}  ATGGTTGaTT GGCAGGGGAA AAAGTACTTA GATGGTGGTT TATCTGATAG
                Consensus  *******_** ********** ********** ********** **********

                           501                                               550
     msa47199.2{394_A909}  TATtCCCGTT GATTTTGCCC GTGGTTTAGG ATTTGACAAG TTGATTGTTG
     msa47199.2{394_H36B}  TATtCCCGTT GATTTTGCCC GTGGTTTAGG ATTTGACAAG TTGATTGTTG
msa47199.2{394_JM9130013}  TATtCCCGTT GATTTTGCCC GTGGTTTAGG ATTTGACAAG TTGATTGTTG
      msa47199.2{394_090}  TATtCCCGTT GATTTTGCCC GTGGTTTAGG ATTTGACAAG TTGATTGTTG
   msa47199.2{394_18RS21}  TATtCCCGTT GATTTTGCCC GTGGTTTAGG ATTTGACAAG TTGATTGTTG
     msa47199.2{394_2603}  TATtCCCGTT GATTTTGCCC GTGGTTTAGG ATTTGACAAG TTGATTGTTG
   msa47199.2{394_CJB110}  TATtCCCGTT GATTTTGCCC GTGGTTTAGG ATTTGACAAG TTGATTGTTG
     msa47199.2{394_COH1}  TATtCCCGTT GATTTTGCCC GTGGTTTAGG ATTTGACAAG TTGATTGTTG
     msa47199.2{394_M732}  TATtCCCGTT GATTTTGCCC GTGGTTTAGG ATTTGACAAG TTGATTGTTG
     msa47199.2{394_M781}  TATtCCCGTT GATTTTGCCC GTGGTTTAGG ATTTGACAAG TTGATTGTTG
   msa47199.2{394_1169NT}  TATcCCCGTT GATTTTGCCC GTGGTTTAGG ATTTGACAAG TTGATTGTTG
                Consensus  ***_****** ********** ********** ********** **********

                           551                                               600
     msa47199.2{394_A909}  TGATGACTAG GCCGCTCAAT TATCAGAAAA AGCCTTCAAG TGGACGATTG
     msa47199.2{394_H36B}  TGATGACTAG GCCGCTCAAT TATCAGAAAA AGCCTTCAAG TGGACGATTG
msa47199.2{394_JM9130013}  TGATGACTAG GCCGCTCAAT TATCAGAAAA AGCCTTCAAG TGGACGATTG
      msa47199.2{394_090}  TGATGACTAG GCCGCTCAAT TATCAGAAAA AGCCTTCAAG TGGACGATTG
   msa47199.2{394_18RS21}  TGATGACTAG GCCGCTCAAT TATCAGAAAA AGCCTTCAAG TGGACGATTG
     msa47199.2{394_2603}  TGATGACTAG GCCGCTCAAT TATCAGAAAA AGCCTTCAAG TGGACGATTG
   msa47199.2{394_CJB110}  TGATGACTAG GCCGCTCAAT TATCAGAAAA AGCCTTCAAG TGGACGATTG
     msa47199.2{394_COH1}  TGATGACTAG GCCGCTCAAT TATCAGAAAA AGCCTTCAAG TGGACGATTG
     msa47199.2{394_M732}  TGATGACTAG GCCGCTCAAT TATCAGAAAA AGCCTTCAAG TGGACGATTG
     msa47199.2{394_M781}  TGATGACTAG GCCGCTCAAT TATCAGAAAA AGCCTTCAAG TGGACGATTG
   msa47199.2{394_1169NT}  TGATGACTAG GCCGCTCAAT TATCAGAAAA AGCCTTCAAG TGGACGATTG
                Consensus  ********** ********** ********** ********** **********

                           601                                               650
     msa47199.2{394_A909}  TATAAAACTC TGTATAGGAA ATATCCTAAT TTTGTAAAGA CAGCCTCGAA
     msa47199.2{394_H36B}  TATAAAACTC TGTATAGGAA ATATCCTAAT TTTGTAAAGA CAGCCTCGAA
msa47199.2{394_JM9130013}  TATAAAACTC TGTATAGGAA ATATCCTAAT TTTGTAAAGA CAGCCTCGAA
      msa47199.2{394_090}  TATAAAACTC TGTATAGGAA ATATCCTAAT TTTGTAAAGA CAGCCTCGAA
   msa47199.2{394_18RS21}  TATAAAACTC TGTATAGGAA ATATCCTAAT TTTGTAAAGA CAGCCTCGAA
     msa47199.2{394_2603}  TATAAAACTC TGTATAGGAA ATATCCTAAT TTTGTAAAGA CAGCCTCGAA
   msa47199.2{394_CJB110}  TATAAAACTC TGTATAGGAA ATATCCTAAT TTTGTAAAGA CAGCCTCGAA
     msa47199.2{394_COH1}  TATAAAACTC TGTATAGGAA ATATCCTAAT TTTGTAAAGA CAGCCTCGAA
     msa47199.2{394_M732}  TATAAAACTC TGTATAGGAA ATATCCTAAT TTTGTAAAGA CAGCCTCGAA
     msa47199.2{394_M781}  TATAAAACTC TGTATAGGAA ATATCCTAAT TTTGTAAAGA CAGCCTCGAA
   msa47199.2{394_1169NT}  TATAAAACTC TGTATAGGAA ATATCCTAAT TTTGTAAAGA CAGCCTCGAA
                Consensus  ********** ********** ********** ********** **********

                           651                                               700
     msa47199.2{394_A909}  cCGGTACCAA CAGTATAATA ATAGcCTTGA AAAGGTCATG AGCCTTGAAA
```

Table 77: Comparative Sequences relating toSAG2059

```
     msa47199.2{394_H36B}  cCGGTACCAA CAGTATAATA ATAGcCTTGA AAAGGTCATG AGCCTTGAAA
msa47199.2{394_JM9130013}  cCGGTACCAA CAGTATAATA ATAGcCTTGA AAAGGTCATG AGCCTTGAAA
      msa47199.2{394_090}  tCGGTACCAA CAGTATAATA ATAGtCTTGA AAAGGTCATG AGCCTTGAAA
   msa47199.2{394_18RS21}  tCGGTACCAA CAGTATAATA ATAGtCTTGA AAAGGTCATG AGCCTTGAAA
     msa47199.2{394_2603}  tCGGTACCAA CAGTATAATA ATAGtCTTGA AAAGGTCATG AGCCTTGAAA
   msa47199.2{394_CJB110}  tCGGTACCAA CAGTATAATA ATAGtCTTGA AAAGGTCATG AGCCTTGAAA
     msa47199.2{394_COH1}  tCGGTACCAA CAGTATAATA ATAGtCTTGA AAAGGTCATG AGCCTTGAAA
     msa47199.2{394_M732}  tCGGTACCAA CAGTATAATA ATAGtCTTGA AAAGGTCATG AGCCTTGAAA
     msa47199.2{394_M781}  tCGGTACCAA CAGTATAATA ATAGtCTTGA AAAGGTCATG AGCCTTGAAA
   msa47199.2{394_1169NT}  tCGGTACCAA CAGTATAATA ATAGcCTTGA AAAGGTCATG AGCCTTGAAA
                Consensus  -********* ********** ****-***** ********** **********

                           701                                                750
     msa47199.2{394_A909}  AAACAGGCGA TCTATTTGCA ATTAGaCCaA GTAAgAGCTT GGTTATTGgC
     msa47199.2{394_H36B}  AAACAGGCGA TCTATTTGCA ATTAGaCCaA GTAAgAGCTT GGTTATTGgC
msa47199.2{394_JM9130013}  AAACAGGCGA TCTATTTGCA ATTAGaCCaA GTAAgAGCTT GGTTATTGgC
      msa47199.2{394_090}  AAACAGGCGA TCTATTTGCA ATTAGaCCgA GTAAgAGCTT GGTTATTGgC
   msa47199.2{394_18RS21}  AAACAGGCGA TCTATTTGCA ATTAGaCCgA GTAAgAGCTT GGTTATTGgC
     msa47199.2{394_2603}  AAACAGGCGA TCTATTTGCA ATTAGaCCgA GTAAgAGCTT GGTTATTGgC
   msa47199.2{394_CJB110}  AAACAGGCGA TCTATTTGCA ATTAGaCCgA GTAAgAGCTT GGTTATTGgC
     msa47199.2{394_COH1}  AAACAGGCGA TCTATTTGCA ATTAGaCCgA GTAAgAGCTT GGTTATTGgC
     msa47199.2{394_M732}  AAACAGGCGA TCTATTTGCA ATTAGaCCgA GTAAgAGCTT GGTTATTGgC
     msa47199.2{394_M781}  AAACAGGCGA TCTATTTGCA ATTAGaCCgA GTAAgAGCTT GGTTATTGgC
   msa47199.2{394_1169NT}  AAACAGGCGA TCTATTTGCA ATTAGgCCgA GTAAaAGCTT GGTTATTGtC
                Consensus  ********** ********** *****-**-* ****-***** ********-*

                           751                                                800
     msa47199.2{394_A909}  CGCTTAGAGA AGAATCCGGA TAAACTTGAT AGTATTTATC AGCTTGGTAT
     msa47199.2{394_H36B}  CGCTTAGAGA AGAATCCGGA TAAACTTGAT AGTATTTATC AGCTTGGTAT
msa47199.2{394_JM9130013}  CGCTTAGAGA AGAATCCGGA TAAACTTGAT AGTATTTATC AGCTTGGTAT
      msa47199.2{394_090}  CGCTTAGAGA AGAATCCGGA TAAACTTGAT AGTATTTATC AGCTTGGTAT
   msa47199.2{394_18RS21}  CGCTTAGAGA AGAATCCGGA TAAACTTGAT AGTATTTATC AGCTTGGTAT
     msa47199.2{394_2603}  CGCTTAGAGA AGAATCCGGA TAAACTTGAT AGTATTTATC AGCTTGGTAT
   msa47199.2{394_CJB110}  CGCTTAGAGA AGAATCCGGA TAAACTTGAT AGTATTTATC AGCTTGGTAT
     msa47199.2{394_COH1}  CGCTTAGAGA AGAATCCGGA TAAACTTGAT AGTATTTATC AGCTTGGTAT
     msa47199.2{394_M732}  CGCTTAGAGA AGAATCCGGA TAAACTTGAT AGTATTTATC AGCTTGGTAT
     msa47199.2{394_M781}  CGCTTAGAGA AGAATCCGGA TAAACTTGAT AGTATTTATC AGCTTGGTAT
   msa47199.2{394_1169NT}  CGCTTAGAGA AGAATCCGGA TAAACTTGAT AGTATTTATC AGCTTGGTAT
                Consensus  ********** ********** ********** ********** **********

                           801                                               849
     msa47199.2{394_A909}  GAAAgATGCT AAAAGTGgGA TGCCTGAGCT GAATAGTTAT CTAATGAAA
     msa47199.2{394_H36B}  GAAAgATGCT AAAAGTGgGA TGCCTGAGCT GAATAGTTAT CTAATGAAA
msa47199.2{394_JM9130013}  GAAAgATGCT AAAAGTGgGA TGCCTGAGCT GAATAGTTAT CTAATGAAA
      msa47199.2{394_090}  GAAAgATGCT AAAAGTGtGA TGCCTGAGCT GAATAGTTAT CTAATGAAA
   msa47199.2{394_18RS21}  GAAAgATGCT AAAAGTGtGA TGCCTGAGCT GAATAGTTAT CTAATGAAA
     msa47199.2{394_2603}  GAAAgATGCT AAAAGTGtGA TGCCTGAGCT GAATAGTTAT CTAATGAAA
   msa47199.2{394_CJB110}  GAAAgATGCT AAAAGTGtGA TGCCTGAGCT GAATAGTTAT CTAATGAAA
     msa47199.2{394_COH1}  GAAAtATGCT AAAAGTGtGA TGCCTGAGCT GAATAGTTAT CTAATGAAA
     msa47199.2{394_M732}  GAAAtATGCT AAAAGTGtGA TGCCTGAGCT GAATAGTTAT CTAATGAAA
     msa47199.2{394_M781}  GAAAtATGCT AAAAGTGtGA TGCCTGAGCT GAATAGTTAT CTAATGAAA
   msa47199.2{394_1169NT}  GAAAgATGCT AAAAGTGtGA TGCCTGAGCT GAATAGTTAT CTAATGAAA
                Consensus  ****-***** *******-** ********** ********** *********
```

SEQ ID NO. 7712
STRAIN 2603 frame: 1
PMLSVGLVLEGGGMRGLYTAGVLDAFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYLSHPKYMSLRSWFRTGNFVNKDFTYYEVPMKLDVFDDEAFKKSSIDFYVVATEMTS
GKPEYFKIDSVFEQMEILRASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVMSLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSVMPELNSYLMK

SEQ ID NO. 7713
STRAIN 090 frame: 1
PMLSVGLVLEGGGMRGLYTAGVLDAFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYLSHPKYMSLRSWFRTGNFVNKDFTYYEVPMKLDVFDDEAFKKSSIDFYVVATEMTS
GKPEYFKIDSVFEQMEILRASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVMSLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSVMPELNSYLMK

SEQ ID NO. 7714
STRAIN A909 frame: 1
PMLSVGLVLEGGGMRGLYTAGVLDAFLDAGIKVDGIISVSAGALFGVNFVSRQRERALRY
NKKYLSHPKYMSLRSWLRTGNFVNKDFTYYEVPMKLDVFDDEAFKKSSIDFYAVATEMTS
GKPEYFKIDSVFEQMEILRASSALPVVSKMVVWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVMSLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7715
STRAIN H36B frame: 1
PMLSVGLVLEGGGMRGLYTAGVLDAFLDAGIKVDGIISVSAGALFGVNFVSRQRERALRY
NKKYLSHPKYMSLRSWLRTGNFVNKDFTYYEVPMKLDVFDDEAFKKSSIDFYAVATEMTS

Table 77: Comparative Sequences relating toSAG2059

GKPEYFKIDSVFEQMEILRASSALPVVSKMVVWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVMSLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7716
STRAIN 18RS21 frame: 1
PMLSVGLVLEGGGMRGLYTAGVLDAFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYLSHPKYMSLRSWFRTGNFVNKDFTYYEVPMKLDVFDDEAFKKSSIDFYVVATEMTS
GKPEYFKIDSVFEQMEILRASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVMSLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSVMPELNSYLMK

SEQ ID NO. 7717
STRAIN M732 frame: 1
PMLSVGLVLEGGGMRGLYTAGVLDAFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYLSHPEYMSLRSWLRTGNFVNKDFTYYEVPMKLDVFDDEAFKKSSIDFYVVATEMTS
GKPEYFKIDSVFEQMEILRASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVMSLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKYAKSVMPELNSYLMK

SEQ ID NO. 7718
STRAIN COH1 frame: 1
PMLSVGLVLEGGGMRGLYTAGVLDAFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYLSHPEYMSLRSWLRTGNFVNKDFTYYEVPMKLDVFDDEAFKKSSIDFYVVATEMTS
GKPEYFKIDSVFEQMEILRASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVMSLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKYAKSVMPELNSYLMK

SEQ ID NO. 7719
STRAIN M781 frame: 1
PMLSVGLVLEGGGMRGLYTAGVLDAFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYLSHPEYMSLRSWLRTGNFVNKDFTYYEVPMKLDVFDDEAFKKSSIDFYVVATEMTS
GKPEYFKIDSVFEQMEILRASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVMSLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKYAKSVMPELNSYLMK

SEQ ID NO. 7720
STRAIN CJB110 frame: 1
PMLSVGLVLEGGGMRGLYTAGVLDAFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYLSHPKYMSLRSWFRTGNFVNKDFTYYEVPMKLDVFDDEAFKKSSIDFYVVATEMTS
GKPEYFKIDSVFEQMEILRASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVMSLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSVMPELNSYLMK

SEQ ID NO. 7721
STRAIN JM9130013 frame: 1
PMLSVGLVLEGGGMRGLYTAGVLDAFLDAGIKVDGIISVSAGALFGVNFVSRQRERALRY
NKKYLSHPKYMSLRSWLRTGNFVNKDFTYYEVPMKLDVFDDEAFKKSSIDFYAVATEMTS
GKPEYFKIDSVFEQMEILRASSALPVVSKMVVWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVMSLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7722
STRAIN 1169NT frame: 1
PMLSVGLVLEGGGMRGLYTAGVLDAFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYLSHPKYMSLRSWLRTGNFVNKDFTYYEVPMKLDVFDDEAFKKSSIDFYAVATEMTS
GKPEYFKIDSVFEQMEILRASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVMSLEKTGDLFAI
RPSKSLVIVRLEKNPDKLDSIYQLGMKDAKSVMPELNSYLMK

```
                               1                                                   50
      msa47322.2{394_A909}     PMLSVGLVLE GGGMRGLYTA GVLDAFLDAG IKvDGIiSVS AGALFGVNFV
      msa47322.2{394_H36B}     PMLSVGLVLE GGGMRGLYTA GVLDAFLDAG IKvDGIiSVS AGALFGVNFV
 msa47322.2{394_JM9130013}     PMLSVGLVLE GGGMRGLYTA GVLDAFLDAG IKvDGIiSVS AGALFGVNFV
       msa47322.2{394_090}     PMLSVGLVLE GGGMRGLYTA GVLDAFLDAG IKiDGIvSVS AGALFGVNFV
    msa47322.2{394_1169NT}     PMLSVGLVLE GGGMRGLYTA GVLDAFLDAG IKiDGIvSVS AGALFGVNFV
    msa47322.2{394_18RS21}     PMLSVGLVLE GGGMRGLYTA GVLDAFLDAG IKiDGIvSVS AGALFGVNFV
      msa47322.2{394_2603}     PMLSVGLVLE GGGMRGLYTA GVLDAFLDAG IKiDGIvSVS AGALFGVNFV
    msa47322.2{394_CJB110}     PMLSVGLVLE GGGMRGLYTA GVLDAFLDAG IKiDGIvSVS AGALFGVNFV
      msa47322.2{394_COH1}     PMLSVGLVLE GGGMRGLYTA GVLDAFLDAG IKiDGIvSVS AGALFGVNFV
      msa47322.2{394_M732}     PMLSVGLVLE GGGMRGLYTA GVLDAFLDAG IKiDGIvSVS AGALFGVNFV
      msa47322.2{394_M781}     PMLSVGLVLE GGGMRGLYTA GVLDAFLDAG IKiDGIvSVS AGALFGVNFV
                 Consensus     ********** ********** ********** **-***-*** **********

                               51                                                 100
      msa47322.2{394_A909}     SRQRERALRY NKKYLSHPkY MSLRSWlRTG NFVNKDFTYY EVPMKLDVFD
      msa47322.2{394_H36B}     SRQRERALRY NKKYLSHPkY MSLRSWlRTG NFVNKDFTYY EVPMKLDVFD
 msa47322.2{394_JM9130013}     SRQRERALRY NKKYLSHPkY MSLRSWlRTG NFVNKDFTYY EVPMKLDVFD
       msa47322.2{394_090}     SRQRERALRY NKKYLSHPkY MSLRSWfRTG NFVNKDFTYY EVPMKLDVFD
    msa47322.2{394_1169NT}     SRQRERALRY NKKYLSHPkY MSLRSWlRTG NFVNKDFTYY EVPMKLDVFD
    msa47322.2{394_18RS21}     SRQRERALRY NKKYLSHPkY MSLRSWfRTG NFVNKDFTYY EVPMKLDVFD
```

Table 77: Comparative Sequences relating toSAG2059

```
     msa47322.2{394_2603}   SRQRERALRY NKKYLSHPkY MSLRSWfRTG NFVNKDFTYY EVPMKLDVFD
   msa47322.2{394_CJB110}   SRQRERALRY NKKYLSHPkY MSLRSWfRTG NFVNKDFTYY EVPMKLDVFD
     msa47322.2{394_COH1}   SRQRERALRY NKKYLSHPeY MSLRSWlRTG NFVNKDFTYY EVPMKLDVFD
     msa47322.2{394_M732}   SRQRERALRY NKKYLSHPeY MSLRSWlRTG NFVNKDFTYY EVPMKLDVFD
     msa47322.2{394_M781}   SRQRERALRY NKKYLSHPeY MSLRSWlRTG NFVNKDFTYY EVPMKLDVFD
                Consensus   ********** ********-* ******-*** ********** **********

                            101                                              150
     msa47322.2{394_A909}   DEAFKKSSID FYaVATEMTS GKPEYFKIDS VFEQMEILRA SSALPVVSKM
     msa47322.2{394_H36B}   DEAFKKSSID FYaVATEMTS GKPEYFKIDS VFEQMEILRA SSALPVVSKM
msa47322.2{394_JM9130013}   DEAFKKSSID FYaVATEMTS GKPEYFKIDS VFEQMEILRA SSALPVVSKM
      msa47322.2{394_090}   DEAFKKSSID FYvVATEMTS GKPEYFKIDS VFEQMEILRA SSALPVVSKM
   msa47322.2{394_1169NT}   DEAFKKSSID FYaVATEMTS GKPEYFKIDS VFEQMEILRA SSALPVVSKM
   msa47322.2{394_18RS21}   DEAFKKSSID FYvVATEMTS GKPEYFKIDS VFEQMEILRA SSALPVVSKM
     msa47322.2{394_2603}   DEAFKKSSID FYvVATEMTS GKPEYFKIDS VFEQMEILRA SSALPVVSKM
   msa47322.2{394_CJB110}   DEAFKKSSID FYvVATEMTS GKPEYFKIDS VFEQMEILRA SSALPVVSKM
     msa47322.2{394_COH1}   DEAFKKSSID FYvVATEMTS GKPEYFKIDS VFEQMEILRA SSALPVVSKM
     msa47322.2{394_M732}   DEAFKKSSID FYvVATEMTS GKPEYFKIDS VFEQMEILRA SSALPVVSKM
     msa47322.2{394_M781}   DEAFKKSSID FYvVATEMTS GKPEYFKIDS VFEQMEILRA SSALPVVSKM
                Consensus   ********** **-******* ********** ********** **********

                            151                                              200
     msa47322.2{394_A909}   VvWQGKKYLD GGLSDSIPVD FARGLGFDKL IVVMTRPLNY QKKPSSGRLY
     msa47322.2{394_H36B}   VvWQGKKYLD GGLSDSIPVD FARGLGFDKL IVVMTRPLNY QKKPSSGRLY
msa47322.2{394_JM9130013}   VvWQGKKYLD GGLSDSIPVD FARGLGFDKL IVVMTRPLNY QKKPSSGRLY
      msa47322.2{394_090}   VdWQGKKYLD GGLSDSIPVD FARGLGFDKL IVVMTRPLNY QKKPSSGRLY
   msa47322.2{394_1169NT}   VdWQGKKYLD GGLSDSIPVD FARGLGFDKL IVVMTRPLNY QKKPSSGRLY
   msa47322.2{394_18RS21}   VdWQGKKYLD GGLSDSIPVD FARGLGFDKL IVVMTRPLNY QKKPSSGRLY
     msa47322.2{394_2603}   VdWQGKKYLD GGLSDSIPVD FARGLGFDKL IVVMTRPLNY QKKPSSGRLY
   msa47322.2{394_CJB110}   VdWQGKKYLD GGLSDSIPVD FARGLGFDKL IVVMTRPLNY QKKPSSGRLY
     msa47322.2{394_COH1}   VdWQGKKYLD GGLSDSIPVD FARGLGFDKL IVVMTRPLNY QKKPSSGRLY
     msa47322.2{394_M732}   VdWQGKKYLD GGLSDSIPVD FARGLGFDKL IVVMTRPLNY QKKPSSGRLY
     msa47322.2{394_M781}   VdWQGKKYLD GGLSDSIPVD FARGLGFDKL IVVMTRPLNY QKKPSSGRLY
                Consensus   *-******** ********** ********** ********** **********

                            201                                              250
     msa47322.2{394_A909}   KTLYRKYPNF VKTASNRYQQ YNNSLEKVMS LEKTGDLFAI RPSKSLVIgR
     msa47322.2{394_H36B}   KTLYRKYPNF VKTASNRYQQ YNNSLEKVMS LEKTGDLFAI RPSKSLVIgR
msa47322.2{394_JM9130013}   KTLYRKYPNF VKTASNRYQQ YNNSLEKVMS LEKTGDLFAI RPSKSLVIgR
      msa47322.2{394_090}   KTLYRKYPNF VKTASNRYQQ YNNSLEKVMS LEKTGDLFAI RPSKSLVIgR
   msa47322.2{394_1169NT}   KTLYRKYPNF VKTASNRYQQ YNNSLEKVMS LEKTGDLFAI RPSKSLVIvR
   msa47322.2{394_18RS21}   KTLYRKYPNF VKTASNRYQQ YNNSLEKVMS LEKTGDLFAI RPSKSLVIgR
     msa47322.2{394_2603}   KTLYRKYPNF VKTASNRYQQ YNNSLEKVMS LEKTGDLFAI RPSKSLVIgR
   msa47322.2{394_CJB110}   KTLYRKYPNF VKTASNRYQQ YNNSLEKVMS LEKTGDLFAI RPSKSLVIgR
     msa47322.2{394_COH1}   KTLYRKYPNF VKTASNRYQQ YNNSLEKVMS LEKTGDLFAI RPSKSLVIgR
     msa47322.2{394_M732}   KTLYRKYPNF VKTASNRYQQ YNNSLEKVMS LEKTGDLFAI RPSKSLVIgR
     msa47322.2{394_M781}   KTLYRKYPNF VKTASNRYQQ YNNSLEKVMS LEKTGDLFAI RPSKSLVIgR
                Consensus   ********** ********** ********** ********** ********-*

                            251                                  282
     msa47322.2{394_A909}   LEKNPDKLDS IYQLGMKdAK SgMPELNSYL MK
     msa47322.2{394_H36B}   LEKNPDKLDS IYQLGMKdAK SgMPELNSYL MK
msa47322.2{394_JM9130013}   LEKNPDKLDS IYQLGMKdAK SgMPELNSYL MK
      msa47322.2{394_090}   LEKNPDKLDS IYQLGMKdAK SvMPELNSYL MK
   msa47322.2{394_1169NT}   LEKNPDKLDS IYQLGMKdAK SvMPELNSYL MK
   msa47322.2{394_18RS21}   LEKNPDKLDS IYQLGMKdAK SvMPELNSYL MK
     msa47322.2{394_2603}   LEKNPDKLDS IYQLGMKdAK SvMPELNSYL MK
   msa47322.2{394_CJB110}   LEKNPDKLDS IYQLGMKdAK SvMPELNSYL MK
     msa47322.2{394_COH1}   LEKNPDKLDS IYQLGMKyAK SvMPELNSYL MK
     msa47322.2{394_M732}   LEKNPDKLDS IYQLGMKyAK SvMPELNSYL MK
     msa47322.2{394_M781}   LEKNPDKLDS IYQLGMKyAK SvMPELNSYL MK
                Consensus   ********** *******-** *-******** **
```

Table 78: Comparative Sequences relating to SAG1016

SEQ ID NO. 7801
STRAIN 2603
ATGAAAGTTTTAGTAGTTGATGATGAACCAGTTGCACGTAACGAATTAATTTACCTTCTT
AATAAGTATGATTCTAACCTCGTTATAGCAGAGGCGCATGATATGGCTACTGCATTAGCT
ATTTTACTTAGAGAAACTTTTGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCT
GGGTTGCAATTAGCAGAGTATATCAATAAAATGCCCAAACCACCATTATTGATATTTGCG
ACTGCTTATGATCAATATGCTATTCAGGCTTTTGAGCATGATGCGCGTGATTATTTGTTA
AAACCCTATGATTTTGATAGGCTAAAGCAAGCTATGGATAGAGTAAAAGGAGCGCTAAGT
ACATCTACAATTATAGAGAGCGTAACTTCCGGTCCTCTCTTCAAGCAACAGTATCCATTG
ACAGTAGAAGATCGAATCTATCTGGTGTCGGCGGATGATATCCTTTTGATTGAAGCTATG
CAAGGAAAACTGATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACAA
CAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTCTTACATTGTG
AACATTAATGCTATTAAAACGATTGAACCTTGGTTTAACCAAACACTTCAGTTACACCTT
TGTAATAAAATAACAGTTCCTGTTAGCAGAGCAAATGTAAAACCCCTAAAACAAATGTTA
GGCATATCTACC

SEQ ID NO. 7802
STRAIN 090
AAAGTTTTAGTAGTTGATGATGAACCAGTTGCACGTAA
CGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAG
AGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAGAAACTTTT
GATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATT
AGCAGAGTATATCAATAAAATGCCCAAACCACCATTATTGATATTTGCGA
CTGCTTATGATCAATATGCTATTCAGGCTTTTGAGCATGATGCGCGTGAT
TATTTGTTAAAACCCTATGATTTTGATAGGCTAAAGCAAGCTATGGATAG
AGTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACTTCCG
GTCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTAT
CTGGTGTCGGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAACT
GATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACAAC
AATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTCT
TACATTGTGAACATTAATGCTATTAAAACGATTGAACCTTGGTTTAACCA
AACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAGAG
CAAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7803
STRAIN A909
AAAGTTTTAGTAGTTGATGATGAACCAGTTGCACGTAAC
GAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAGA
GGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAGAAACTTTTG
ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATTA
GCAGAGTATATCAATAAAATGCCCAAACCACCATTATTGATATTCGCGAC
TGCTTATGATCAATATGCTATTCAAGCTTTTGAGCATGATGCGCGTGATT
ATTTGTTAAAACCCTATGAGTTTGATAGGCTAAAGCAAGCTATGGATAGA
GTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACTTCCGG
CCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTATC
TGGTGTCGGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAACTG
ATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACAACA
ATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTGCACCGCTCTT
ACATTGTGAATATTAATGCTATTAAAACGATTGAACCTTGGTTTAACCAA
ACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAGAGC
AAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7804
STRAIN H36B
AAAGTTTTAGTAGTTGATGATGAACCAGTTGCACGT
AACGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGC
AGAGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAGAAACTT
TTGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAA
TTAGCAGAGTATATCAATAAAATGCCCAAACCACCATTATTGATATTCGC
GACTGCTTATGATCAATATGCTATTCAAGCTTTTGAGCATGATGCGCGTG
ATTATTTGTTAAAACCCTATGAGTTTGATAGGCTAAAGCAAGCTATGGAT
AGAGTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACTTC
CGGCCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCT
ATCTGGTGTCGGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAA
CTGATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACA
ACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTGCACCGCT
CTTACATTGTGAATATTAATGCTATTAAAACGATTGAACCTTGGTTTAAC
CAAACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAG
AGCAAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7805
STRAIN 18RS21
AAAGTTTTAGTAGTTGATGATGAACCAGTTGCACGTAAC
GAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAGA
GGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAGAAACTTTTG
ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATTA
GCAGAGTATATCAATAAAATGCCCAAACCACCATTATTGATATTTGCGAC
TGCTTATGATCAATATGCTATTCAGGCTTTTGAGCATGATGCGCGTGATT
ATTTGTTAAAACCCTATGATTTTGATAGGCTAAAGCAAGCTATGGATAGA
GTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACTTCCGG
TCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTATC
TGGTGTCGGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAACTG

Table 78: Comparative Sequences relating to SAG1016

ATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACAACA
ATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTCTT
ACATTGTGAACATTAATGCTATTAAAACGATTGAACCTTGGTTTAACCAA
ACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAGAGC
AAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7806
STRAIN M732
AAAGTTTTAGTAGTTGATGATGAACCAGTT
GCACGTAACGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGT
TATAGCAGAGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAG
AAACTTTTGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGG
TTGCAATTAGCAGAGTATATCAATAAAATGCCCAAACCACCATTATTGAT
ATTCGCGACTGCTTATGATCAATATGCTATTCAGGCTTTTGAGCAGGATG
CGCGTGATTATTTGTTAAAACCCTATGAGTTTGATAGGTTAAAGCAAGCT
ATGGATAGAGTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGT
AGCTTCCGGTCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATC
GAATCTATCTGGTGTCGGCGGATGATATCCTTTTGATTGAAGCTATGCAA
GGAAAACTGATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTC
TCTACAACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTAC
ATCGCTCTTACATTGTGAATATTAATGCTATTAAAACGATTGAACCTTGG
TTTAACCAAACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGT
TAGCAGAGCAAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7807
STRAIN COH1
AAAGTTTTAGTAGTTGATGATGAACCAGTTGCACGTA
ACGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCA
GAGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAGAAACTTT
TGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAAT
TAGCAGAGTATATCAATAAAATGCCCAAACCACCATTATTGATATTCGCG
ACTGCTTATGATCAATATGCTATTCAGGCTTTTGAGCAGGATGCGCGTGA
TTATTTGTTAAAACCCTATGAGTTTGATAGGTTAAAGCAAGCTATGGATA
GAGTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAGCTTCC
GGTCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTA
TCTGGTGTCGGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAAC
TGATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACAA
CAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTC
TTACATTGTGAATATTAATGCTATTAAAACGATTGAACCTTGGTTTAACC
AAACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAGA
GCAAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7808
STRAIN M781
AAAGTTTTAGTAGTTGATGATGAACCAGTTGCACGTAAC
GAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAGA
GGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAGAAACTTTTG
ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATTA
GCAGAGTATATCAATAAAATGCCCAAACCACCATTATTGATATTCGCGAC
TGCTTATGATCAATATGCTATTCAGGCTTTTGAGCAGGATGCGCGTGATT
ATTTGTTAAAACCCTATGAGTTTGATAGGTTAAAGCAAGCTATGGATAGA
GTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAGCTTCCGG
TCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTATC
TGGTGTCGGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAACTG
ATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTCTACAACA
ATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTCTT
ACATTGTGAATATTAATGCTATTAAAACGATTGAACCTTGGTTTAACCAA
ACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAGAGC
AAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7809
STRAIN CJB110
CTTAATAAGTATGATTCTAACCTCGTTATAGCAGAGGCGCATGATATGGC
TACTGCATTAGCTATTTTACTTAGAGAAACTTTTGATGTAGCACTGTTAG
ATATCCATCTCAGAGATGATTCTGGGTTGCAATTAGCAGAGTATATCAAT
AAAATGCCCAAACCACCATTATTGATATTCGCGACTGCTTATGATCAATA
TGCTATTCAAGCTTTTGAGCATGATGCGCGTGATTATTTGTTAAAACCCT
ATGAGTTTGATAGGCTAAAGCAAGnTATGGATAGAGTAAAAGGAGCGCTA
AGTACATCTACAATTATAGAGAGCGTAACTTCCGGCCCTCTCTTCAAGCA
ACAGTATCCATTGACAGTAGAAGATnGAATCTATCTGGTGTCGGCGGATG
ATATCCTTTTGATTGAAGCTATGCAAGGAAAACTGATTATACAAACACCT
GATAAAAATTATGAAATTGATGGCTCTCTACAACAATGGCAAGATAAACT
ACCATCATCTCAATTTGTACGGGTGCACCGCTCTTACATTGTGAATATTA
ATGCTATTAAAACGATTGAACCTTGGTTTAACCAAACACTTCAGTTACAC
CTTTGTAATAAAATAACAGTTCCTGTTAGCAGAGCAAATGTAAAACCCCT
AAAACAAATGTTAGG

SEQ ID NO. 7810
STRAIN 1169NT
AAAGTTTTAGTAGTTGATGATGAACCAG
TTGCACGTAACGAATTAATTTATCTTCTTAATAAGTATGATTCTAACCTC
GTTATAGCAGAGGCGCATGATATAGCTACTGCATTAGCTATTTTACTTAG

Table 78: Comparative Sequences relating to SAG1016

AGAAACTTTTGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTG
GGTTGCAATTAGCAGAGTATATCAATAAAATGCCCAAACCACCATTATTG
ATATTCGCGACTGCTTATGATCAATATGCTATTCAGGCTTTTGAGCATGA
TGCGCGTGATTATTTGTTAAAACCCTATGAGTTTGATAGGCTAAAGCAAG
CTATGGATAGAGTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGC
GTAACTTCCGGCCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGA
TCGAATCTATCTGGTGTCGGCGGATGATATCCTTTTGATTGAAGCTATGC
AAGGAAAACTGATTATACAAACACCTGATAAAAATTATGAAATTGATGGC
TCTCTACAACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGT
GCACCGCTCTTACATTGTGAATATTAATGCTATTAAAACGATTGAACCTT
GGTTTAACCAAACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCCT
GTTAGCAGAGCAAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTAC
C

SEQ ID NO. 7811
STRAIN JM9130013
AAAGTTTTAGTAGTTGATGATGAACCAGT
TGCACGTAACGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCG
TTATAGCAGAGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGA
GAAACTTTTGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGG
GTTGCAATTAGCAGAGTATATCAATAAAATGCCCAAACCACCATTATTGA
TATTCGCGACTGCTTATGATCAATATGCTATTCAAGCTTTTGAGCATGAT
GCGCGTGATTATTTGTTAAAACCCTATGAGTTTGATAGGCTAAAGCAAGC
TATGGATAGAGTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCG
TAACTTCCGGCCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGAT
CGAATCTATCTGGTGTCGGCGGATGATATCCTTTTGATTGAAGCTATGCA
AGGAAAACTGATTATACAAACACCTGATAAAAATTATGAAATTGATGGCT
CTCTACAACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTG
CACCGCTCTTACATTGTGAATATTAATGCTATTAAAACGATTGAACCTTG
GTTTAACCAAACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTG
TTAGCAGAGCAAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTACC

```
MSA Alignment Results: Pretty output
PRETTY of: /biotmp/msa141507.2{*}   April 10, 2003 06:36  ..

                                   1                                                  50
      msa141507.2{399_A909}   ---aaagttt tagtagttga tgatgaacca gttgcacgta acgaattaat
    msa141507.2{399_CJB110}   ---------- ---------- ---------- ---------- ----------
      msa141507.2{399_H36B}   ---aaagttt tagtagttga tgatgaacca gttgcacgta acgaattaat
 msa141507.2{399_JM9130013}   ---aaagttt tagtagttga tgatgaacca gttgcacgta acgaattaat
    msa141507.2{399_1169NT}   ---aaagttt tagtagttga tgatgaacca gttgcacgta acgaattaat
       msa141507.2{399_090}   ---aaagttt tagtagttga tgatgaacca gttgcacgta acgaattaat
    msa141507.2{399_18RS21}   ---aaagttt tagtagttga tgatgaacca gttgcacgta acgaattaat
      msa141507.2{399_2603}   atgaaagttt tagtagttga tgatgaacca gttgcacgta acgaattaat
      msa141507.2{399_COH1}   ---aaagttt tagtagttga tgatgaacca gttgcacgta acgaattaat
      msa141507.2{399_M732}   ---aaagttt tagtagttga tgatgaacca gttgcacgta acgaattaat
      msa141507.2{399_M781}   ---aaagttt tagtagttga tgatgaacca gttgcacgta acgaattaat
                  Consensus   ***------- ---------- ---------- ---------- ----------

                              51                                                 100
      msa141507.2{399_A909}   ttaccttCTT AATAAGTATG ATTCTAACCT CGTTATAGCA GAGGCGCATG
    msa141507.2{399_CJB110}   -------CTT AATAAGTATG ATTCTAACCT CGTTATAGCA GAGGCGCATG
      msa141507.2{399_H36B}   ttaccttCTT AATAAGTATG ATTCTAACCT CGTTATAGCA GAGGCGCATG
 msa141507.2{399_JM9130013}   ttaccttCTT AATAAGTATG ATTCTAACCT CGTTATAGCA GAGGCGCATG
    msa141507.2{399_1169NT}   ttatcttCTT AATAAGTATG ATTCTAACCT CGTTATAGCA GAGGCGCATG
       msa141507.2{399_090}   ttaccttCTT AATAAGTATG ATTCTAACCT CGTTATAGCA GAGGCGCATG
    msa141507.2{399_18RS21}   ttaccttCTT AATAAGTATG ATTCTAACCT CGTTATAGCA GAGGCGCATG
      msa141507.2{399_2603}   ttaccttCTT AATAAGTATG ATTCTAACCT CGTTATAGCA GAGGCGCATG
      msa141507.2{399_COH1}   ttaccttCTT AATAAGTATG ATTCTAACCT CGTTATAGCA GAGGCGCATG
      msa141507.2{399_M732}   ttaccttCTT AATAAGTATG ATTCTAACCT CGTTATAGCA GAGGCGCATG
      msa141507.2{399_M781}   ttaccttCTT AATAAGTATG ATTCTAACCT CGTTATAGCA GAGGCGCATG
                  Consensus   -------*** ********** ********** ********** **********

                              101                                                150
      msa141507.2{399_A909}   ATATgGCTAC TGCATTAGCT ATTTTACTTA GAGAAACTTT TGATGTAGCA
    msa141507.2{399_CJB110}   ATATgGCTAC TGCATTAGCT ATTTTACTTA GAGAAACTTT TGATGTAGCA
      msa141507.2{399_H36B}   ATATgGCTAC TGCATTAGCT ATTTTACTTA GAGAAACTTT TGATGTAGCA
 msa141507.2{399_JM9130013}   ATATgGCTAC TGCATTAGCT ATTTTACTTA GAGAAACTTT TGATGTAGCA
    msa141507.2{399_1169NT}   ATATaGCTAC TGCATTAGCT ATTTTACTTA GAGAAACTTT TGATGTAGCA
       msa141507.2{399_090}   ATATgGCTAC TGCATTAGCT ATTTTACTTA GAGAAACTTT TGATGTAGCA
    msa141507.2{399_18RS21}   ATATgGCTAC TGCATTAGCT ATTTTACTTA GAGAAACTTT TGATGTAGCA
      msa141507.2{399_2603}   ATATgGCTAC TGCATTAGCT ATTTTACTTA GAGAAACTTT TGATGTAGCA
      msa141507.2{399_COH1}   ATATgGCTAC TGCATTAGCT ATTTTACTTA GAGAAACTTT TGATGTAGCA
      msa141507.2{399_M732}   ATATgGCTAC TGCATTAGCT ATTTTACTTA GAGAAACTTT TGATGTAGCA
      msa141507.2{399_M781}   ATATgGCTAC TGCATTAGCT ATTTTACTTA GAGAAACTTT TGATGTAGCA
                  Consensus   ****-***** ********** ********** ********** **********

                              151                                                200
      msa141507.2{399_A909}   CTGTTAGATA TCCATCTCAG AGATGATTCT GGGTTGCAAT TAGCAGAGTA
    msa141507.2{399_CJB110}   CTGTTAGATA TCCATCTCAG AGATGATTCT GGGTTGCAAT TAGCAGAGTA
      msa141507.2{399_H36B}   CTGTTAGATA TCCATCTCAG AGATGATTCT GGGTTGCAAT TAGCAGAGTA
 msa141507.2{399_JM9130013}   CTGTTAGATA TCCATCTCAG AGATGATTCT GGGTTGCAAT TAGCAGAGTA
    msa141507.2{399_1169NT}   CTGTTAGATA TCCATCTCAG AGATGATTCT GGGTTGCAAT TAGCAGAGTA
```

Table 78: Comparative Sequences relating to SAG1016

```
      msa141507.2{399_090}  CTGTTAGATA TCCATCTCAG AGATGATTCT GGGTTGCAAT TAGCAGAGTA
   msa141507.2{399_18RS21}  CTGTTAGATA TCCATCTCAG AGATGATTCT GGGTTGCAAT TAGCAGAGTA
     msa141507.2{399_2603}  CTGTTAGATA TCCATCTCAG AGATGATTCT GGGTTGCAAT TAGCAGAGTA
     msa141507.2{399_COH1}  CTGTTAGATA TCCATCTCAG AGATGATTCT GGGTTGCAAT TAGCAGAGTA
     msa141507.2{399_M732}  CTGTTAGATA TCCATCTCAG AGATGATTCT GGGTTGCAAT TAGCAGAGTA
     msa141507.2{399_M781}  CTGTTAGATA TCCATCTCAG AGATGATTCT GGGTTGCAAT TAGCAGAGTA
                 Consensus  ********** ********** ********** ********** **********

                            201                                                250
     msa141507.2{399_A909}  TATCAATAAA ATGCCCAAAC CACCATTATT GATATTcGCG ACTGCTTATG
   msa141507.2{399_CJB110}  TATCAATAAA ATGCCCAAAC CACCATTATT GATATTcGCG ACTGCTTATG
     msa141507.2{399_H36B}  TATCAATAAA ATGCCCAAAC CACCATTATT GATATTcGCG ACTGCTTATG
msa141507.2{399_JM9130013}  TATCAATAAA ATGCCCAAAC CACCATTATT GATATTcGCG ACTGCTTATG
   msa141507.2{399_1169NT}  TATCAATAAA ATGCCCAAAC CACCATTATT GATATTcGCG ACTGCTTATG
      msa141507.2{399_090}  TATCAATAAA ATGCCCAAAC CACCATTATT GATATTtGCG ACTGCTTATG
   msa141507.2{399_18RS21}  TATCAATAAA ATGCCCAAAC CACCATTATT GATATTtGCG ACTGCTTATG
     msa141507.2{399_2603}  TATCAATAAA ATGCCCAAAC CACCATTATT GATATTtGCG ACTGCTTATG
     msa141507.2{399_COH1}  TATCAATAAA ATGCCCAAAC CACCATTATT GATATTcGCG ACTGCTTATG
     msa141507.2{399_M732}  TATCAATAAA ATGCCCAAAC CACCATTATT GATATTcGCG ACTGCTTATG
     msa141507.2{399_M781}  TATCAATAAA ATGCCCAAAC CACCATTATT GATATTcGCG ACTGCTTATG
                 Consensus  ********** ********** ********** ******_*** **********

                            251                                                300
     msa141507.2{399_A909}  ATCAATATGC TATTCAaGCT TTTGAGCAtG ATGCGCGTGA TTATTTGTTA
   msa141507.2{399_CJB110}  ATCAATATGC TATTCAaGCT TTTGAGCAtG ATGCGCGTGA TTATTTGTTA
     msa141507.2{399_H36B}  ATCAATATGC TATTCAaGCT TTTGAGCAtG ATGCGCGTGA TTATTTGTTA
msa141507.2{399_JM9130013}  ATCAATATGC TATTCAaGCT TTTGAGCAtG ATGCGCGTGA TTATTTGTTA
   msa141507.2{399_1169NT}  ATCAATATGC TATTCAgGCT TTTGAGCAtG ATGCGCGTGA TTATTTGTTA
      msa141507.2{399_090}  ATCAATATGC TATTCAgGCT TTTGAGCAtG ATGCGCGTGA TTATTTGTTA
   msa141507.2{399_18RS21}  ATCAATATGC TATTCAgGCT TTTGAGCAtG ATGCGCGTGA TTATTTGTTA
     msa141507.2{399_2603}  ATCAATATGC TATTCAgGCT TTTGAGCAtG ATGCGCGTGA TTATTTGTTA
     msa141507.2{399_COH1}  ATCAATATGC TATTCAgGCT TTTGAGCAgG ATGCGCGTGA TTATTTGTTA
     msa141507.2{399_M732}  ATCAATATGC TATTCAgGCT TTTGAGCAgG ATGCGCGTGA TTATTTGTTA
     msa141507.2{399_M781}  ATCAATATGC TATTCAgGCT TTTGAGCAgG ATGCGCGTGA TTATTTGTTA
                 Consensus  ********** ******_*** ********_* ********** **********

                            301                                                350
     msa141507.2{399_A909}  AAACCCTATG AgTTTGATAG GcTAAAGCAA GcTATGGATA GAGTAAAAGG
   msa141507.2{399_CJB110}  AAACCCTATG AgTTTGATAG GcTAAAGCAA GnTATGGATA GAGTAAAAGG
     msa141507.2{399_H36B}  AAACCCTATG AgTTTGATAG GcTAAAGCAA GcTATGGATA GAGTAAAAGG
msa141507.2{399_JM9130013}  AAACCCTATG AgTTTGATAG GcTAAAGCAA GcTATGGATA GAGTAAAAGG
   msa141507.2{399_1169NT}  AAACCCTATG AgTTTGATAG GcTAAAGCAA GcTATGGATA GAGTAAAAGG
      msa141507.2{399_090}  AAACCCTATG AtTTTGATAG GcTAAAGCAA GcTATGGATA GAGTAAAAGG
   msa141507.2{399_18RS21}  AAACCCTATG AtTTTGATAG GcTAAAGCAA GcTATGGATA GAGTAAAAGG
     msa141507.2{399_2603}  AAACCCTATG AtTTTGATAG GcTAAAGCAA GcTATGGATA GAGTAAAAGG
     msa141507.2{399_COH1}  AAACCCTATG AgTTTGATAG GtTAAAGCAA GcTATGGATA GAGTAAAAGG
     msa141507.2{399_M732}  AAACCCTATG AgTTTGATAG GtTAAAGCAA GcTATGGATA GAGTAAAAGG
     msa141507.2{399_M781}  AAACCCTATG AgTTTGATAG GtTAAAGCAA GcTATGGATA GAGTAAAAGG
                 Consensus  ********** *_******** *_******** *_******** **********

                            351                                                400
     msa141507.2{399_A909}  AGCGCTAAGT ACATCTACAA TTATAGAGAG CGTAaCTTCC GGcCCTCTCT
   msa141507.2{399_CJB110}  AGCGCTAAGT ACATCTACAA TTATAGAGAG CGTAaCTTCC GGcCCTCTCT
     msa141507.2{399_H36B}  AGCGCTAAGT ACATCTACAA TTATAGAGAG CGTAaCTTCC GGcCCTCTCT
msa141507.2{399_JM9130013}  AGCGCTAAGT ACATCTACAA TTATAGAGAG CGTAaCTTCC GGcCCTCTCT
   msa141507.2{399_1169NT}  AGCGCTAAGT ACATCTACAA TTATAGAGAG CGTAaCTTCC GGcCCTCTCT
      msa141507.2{399_090}  AGCGCTAAGT ACATCTACAA TTATAGAGAG CGTAaCTTCC GGtCCTCTCT
   msa141507.2{399_18RS21}  AGCGCTAAGT ACATCTACAA TTATAGAGAG CGTAaCTTCC GGtCCTCTCT
     msa141507.2{399_2603}  AGCGCTAAGT ACATCTACAA TTATAGAGAG CGTAaCTTCC GGtCCTCTCT
     msa141507.2{399_COH1}  AGCGCTAAGT ACATCTACAA TTATAGAGAG CGTAgCTTCC GGtCCTCTCT
     msa141507.2{399_M732}  AGCGCTAAGT ACATCTACAA TTATAGAGAG CGTAgCTTCC GGtCCTCTCT
     msa141507.2{399_M781}  AGCGCTAAGT ACATCTACAA TTATAGAGAG CGTAgCTTCC GGtCCTCTCT
                 Consensus  ********** ********** ********** ****_***** **_*******

                            401                                                450
     msa141507.2{399_A909}  TCAAGCAACA GTATCCATTG ACAGTAGAAG ATcGAATCTA TCTGGTGTCG
   msa141507.2{399_CJB110}  TCAAGCAACA GTATCCATTG ACAGTAGAAG ATnGAATCTA TCTGGTGTCG
     msa141507.2{399_H36B}  TCAAGCAACA GTATCCATTG ACAGTAGAAG ATcGAATCTA TCTGGTGTCG
msa141507.2{399_JM9130013}  TCAAGCAACA GTATCCATTG ACAGTAGAAG ATcGAATCTA TCTGGTGTCG
   msa141507.2{399_1169NT}  TCAAGCAACA GTATCCATTG ACAGTAGAAG ATcGAATCTA TCTGGTGTCG
      msa141507.2{399_090}  TCAAGCAACA GTATCCATTG ACAGTAGAAG ATcGAATCTA TCTGGTGTCG
   msa141507.2{399_18RS21}  TCAAGCAACA GTATCCATTG ACAGTAGAAG ATcGAATCTA TCTGGTGTCG
     msa141507.2{399_2603}  TCAAGCAACA GTATCCATTG ACAGTAGAAG ATcGAATCTA TCTGGTGTCG
     msa141507.2{399_COH1}  TCAAGCAACA GTATCCATTG ACAGTAGAAG ATcGAATCTA TCTGGTGTCG
     msa141507.2{399_M732}  TCAAGCAACA GTATCCATTG ACAGTAGAAG ATcGAATCTA TCTGGTGTCG
     msa141507.2{399_M781}  TCAAGCAACA GTATCCATTG ACAGTAGAAG ATcGAATCTA TCTGGTGTCG
                 Consensus  ********** ********** ********** **_******* **********

                            451                                                500
     msa141507.2{399_A909}  GCGGATGATA TCCTTTTGAT TGAAGCTATG CAAGGAAAAC TGATTATACA
   msa141507.2{399_CJB110}  GCGGATGATA TCCTTTTGAT TGAAGCTATG CAAGGAAAAC TGATTATACA
     msa141507.2{399_H36B}  GCGGATGATA TCCTTTTGAT TGAAGCTATG CAAGGAAAAC TGATTATACA
msa141507.2{399_JM9130013}  GCGGATGATA TCCTTTTGAT TGAAGCTATG CAAGGAAAAC TGATTATACA
```

Table 78: Comparative Sequences relating to SAG1016

```
  msa141507.2{399_1169NT}  GCGGATGATA TCCTTTTGAT TGAAGCTATG CAAGGAAAAC TGATTATACA
     msa141507.2{399_090}  GCGGATGATA TCCTTTTGAT TGAAGCTATG CAAGGAAAAC TGATTATACA
   msa141507.2{399_18RS21}  GCGGATGATA TCCTTTTGAT TGAAGCTATG CAAGGAAAAC TGATTATACA
    msa141507.2{399_2603}  GCGGATGATA TCCTTTTGAT TGAAGCTATG CAAGGAAAAC TGATTATACA
    msa141507.2{399_COH1}  GCGGATGATA TCCTTTTGAT TGAAGCTATG CAAGGAAAAC TGATTATACA
    msa141507.2{399_M732}  GCGGATGATA TCCTTTTGAT TGAAGCTATG CAAGGAAAAC TGATTATACA
    msa141507.2{399_M781}  GCGGATGATA TCCTTTTGAT TGAAGCTATG CAAGGAAAAC TGATTATACA
                Consensus  ********** ********** ********** ********** **********

                           501                                                550
    msa141507.2{399_A909}  AACACCTGAT AAAAATTATG AAATTGATGG CTCTCTACAA CAATGGCAAG
  msa141507.2{399_CJB110}  AACACCTGAT AAAAATTATG AAATTGATGG CTCTCTACAA CAATGGCAAG
    msa141507.2{399_H36B}  AACACCTGAT AAAAATTATG AAATTGATGG CTCTCTACAA CAATGGCAAG
msa141507.2{399_JM9130013}  AACACCTGAT AAAAATTATG AAATTGATGG CTCTCTACAA CAATGGCAAG
  msa141507.2{399_1169NT}  AACACCTGAT AAAAATTATG AAATTGATGG CTCTCTACAA CAATGGCAAG
     msa141507.2{399_090}  AACACCTGAT AAAAATTATG AAATTGATGG CTCTCTACAA CAATGGCAAG
  msa141507.2{399_18RS21}  AACACCTGAT AAAAATTATG AAATTGATGG CTCTCTACAA CAATGGCAAG
    msa141507.2{399_2603}  AACACCTGAT AAAAATTATG AAATTGATGG CTCTCTACAA CAATGGCAAG
    msa141507.2{399_COH1}  AACACCTGAT AAAAATTATG AAATTGATGG CTCTCTACAA CAATGGCAAG
    msa141507.2{399_M732}  AACACCTGAT AAAAATTATG AAATTGATGG CTCTCTACAA CAATGGCAAG
    msa141507.2{399_M781}  AACACCTGAT AAAAATTATG AAATTGATGG CTCTCTACAA CAATGGCAAG
                Consensus  ********** ********** ********** ********** **********

                           551                                                600
    msa141507.2{399_A909}  ATAAACTACC ATCATCTCAA TTTGTACGGG TgCAcCGCTC TTACATTGTG
  msa141507.2{399_CJB110}  ATAAACTACC ATCATCTCAA TTTGTACGGG TgCAcCGCTC TTACATTGTG
    msa141507.2{399_H36B}  ATAAACTACC ATCATCTCAA TTTGTACGGG TgCAcCGCTC TTACATTGTG
msa141507.2{399_JM9130013}  ATAAACTACC ATCATCTCAA TTTGTACGGG TgCAcCGCTC TTACATTGTG
  msa141507.2{399_1169NT}  ATAAACTACC ATCATCTCAA TTTGTACGGG TgCAcCGCTC TTACATTGTG
     msa141507.2{399_090}  ATAAACTACC ATCATCTCAA TTTGTACGGG TaCAtCGCTC TTACATTGTG
  msa141507.2{399_18RS21}  ATAAACTACC ATCATCTCAA TTTGTACGGG TaCAtCGCTC TTACATTGTG
    msa141507.2{399_2603}  ATAAACTACC ATCATCTCAA TTTGTACGGG TaCAtCGCTC TTACATTGTG
    msa141507.2{399_COH1}  ATAAACTACC ATCATCTCAA TTTGTACGGG TaCAtCGCTC TTACATTGTG
    msa141507.2{399_M732}  ATAAACTACC ATCATCTCAA TTTGTACGGG TaCAtCGCTC TTACATTGTG
    msa141507.2{399_M781}  ATAAACTACC ATCATCTCAA TTTGTACGGG TaCAtCGCTC TTACATTGTG
                Consensus  ********** ********** ********** *-**-***** **********

                           601                                                650
    msa141507.2{399_A909}  AAtATTAATG CTATTAAAAC GATTGAACCT TGGTTTAACC AAACACTTCA
  msa141507.2{399_CJB110}  AAtATTAATG CTATTAAAAC GATTGAACCT TGGTTTAACC AAACACTTCA
    msa141507.2{399_H36B}  AAtATTAATG CTATTAAAAC GATTGAACCT TGGTTTAACC AAACACTTCA
msa141507.2{399_JM9130013}  AAtATTAATG CTATTAAAAC GATTGAACCT TGGTTTAACC AAACACTTCA
  msa141507.2{399_1169NT}  AAtATTAATG CTATTAAAAC GATTGAACCT TGGTTTAACC AAACACTTCA
     msa141507.2{399_090}  AAcATTAATG CTATTAAAAC GATTGAACCT TGGTTTAACC AAACACTTCA
  msa141507.2{399_18RS21}  AAcATTAATG CTATTAAAAC GATTGAACCT TGGTTTAACC AAACACTTCA
    msa141507.2{399_2603}  AAcATTAATG CTATTAAAAC GATTGAACCT TGGTTTAACC AAACACTTCA
    msa141507.2{399_COH1}  AAtATTAATG CTATTAAAAC GATTGAACCT TGGTTTAACC AAACACTTCA
    msa141507.2{399_M732}  AAtATTAATG CTATTAAAAC GATTGAACCT TGGTTTAACC AAACACTTCA
    msa141507.2{399_M781}  AAtATTAATG CTATTAAAAC GATTGAACCT TGGTTTAACC AAACACTTCA
                Consensus  **-******* ********** ********** ********** **********

                           651                                                700
    msa141507.2{399_A909}  GTTACACCTT TGTAATAAAA TAACAGTTCC TGTTAGCAGA GCAAATGTAA
  msa141507.2{399_CJB110}  GTTACACCTT TGTAATAAAA TAACAGTTCC TGTTAGCAGA GCAAATGTAA
    msa141507.2{399_H36B}  GTTACACCTT TGTAATAAAA TAACAGTTCC TGTTAGCAGA GCAAATGTAA
msa141507.2{399_JM9130013}  GTTACACCTT TGTAATAAAA TAACAGTTCC TGTTAGCAGA GCAAATGTAA
  msa141507.2{399_1169NT}  GTTACACCTT TGTAATAAAA TAACAGTTCC TGTTAGCAGA GCAAATGTAA
     msa141507.2{399_090}  GTTACACCTT TGTAATAAAA TAACAGTTCC TGTTAGCAGA GCAAATGTAA
  msa141507.2{399_18RS21}  GTTACACCTT TGTAATAAAA TAACAGTTCC TGTTAGCAGA GCAAATGTAA
    msa141507.2{399_2603}  GTTACACCTT TGTAATAAAA TAACAGTTCC TGTTAGCAGA GCAAATGTAA
    msa141507.2{399_COH1}  GTTACACCTT TGTAATAAAA TAACAGTTCC TGTTAGCAGA GCAAATGTAA
    msa141507.2{399_M732}  GTTACACCTT TGTAATAAAA TAACAGTTCC TGTTAGCAGA GCAAATGTAA
    msa141507.2{399_M781}  GTTACACCTT TGTAATAAAA TAACAGTTCC TGTTAGCAGA GCAAATGTAA
                Consensus  ********** ********** ********** ********** **********

                           701                             732
    msa141507.2{399_A909}  AACCCCTAAA ACAAATGTTA GGcatatcta cc
  msa141507.2{399_CJB110}  AACCCCTAAA ACAAATGTTA GG-------- --
    msa141507.2{399_H36B}  AACCCCTAAA ACAAATGTTA GGcatatcta cc
msa141507.2{399_JM9130013}  AACCCCTAAA ACAAATGTTA GGcatatcta cc
  msa141507.2{399_1169NT}  AACCCCTAAA ACAAATGTTA GGcatatcta cc
     msa141507.2{399_090}  AACCCCTAAA ACAAATGTTA GGcatatcta cc
  msa141507.2{399_18RS21}  AACCCCTAAA ACAAATGTTA GGcatatcta cc
    msa141507.2{399_2603}  AACCCCTAAA ACAAATGTTA GGcatatcta cc
    msa141507.2{399_COH1}  AACCCCTAAA ACAAATGTTA GGcatatcta cc
    msa141507.2{399_M732}  AACCCCTAAA ACAAATGTTA GGcatatcta cc
    msa141507.2{399_M781}  AACCCCTAAA ACAAATGTTA GGcatatcta cc
                Consensus  ********** ********** **-------- --
```

SEQ ID NO. 7812
STRAIN 2603 frame: 1
KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLIFATAYDQYAIQAFEHDARDYLLKPYDFDRLKQAMDRVKGALST

Table 78: Comparative Sequences relating to SAG1016

STIIESVTSGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLIIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7813
STRAIN 090 frame: 1
KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLIFATAYDQYAIQAFEHDARDYLLKPYDFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLIIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7814
STRAIN A909 frame: 1
KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLIFATAYDQYAIQAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLIIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7815
STRAIN H36B frame: 1
KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLIFATAYDQYAIQAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLIIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7816
STRAIN 18RS21 frame: 1
KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLIFATAYDQYAIQAFEHDARDYLLKPYDFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLIIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7817
STRAIN M732 frame: 1
KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLIFATAYDQYAIQAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVASGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLIIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7818
STRAIN COH1 frame: 1
KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLIFATAYDQYAIQAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVASGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLIIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7819
STRAIN M781 frame: 1
KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLIFATAYDQYAIQAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVASGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLIIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7820
STRAIN CJB110 frame: 1
LNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSGLQLAEYINKMPKPPLLIF
ATAYDQYAIQAFEHDARDYLLKPYEFDRLKQXMDRVKGALSTSTIIESVTSGPLFKQQYP
LTVEDXIYLVSADDILLIEAMQGKLIIQTPDKNYEIDGSLQQWQDKLPSSQFVRVHRSYI
VNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQML

SEQ ID NO. 7821
STRAIN 1169NT frame: 1
KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDIATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLIFATAYDQYAIQAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLIIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7822
STRAIN JM9130013 frame: 1
KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLIFATAYDQYAIQAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLIIQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

Table 78: Comparative Sequences relating to SAG1016

```
PRETTY of: /biotmp/msa141801.2{*}   April 10, 2003 06:38  ..

                                 1                                                   50
      msa141801.2{399_COH1}      kvlvvddepv arneliylLN KYDSNLVIAE AHDmATALAI LLRETFDVAL
      msa141801.2{399_M732}      kvlvvddepv arneliylLN KYDSNLVIAE AHDmATALAI LLRETFDVAL
      msa141801.2{399_M781}      kvlvvddepv arneliylLN KYDSNLVIAE AHDmATALAI LLRETFDVAL
       msa141801.2{399_090}      kvlvvddepv arneliylLN KYDSNLVIAE AHDmATALAI LLRETFDVAL
    msa141801.2{399_18RS21}      kvlvvddepv arneliylLN KYDSNLVIAE AHDmATALAI LLRETFDVAL
      msa141801.2{399_2603}      kvlvvddepv arneliylLN KYDSNLVIAE AHDmATALAI LLRETFDVAL
      msa141801.2{399_A909}      kvlvvddepv arneliylLN KYDSNLVIAE AHDmATALAI LLRETFDVAL
      msa141801.2{399_H36B}      kvlvvddepv arneliylLN KYDSNLVIAE AHDmATALAI LLRETFDVAL
msa141801.2{399_JM9130013}      kvlvvddepv arneliylLN KYDSNLVIAE AHDmATALAI LLRETFDVAL
    msa141801.2{399_1169NT}      kvlvvddepv arneliylLN KYDSNLVIAE AHDiATALAI LLRETFDVAL
    msa141801.2{399_CJB110}      ~~~~~~~~~~ ~~~~~~~~LN KYDSNLVIAE AHDmATALAI LLRETFDVAL
                  Consensus      ---------- --------** ********** ***-****** **********

                                 51                                                 100
      msa141801.2{399_COH1}      LDIHLRDDSG LQLAEYINKM PKPPLLIFAT AYDQYAIQAF EqDARDYLLK
      msa141801.2{399_M732}      LDIHLRDDSG LQLAEYINKM PKPPLLIFAT AYDQYAIQAF EqDARDYLLK
      msa141801.2{399_M781}      LDIHLRDDSG LQLAEYINKM PKPPLLIFAT AYDQYAIQAF EqDARDYLLK
       msa141801.2{399_090}      LDIHLRDDSG LQLAEYINKM PKPPLLIFAT AYDQYAIQAF EhDARDYLLK
    msa141801.2{399_18RS21}      LDIHLRDDSG LQLAEYINKM PKPPLLIFAT AYDQYAIQAF EhDARDYLLK
      msa141801.2{399_2603}      LDIHLRDDSG LQLAEYINKM PKPPLLIFAT AYDQYAIQAF EhDARDYLLK
      msa141801.2{399_A909}      LDIHLRDDSG LQLAEYINKM PKPPLLIFAT AYDQYAIQAF EhDARDYLLK
      msa141801.2{399_H36B}      LDIHLRDDSG LQLAEYINKM PKPPLLIFAT AYDQYAIQAF EhDARDYLLK
msa141801.2{399_JM9130013}      LDIHLRDDSG LQLAEYINKM PKPPLLIFAT AYDQYAIQAF EhDARDYLLK
    msa141801.2{399_1169NT}      LDIHLRDDSG LQLAEYINKM PKPPLLIFAT AYDQYAIQAF EhDARDYLLK
    msa141801.2{399_CJB110}      LDIHLRDDSG LQLAEYINKM PKPPLLIFAT AYDQYAIQAF EhDARDYLLK
                  Consensus      ********** ********** ********** ********** *-********

                                 101                                                150
      msa141801.2{399_COH1}      PYeFDRLKQa MDRVKGALST STIIESVaSG PLFKQQYPLT VEDrIYLVSA
      msa141801.2{399_M732}      PYeFDRLKQa MDRVKGALST STIIESVaSG PLFKQQYPLT VEDrIYLVSA
      msa141801.2{399_M781}      PYeFDRLKQa MDRVKGALST STIIESVaSG PLFKQQYPLT VEDrIYLVSA
       msa141801.2{399_090}      PYdFDRLKQa MDRVKGALST STIIESVtSG PLFKQQYPLT VEDrIYLVSA
    msa141801.2{399_18RS21}      PYdFDRLKQa MDRVKGALST STIIESVtSG PLFKQQYPLT VEDrIYLVSA
      msa141801.2{399_2603}      PYdFDRLKQa MDRVKGALST STIIESVtSG PLFKQQYPLT VEDrIYLVSA
      msa141801.2{399_A909}      PYeFDRLKQa MDRVKGALST STIIESVtSG PLFKQQYPLT VEDrIYLVSA
      msa141801.2{399_H36B}      PYeFDRLKQa MDRVKGALST STIIESVtSG PLFKQQYPLT VEDrIYLVSA
msa141801.2{399_JM9130013}      PYeFDRLKQa MDRVKGALST STIIESVtSG PLFKQQYPLT VEDrIYLVSA
    msa141801.2{399_1169NT}      PYeFDRLKQa MDRVKGALST STIIESVtSG PLFKQQYPLT VEDrIYLVSA
    msa141801.2{399_CJB110}      PYeFDRLKQx MDRVKGALST STIIESVtSG PLFKQQYPLT VEDxIYLVSA
                  Consensus      **-******- ********** *******-** ********** ***-******

                                 151                                                200
      msa141801.2{399_COH1}      DDILLIEAMQ GKLIIQTPDK NYEIDGSLQQ WQDKLPSSQF VRVHRSYIVN
      msa141801.2{399_M732}      DDILLIEAMQ GKLIIQTPDK NYEIDGSLQQ WQDKLPSSQF VRVHRSYIVN
      msa141801.2{399_M781}      DDILLIEAMQ GKLIIQTPDK NYEIDGSLQQ WQDKLPSSQF VRVHRSYIVN
       msa141801.2{399_090}      DDILLIEAMQ GKLIIQTPDK NYEIDGSLQQ WQDKLPSSQF VRVHRSYIVN
    msa141801.2{399_18RS21}      DDILLIEAMQ GKLIIQTPDK NYEIDGSLQQ WQDKLPSSQF VRVHRSYIVN
      msa141801.2{399_2603}      DDILLIEAMQ GKLIIQTPDK NYEIDGSLQQ WQDKLPSSQF VRVHRSYIVN
      msa141801.2{399_A909}      DDILLIEAMQ GKLIIQTPDK NYEIDGSLQQ WQDKLPSSQF VRVHRSYIVN
      msa141801.2{399_H36B}      DDILLIEAMQ GKLIIQTPDK NYEIDGSLQQ WQDKLPSSQF VRVHRSYIVN
msa141801.2{399_JM9130013}      DDILLIEAMQ GKLIIQTPDK NYEIDGSLQQ WQDKLPSSQF VRVHRSYIVN
    msa141801.2{399_1169NT}      DDILLIEAMQ GKLIIQTPDK NYEIDGSLQQ WQDKLPSSQF VRVHRSYIVN
    msa141801.2{399_CJB110}      DDILLIEAMQ GKLIIQTPDK NYEIDGSLQQ WQDKLPSSQF VRVHRSYIVN
                  Consensus      ********** ********** ********** ********** **********

                                 201                                   243
      msa141801.2{399_COH1}      INAIKTIEPW FNQTLQLHLC NKITVPVSRA NVKPLKQMLg ist
      msa141801.2{399_M732}      INAIKTIEPW FNQTLQLHLC NKITVPVSRA NVKPLKQMLg ist
      msa141801.2{399_M781}      INAIKTIEPW FNQTLQLHLC NKITVPVSRA NVKPLKQMLg ist
       msa141801.2{399_090}      INAIKTIEPW FNQTLQLHLC NKITVPVSRA NVKPLKQMLg ist
    msa141801.2{399_18RS21}      INAIKTIEPW FNQTLQLHLC NKITVPVSRA NVKPLKQMLg ist
      msa141801.2{399_2603}      INAIKTIEPW FNQTLQLHLC NKITVPVSRA NVKPLKQMLg ist
      msa141801.2{399_A909}      INAIKTIEPW FNQTLQLHLC NKITVPVSRA NVKPLKQMLg ist
      msa141801.2{399_H36B}      INAIKTIEPW FNQTLQLHLC NKITVPVSRA NVKPLKQMLg ist
msa141801.2{399_JM9130013}      INAIKTIEPW FNQTLQLHLC NKITVPVSRA NVKPLKQMLg ist
    msa141801.2{399_1169NT}      INAIKTIEPW FNQTLQLHLC NKITVPVSRA NVKPLKQMLg ist
    msa141801.2{399_CJB110}      INAIKTIEPW FNQTLQLHLC NKITVPVSRA NVKPLKQML~ ~~~
                  Consensus      ********** ********** ********** *********- ---
```

Table 79: Comparative Sequences relating to SAG2150

SEQ ID NO. 7901
STRAIN 2603
ATGGGAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCCGGCACTCCTTTTGAAGGG
CGTGCCCTTTTTGACGTCAATCTGAAAATTGAAGATGCTTCCTATACCGCGTTCATTGGG
CACACAGGTTCTGGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCCTACA
AAAGGTGAGGTAATTGTCGATGATTTTTCTATTAAAGCAGGGGACAAGAACAAAGAAATC
AAATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCAATTTCCAGAAAGTCAGCTTTTTGAA
GAGACAGTTTTAAAGGATGTTGCTTTTGGACCACAAAATTTTGGTATTTCTCAGATTGAA
GCTGAAAGGCTGGCTGAAGAAAAATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGAT
AAAAATCCATTTGAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTA
GCGATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATCCTAAGGGA
AGAAAAGAATTAATGACTCTTTTTAAAAATCTTCATAAAAAAGGAATGACTATCGTCTTA
GTGACTCACTTAATGGACGATGTAGCGGATTATGCTGACTATGTGTATGTTTTAGAAGCA
GGGAAAGTAACCTTATCAGGACAACCAAAACAGATTTTTCAAGAAGTAGAACTTTTAGAA
AGTAAACAATTAGGAGTTCCCAAAATCACCAAGTTTGCTCAAAGACTATCTCATAAGGGA
TTAAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7902
STRAIN 090
GGAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCC
GGCACTCCTTTTGAAGGGCGTGCCCTTTTTGACGTCAATCTGAAAATTGA
AGATGCTTCCTATACCGCGTTCATTGGGCACACAGGTTCTGGAAAATCAA
CTATTATGCAACTTTTGAATGGTTTACATATTCCTACAAAAGGTGAGGTA
ATTGTCGATGATTTTTCTATTAAAGCAGGGGACAAGAACAAAGAAATCAA
ATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCAATTTCCAGAAAGTCAGC
TTTTTGAAGAGACAGTTTTAAAGGATGTTGCTTTTGGACCACAAAATTTT
GGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAAAATTAAGGTT
AGTTGGTATCAGTGAGGATTTATTCGATAAAAATCCATTTGAACTTTCTG
GAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGCGATGGAACCC
AAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATCCTAAGGGAAG
AAAAGAATTAATGACTCTTTTTAAAAATCTTCATAAAAAAGGAATGACTA
TCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTATGCTGACTAT
GTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGACAACCAAAACA
GATTTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTAGGAGTTCCCA
AAATCACCAAGTTTGCTCAAAGACTATCTCATAAGGGATTAAATTTACCT
AGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7903
STRAIN A909
GGAATTGAATTTAAAAATGTAAGTTATACCTATCAA
GCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTTGACGTCAATCTGAAAAT
TGAAGATGCTTCCTATACCGCGTTCATTGGGCACACAGGTTCTGGAAAAT
CAACTATTATGCAACTTTTGAATGGTTTACATATTCCTACAAAAGGTGAG
GTAATTGTCGATGATTTTTCTATTAAAGCAGGGGACAAGAACAAAGAAAT
CAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCAATTTCCAGAAAGTC
AGCTTTTTGAAGAGACAGTTTTAAAAGATGTTGCTTTTGGACCACAAAAT
TTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAAAATTAAG
GTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAATCCATTTGAACTTT
CTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGCGATGGAA
CCCAAAGTACTAGTACTAGATGAGCCAACAGCTGGACTTGATCCTAAGGG
AAGAAAAGAATTAATGACTCTTTTTAAAAATCTTCATAAAAAAGGAATGA
CTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTATGCTGAC
TATGTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGACAACCAAA
GCAGATTTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTAGGAGTTC
CCAAAATCACCAAGTTTGCTCAAAGGCTATCTCATAAGGGATTAAATTTA
CCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTAAGCATGG
A

SEQ ID NO. 7904
STRAIN H36B
GGAATTGAATTTAAAAATGTAAGTTATAC
CTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTTGACGTCAATC
TGAAAATTGAAGATGCTTCCTATACCGCGTTCATTGGGCACACAGGTTCT
GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCCTACAAA
AGGTGAGGTAATTGTCGATGATTTTTCTATTAAAGCAGGGGACAAGAACA
AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCAATTTCCA
GAAAGTCAGCTTTTTGAAGAGACAGTTTTAAAAGATGTTGCTTTTGGACC
ACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAATCCATTT
GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGC
GATGGAACCCAAAGTACTAGTACTAGATGAGCCAACAGCTGGACTTGATC
CTAAGGGAAGAAAAGAATTAATGACTCTTTTTAAAAATCTTCATAAAAAA
GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
TGCTGACTATGTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGAC
AACCAAAGCAGATTTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTA
GGAGTTCCCAAAATCACCAAGTTTGCTCAAAGGCTATCTCATAAGGGATT
AAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTA
AGCATGGA

SEQ ID NO. 7905
STRAIN 18RS21
GGAATTGAATTTAAAAATGTAAGTTATAC
CTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTTGACGTCAATC

Table 79: Comparative Sequences relating to SAG2150

TGAAAATTGAAGATGCTTCCTATACCGCGTTCATTGGGCACACAGGTTCT
GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCCTACAAA
AGGTGAGGTAATTGTCGATGATTTTTCTATTAAAGCAGGGGACAAGAACA
AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCAATTTCCA
GAAAGTCAGCTTTTTGAAGAGACAGTTTTAAAGGATGTTGCTTTTGGACC
ACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAATCCATTT
GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGC
GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
CTAAGGGAAGAAAAGAATTAATGACTCTTTTTAAAAATCTTCATAAAAAA
GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
TGCTGACTATGTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGAC
AACCAAAACAGATTTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTA
GGAGTTCCCAAAATCACCAAGTTTGCTCAAAGACTATCTCATAAGGGATT
AAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTA
AGCATGGA

SEQ ID NO. 7906
STRAIN M732
GGAATTGAATTTAAAAATGTAAGTTATAC
CTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTTGACGTCAATC
TGAAAATTGAAGATGTTTCCTATACCGCGTTCATTGGGCACACAGGTTCT
GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCCTACAAA
AGGTGAGGTAATTGTCGATGATTTTTCTATTAAAGCAGGGGACAAGAACA
AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCAATTTCCA
GAAAGTCAGCTTTTTGAAGAGACAGTTTTAAAGGATGTTGCTTTTGGACC
ACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAATCCATTT
GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGC
GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
CTAAGGGAAGAAAAGAATTAATGACTCTTTTTAAAAATCTTCATAAAAAA
GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
TGCTGACTATGTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGAC
AACCAAAACAGATTTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTA
GGAGTTCCCAAAATCACCAAGTTTGCTCAAAGACTATCTCATAAGGGATT
AAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTA
AGCATGGA

SEQ ID NO. 7907
STRAIN COH1
GGAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCC
GGCACTCCTTTTGAAGGGCGTGCCCTTTTTGACGTCAATCTGAAAATTGA
AGATGTTTCCTATACCGCGTTCATTGGGCACACAGGTTCTGGAAAATCAA
CTATTATGCAACTTTTGAATGGTTTACATATTCCTACAAAAGGTGAGGTA
ATTGTCGATGATTTTTCTATTAAAGCAGGGGACAAGAACAAAGAAATCAA
ATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCAATTTCCAGAAAGTCAGC
TTTTTGAAGAGACAGTTTTAAAGGATGTTGCTTTTGGACCACAAAATTTT
GGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAAAATTAAGGTT
AGTTGGTATCAGTGAGGATTTATTCGATAAAAATCCATTTGAACTTTCTG
GAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGCGATGGAACCC
AAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATCCTAAGGGAAG
AAAAGAATTAATGACTCTTTTTAAAAATCTTCATAAAAAAGGAATGACTA
TCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTATGCTGACTAT
GTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGACAACCAAAACA
GATTTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTAGGAGTTCCCA
AAATCACCAAGTTTGCTCAAAGACTATCTCATAAGGGATTAAATTTACCT
AGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7908
STRAIN M781
GGAATTGAATTTAAAAATGTAAGTTATAC
CTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTTGACGTCAATC
TGAAAATTGAAGATGTTTCCTATACCGCGTTCATTGGGCACACAGGTTCT
GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCCTACAAA
AGGTGAGGTAATTGTCGATGATTTTTCTATTAAAGCAGGGGACAAGAACA
AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCAATTTCCA
GAAAGTCAGCTTTTTGAAGAGACAGTTTTAAAGGATGTTGCTTTTGGACC
ACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAATCCATTT
GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGC
GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
CTAAGGGAAGAAAAGAATTAATGACTCTTTTTAAAAATCTTCATAAAAAA
GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
TGCTGACTATGTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGAC
AACCAAAACAGATTTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTA
GGAGTTCCCAAAATCACCAAGTTTGCTCAAAGACTATCTCATAAGGGATT
AAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTA
AGCATGGA

SEQ ID NO. 7909
STRAIN CJB110
GGAATTGAATTTAAAAATGTAAGTTATAC
CTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTTGACGTCAATC

Table 79: Comparative Sequences relating to SAG2150

TGAAAATTGAAGATGCTTCCTATACCGCGTTCATTGGGCACACAGGTTCT
GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCCTACAAA
AGGTGAGGTAATTGTCGATGATTTTTCTATTAAAGCAGGGGACAAGAACA
AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCAATTTCCA
GAAAGTCAGCTTTTTGAAGAGACAGTTTTAAAGGATGTTGCTTTTGGACC
ACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAATCCATTT
GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGC
GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
CTAAGGGAAGAAAAGAATTAATGACTCTTTTTAAAAATCTTCATAAAAAA
GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
TGCTGACTATGTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCAGGAC
AACCAAAACAGATTTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTA
GGAGTTCCCAAAATCACCAAGTTTGCTCAAAGACTATCTCATAAGGGATT
AAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTA
AGCATGGA

SEQ ID NO. 7910
STRAIN 1169NT
GGAATTGAATTTAAAAATGTAA
GTTATACCTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTTGAC
GTCAATCTGAAAATTGAAGATGCTTCCTATACCGCGTTCATTGGGCACAC
AGGTTCTGGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTC
CTACAAAAGGTGAGGTAATTGTCGATGATTTTTCTATTAAAGCAGGGGAC
AAGAACAAAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCA
ATTTCCAGAAAGTCAGCTTTTTGAAGAGACAGTTTTAAAGGATGTTGCTT
TTGGACCACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCT
GAAGAAAAATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAA
TCCATTTGAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTA
TTTTAGCGATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGA
CTTGATCCTAAGGGAAGAAAAGAATTAATGACTCTTTTTAAAAATCTTCA
TAAAAAAGGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAG
CGGATTATGCTGACTATGTGTATGTTTTAGAAGCAGGGAAAGTAACCTTA
TCAGGACAACCAAAACAGATTTTTCAAGAAGTAGAACTTTTAGAAAGTAA
ACAATTAGGAGTTCCCAAAATCACCAAGTTTGCTCAAAGACTATCTCATA
AGGGATTAAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAG
GCTATTAAGCATGGA

SEQ ID NO. 7911
STRAIN JM9130013
GGAATTGAATTTAAAAATGTAAGTT
ATACCTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTTGACGTT
AATCTGAAAATTGAAGATGCTTCCTATACCGCATTCATTGGGCACACAGG
TTCTGGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCCTA
CAAAAGGTGAGGTAATTGTCGATGATTTTTCTATTAAAGCAGGGGACAAG
AACAAAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTTCAATT
TCCAGAAAGTCAGCTTTTTGAAGAGACAGTTTTAAAGGATGTTGCTTTTG
GACCACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAA
GAAAAATTAAGGTTAGTTGGTATTAGTGAGGATTTATTCGATAAAAATCC
ATTTGAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTT
TAGCGATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTT
GATCCTAAGGGAAGAAAAGAATTAATGACTCTTTTTAAAAATCTTCATAA
AAAAGGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGG
ATTATGCTGACTATGTGTATGTTTTAGAAGCAGGGAAAGTAACCTTATCA
GGACAACCAAAACAGATTTTTCAAGAAGTAGAACTTTTAGAAAGTAAACA
ATTAGGAGTTCCCAAAATCACCAAGTTTGCTCAAAGACTATCTCATAAGG
GATTAAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCT
ATTAAGCATGGA

```
PRETTY of: /biotmp/msa238454.2{*}   May 14, 2003 06:55  ..

                               1                                                  50
      msa238454.2{401_A909}    ---GGAATTG AATTTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC
      msa238454.2{401_H36B}    ---GGAATTG AATTTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC
       msa238454.2{401_090}    ---GGAATTG AATTTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC
    msa238454.2{401_1169NT}    ---GGAATTG AATTTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC
    msa238454.2{401_18RS21}    ---GGAATTG AATTTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC
      msa238454.2{401_2603}    atgGGAATTG AATTTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC
    msa238454.2{401_CJB110}    ---GGAATTG AATTTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC
      msa238454.2{401_COH1}    ---GGAATTG AATTTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC
      msa238454.2{401_M732}    ---GGAATTG AATTTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC
      msa238454.2{401_M781}    ---GGAATTG AATTTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC
  msa238454.2{401_JM9130013}   ---GGAATTG AATTTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC
                  Consensus    ********** ********** ********** ********** **********

                               51                                                100
      msa238454.2{401_A909}    TTTTGAAGGG CGTGCCCTTT TTGACGTcAA TCTGAAAATT GAAGATGcTT
      msa238454.2{401_H36B}    TTTTGAAGGG CGTGCCCTTT TTGACGTcAA TCTGAAAATT GAAGATGcTT
       msa238454.2{401_090}    TTTTGAAGGG CGTGCCCTTT TTGACGTcAA TCTGAAAATT GAAGATGcTT
    msa238454.2{401_1169NT}    TTTTGAAGGG CGTGCCCTTT TTGACGTcAA TCTGAAAATT GAAGATGcTT
    msa238454.2{401_18RS21}    TTTTGAAGGG CGTGCCCTTT TTGACGTcAA TCTGAAAATT GAAGATGcTT
      msa238454.2{401_2603}    TTTTGAAGGG CGTGCCCTTT TTGACGTcAA TCTGAAAATT GAAGATGcTT
    msa238454.2{401_CJB110}    TTTTGAAGGG CGTGCCCTTT TTGACGTcAA TCTGAAAATT GAAGATGcTT
```

Table 79: Comparative Sequences relating to SAG2150

```
     msa238454.2{401_COH1}  TTTTGAAGGG CGTGCCCTTT TTGACGTcAA TCTGAAAATT GAAGATGtTT
     msa238454.2{401_M732}  TTTTGAAGGG CGTGCCCTTT TTGACGTcAA TCTGAAAATT GAAGATGtTT
     msa238454.2{401_M781}  TTTTGAAGGG CGTGCCCTTT TTGACGTcAA TCTGAAAATT GAAGATGtTT
msa238454.2{401_JM9130013}  TTTTGAAGGG CGTGCCCTTT TTGACGTtAA TCTGAAAATT GAAGATGcTT
                 Consensus  ********** ********** *******_** ********** *******_**

                            101                                                150
     msa238454.2{401_A909}  CCTATACCGC gTTCATTGGG CACACAGGTT CTGGAAAATC AACTATTATG
     msa238454.2{401_H36B}  CCTATACCGC gTTCATTGGG CACACAGGTT CTGGAAAATC AACTATTATG
      msa238454.2{401_090}  CCTATACCGC gTTCATTGGG CACACAGGTT CTGGAAAATC AACTATTATG
   msa238454.2{401_1169NT}  CCTATACCGC gTTCATTGGG CACACAGGTT CTGGAAAATC AACTATTATG
   msa238454.2{401_18RS21}  CCTATACCGC gTTCATTGGG CACACAGGTT CTGGAAAATC AACTATTATG
     msa238454.2{401_2603}  CCTATACCGC gTTCATTGGG CACACAGGTT CTGGAAAATC AACTATTATG
   msa238454.2{401_CJB110}  CCTATACCGC gTTCATTGGG CACACAGGTT CTGGAAAATC AACTATTATG
     msa238454.2{401_COH1}  CCTATACCGC gTTCATTGGG CACACAGGTT CTGGAAAATC AACTATTATG
     msa238454.2{401_M732}  CCTATACCGC gTTCATTGGG CACACAGGTT CTGGAAAATC AACTATTATG
     msa238454.2{401_M781}  CCTATACCGC gTTCATTGGG CACACAGGTT CTGGAAAATC AACTATTATG
msa238454.2{401_JM9130013}  CCTATACCGC aTTCATTGGG CACACAGGTT CTGGAAAATC AACTATTATG
                 Consensus  ********** _********* ********** ********** **********

                            151                                                200
     msa238454.2{401_A909}  CAACTTTTGA ATGGTTTACA TATTCCTACA AAAGGTGAGG TAATTGTCGA
     msa238454.2{401_H36B}  CAACTTTTGA ATGGTTTACA TATTCCTACA AAAGGTGAGG TAATTGTCGA
      msa238454.2{401_090}  CAACTTTTGA ATGGTTTACA TATTCCTACA AAAGGTGAGG TAATTGTCGA
   msa238454.2{401_1169NT}  CAACTTTTGA ATGGTTTACA TATTCCTACA AAAGGTGAGG TAATTGTCGA
   msa238454.2{401_18RS21}  CAACTTTTGA ATGGTTTACA TATTCCTACA AAAGGTGAGG TAATTGTCGA
     msa238454.2{401_2603}  CAACTTTTGA ATGGTTTACA TATTCCTACA AAAGGTGAGG TAATTGTCGA
   msa238454.2{401_CJB110}  CAACTTTTGA ATGGTTTACA TATTCCTACA AAAGGTGAGG TAATTGTCGA
     msa238454.2{401_COH1}  CAACTTTTGA ATGGTTTACA TATTCCTACA AAAGGTGAGG TAATTGTCGA
     msa238454.2{401_M732}  CAACTTTTGA ATGGTTTACA TATTCCTACA AAAGGTGAGG TAATTGTCGA
     msa238454.2{401_M781}  CAACTTTTGA ATGGTTTACA TATTCCTACA AAAGGTGAGG TAATTGTCGA
msa238454.2{401_JM9130013}  CAACTTTTGA ATGGTTTACA TATTCCTACA AAAGGTGAGG TAATTGTCGA
                 Consensus  ********** ********** ********** ********** **********

                            201                                                250
     msa238454.2{401_A909}  TGATTTTTCT ATTAAAGCAG GGGACAAGAA CAAAGAAATC AAATTTATAA
     msa238454.2{401_H36B}  TGATTTTTCT ATTAAAGCAG GGGACAAGAA CAAAGAAATC AAATTTATAA
      msa238454.2{401_090}  TGATTTTTCT ATTAAAGCAG GGGACAAGAA CAAAGAAATC AAATTTATAA
   msa238454.2{401_1169NT}  TGATTTTTCT ATTAAAGCAG GGGACAAGAA CAAAGAAATC AAATTTATAA
   msa238454.2{401_18RS21}  TGATTTTTCT ATTAAAGCAG GGGACAAGAA CAAAGAAATC AAATTTATAA
     msa238454.2{401_2603}  TGATTTTTCT ATTAAAGCAG GGGACAAGAA CAAAGAAATC AAATTTATAA
   msa238454.2{401_CJB110}  TGATTTTTCT ATTAAAGCAG GGGACAAGAA CAAAGAAATC AAATTTATAA
     msa238454.2{401_COH1}  TGATTTTTCT ATTAAAGCAG GGGACAAGAA CAAAGAAATC AAATTTATAA
     msa238454.2{401_M732}  TGATTTTTCT ATTAAAGCAG GGGACAAGAA CAAAGAAATC AAATTTATAA
     msa238454.2{401_M781}  TGATTTTTCT ATTAAAGCAG GGGACAAGAA CAAAGAAATC AAATTTATAA
msa238454.2{401_JM9130013}  TGATTTTTCT ATTAAAGCAG GGGACAAGAA CAAAGAAATC AAATTTATAA
                 Consensus  ********** ********** ********** ********** **********

                            251                                                300
     msa238454.2{401_A909}  GGCAAAAAGT TGGTTTAGTT TTTCAATTTC CAGAAAGTCA GCTTTTTGAA
     msa238454.2{401_H36B}  GGCAAAAAGT TGGTTTAGTT TTTCAATTTC CAGAAAGTCA GCTTTTTGAA
      msa238454.2{401_090}  GGCAAAAAGT TGGTTTAGTT TTTCAATTTC CAGAAAGTCA GCTTTTTGAA
   msa238454.2{401_1169NT}  GGCAAAAAGT TGGTTTAGTT TTTCAATTTC CAGAAAGTCA GCTTTTTGAA
   msa238454.2{401_18RS21}  GGCAAAAAGT TGGTTTAGTT TTTCAATTTC CAGAAAGTCA GCTTTTTGAA
     msa238454.2{401_2603}  GGCAAAAAGT TGGTTTAGTT TTTCAATTTC CAGAAAGTCA GCTTTTTGAA
   msa238454.2{401_CJB110}  GGCAAAAAGT TGGTTTAGTT TTTCAATTTC CAGAAAGTCA GCTTTTTGAA
     msa238454.2{401_COH1}  GGCAAAAAGT TGGTTTAGTT TTTCAATTTC CAGAAAGTCA GCTTTTTGAA
     msa238454.2{401_M732}  GGCAAAAAGT TGGTTTAGTT TTTCAATTTC CAGAAAGTCA GCTTTTTGAA
     msa238454.2{401_M781}  GGCAAAAAGT TGGTTTAGTT TTTCAATTTC CAGAAAGTCA GCTTTTTGAA
msa238454.2{401_JM9130013}  GGCAAAAAGT TGGTTTAGTT TTTCAATTTC CAGAAAGTCA GCTTTTTGAA
                 Consensus  ********** ********** ********** ********** **********

                            301                                                350
     msa238454.2{401_A909}  GAGACAGTTT TAAAaGATGT TGCTTTTGGA CCACAAAATT TTGGTATTTC
     msa238454.2{401_H36B}  GAGACAGTTT TAAAaGATGT TGCTTTTGGA CCACAAAATT TTGGTATTTC
      msa238454.2{401_090}  GAGACAGTTT TAAAgGATGT TGCTTTTGGA CCACAAAATT TTGGTATTTC
   msa238454.2{401_1169NT}  GAGACAGTTT TAAAgGATGT TGCTTTTGGA CCACAAAATT TTGGTATTTC
   msa238454.2{401_18RS21}  GAGACAGTTT TAAAgGATGT TGCTTTTGGA CCACAAAATT TTGGTATTTC
     msa238454.2{401_2603}  GAGACAGTTT TAAAgGATGT TGCTTTTGGA CCACAAAATT TTGGTATTTC
   msa238454.2{401_CJB110}  GAGACAGTTT TAAAgGATGT TGCTTTTGGA CCACAAAATT TTGGTATTTC
     msa238454.2{401_COH1}  GAGACAGTTT TAAAgGATGT TGCTTTTGGA CCACAAAATT TTGGTATTTC
     msa238454.2{401_M732}  GAGACAGTTT TAAAgGATGT TGCTTTTGGA CCACAAAATT TTGGTATTTC
     msa238454.2{401_M781}  GAGACAGTTT TAAAgGATGT TGCTTTTGGA CCACAAAATT TTGGTATTTC
msa238454.2{401_JM9130013}  GAGACAGTTT TAAAgGATGT TGCTTTTGGA CCACAAAATT TTGGTATTTC
                 Consensus  ********** ****_***** ********** ********** **********

                            351                                                400
     msa238454.2{401_A909}  TCAGATTGAA GCTGAAAGGC TGGCTGAAGA AAAATTAAGG TTAGTTGGTA
     msa238454.2{401_H36B}  TCAGATTGAA GCTGAAAGGC TGGCTGAAGA AAAATTAAGG TTAGTTGGTA
      msa238454.2{401_090}  TCAGATTGAA GCTGAAAGGC TGGCTGAAGA AAAATTAAGG TTAGTTGGTA
   msa238454.2{401_1169NT}  TCAGATTGAA GCTGAAAGGC TGGCTGAAGA AAAATTAAGG TTAGTTGGTA
   msa238454.2{401_18RS21}  TCAGATTGAA GCTGAAAGGC TGGCTGAAGA AAAATTAAGG TTAGTTGGTA
     msa238454.2{401_2603}  TCAGATTGAA GCTGAAAGGC TGGCTGAAGA AAAATTAAGG TTAGTTGGTA
```

Table 79: Comparative Sequences relating to SAG2150

```
    msa238454.2{401_CJB110}  TCAGATTGAA GCTGAAAGGC TGGCTGAAGA AAAATTAAGG TTAGTTGGTA
      msa238454.2{401_COH1}  TCAGATTGAA GCTGAAAGGC TGGCTGAAGA AAAATTAAGG TTAGTTGGTA
      msa238454.2{401_M732}  TCAGATTGAA GCTGAAAGGC TGGCTGAAGA AAAATTAAGG TTAGTTGGTA
      msa238454.2{401_M781}  TCAGATTGAA GCTGAAAGGC TGGCTGAAGA AAAATTAAGG TTAGTTGGTA
 msa238454.2{401_JM9130013}  TCAGATTGAA GCTGAAAGGC TGGCTGAAGA AAAATTAAGG TTAGTTGGTA
                  Consensus  ********** ********** ********** ********** **********

                             401                                               450
      msa238454.2{401_A909}  TcAGTGAGGA TTTATTCGAT AAAAATCCAT TTGAACTTTC TGGAGGGCAG
      msa238454.2{401_H36B}  TcAGTGAGGA TTTATTCGAT AAAAATCCAT TTGAACTTTC TGGAGGGCAG
       msa238454.2{401_090}  TcAGTGAGGA TTTATTCGAT AAAAATCCAT TTGAACTTTC TGGAGGGCAG
    msa238454.2{401_1169NT}  TcAGTGAGGA TTTATTCGAT AAAAATCCAT TTGAACTTTC TGGAGGGCAG
    msa238454.2{401_18RS21}  TcAGTGAGGA TTTATTCGAT AAAAATCCAT TTGAACTTTC TGGAGGGCAG
      msa238454.2{401_2603}  TcAGTGAGGA TTTATTCGAT AAAAATCCAT TTGAACTTTC TGGAGGGCAG
    msa238454.2{401_CJB110}  TcAGTGAGGA TTTATTCGAT AAAAATCCAT TTGAACTTTC TGGAGGGCAG
      msa238454.2{401_COH1}  TcAGTGAGGA TTTATTCGAT AAAAATCCAT TTGAACTTTC TGGAGGGCAG
      msa238454.2{401_M732}  TcAGTGAGGA TTTATTCGAT AAAAATCCAT TTGAACTTTC TGGAGGGCAG
      msa238454.2{401_M781}  TcAGTGAGGA TTTATTCGAT AAAAATCCAT TTGAACTTTC TGGAGGGCAG
 msa238454.2{401_JM9130013}  TtAGTGAGGA TTTATTCGAT AAAAATCCAT TTGAACTTTC TGGAGGGCAG
                  Consensus  *-******** ********** ********** ********** **********

                             451                                               500
      msa238454.2{401_A909}  ATGAGGCGGG TTGCTATAGC TGGTATTTTA GCGATGGAAC CCAAAGTACT
      msa238454.2{401_H36B}  ATGAGGCGGG TTGCTATAGC TGGTATTTTA GCGATGGAAC CCAAAGTACT
       msa238454.2{401_090}  ATGAGGCGGG TTGCTATAGC TGGTATTTTA GCGATGGAAC CCAAAGTACT
    msa238454.2{401_1169NT}  ATGAGGCGGG TTGCTATAGC TGGTATTTTA GCGATGGAAC CCAAAGTACT
    msa238454.2{401_18RS21}  ATGAGGCGGG TTGCTATAGC TGGTATTTTA GCGATGGAAC CCAAAGTACT
      msa238454.2{401_2603}  ATGAGGCGGG TTGCTATAGC TGGTATTTTA GCGATGGAAC CCAAAGTACT
    msa238454.2{401_CJB110}  ATGAGGCGGG TTGCTATAGC TGGTATTTTA GCGATGGAAC CCAAAGTACT
      msa238454.2{401_COH1}  ATGAGGCGGG TTGCTATAGC TGGTATTTTA GCGATGGAAC CCAAAGTACT
      msa238454.2{401_M732}  ATGAGGCGGG TTGCTATAGC TGGTATTTTA GCGATGGAAC CCAAAGTACT
      msa238454.2{401_M781}  ATGAGGCGGG TTGCTATAGC TGGTATTTTA GCGATGGAAC CCAAAGTACT
 msa238454.2{401_JM9130013}  ATGAGGCGGG TTGCTATAGC TGGTATTTTA GCGATGGAAC CCAAAGTACT
                  Consensus  ********** ********** ********** ********** **********

                             501                                               550
      msa238454.2{401_A909}  AGTACTaGAT GAGCCAACAG CTGGACTTGA TCCTAAGGGA AGAAAAGAAT
      msa238454.2{401_H36B}  AGTACTaGAT GAGCCAACAG CTGGACTTGA TCCTAAGGGA AGAAAAGAAT
       msa238454.2{401_090}  AGTACTgGAT GAGCCAACAG CTGGACTTGA TCCTAAGGGA AGAAAAGAAT
    msa238454.2{401_1169NT}  AGTACTgGAT GAGCCAACAG CTGGACTTGA TCCTAAGGGA AGAAAAGAAT
    msa238454.2{401_18RS21}  AGTACTgGAT GAGCCAACAG CTGGACTTGA TCCTAAGGGA AGAAAAGAAT
      msa238454.2{401_2603}  AGTACTgGAT GAGCCAACAG CTGGACTTGA TCCTAAGGGA AGAAAAGAAT
    msa238454.2{401_CJB110}  AGTACTgGAT GAGCCAACAG CTGGACTTGA TCCTAAGGGA AGAAAAGAAT
      msa238454.2{401_COH1}  AGTACTgGAT GAGCCAACAG CTGGACTTGA TCCTAAGGGA AGAAAAGAAT
      msa238454.2{401_M732}  AGTACTgGAT GAGCCAACAG CTGGACTTGA TCCTAAGGGA AGAAAAGAAT
      msa238454.2{401_M781}  AGTACTgGAT GAGCCAACAG CTGGACTTGA TCCTAAGGGA AGAAAAGAAT
 msa238454.2{401_JM9130013}  AGTACTgGAT GAGCCAACAG CTGGACTTGA TCCTAAGGGA AGAAAAGAAT
                  Consensus  ******-*** ********** ********** ********** **********

                             551                                               600
      msa238454.2{401_A909}  TAATGACTCT TTTTAAAAAT CTTCATAAAA AAGGAATGAC TATCGTCTTA
      msa238454.2{401_H36B}  TAATGACTCT TTTTAAAAAT CTTCATAAAA AAGGAATGAC TATCGTCTTA
       msa238454.2{401_090}  TAATGACTCT TTTTAAAAAT CTTCATAAAA AAGGAATGAC TATCGTCTTA
    msa238454.2{401_1169NT}  TAATGACTCT TTTTAAAAAT CTTCATAAAA AAGGAATGAC TATCGTCTTA
    msa238454.2{401_18RS21}  TAATGACTCT TTTTAAAAAT CTTCATAAAA AAGGAATGAC TATCGTCTTA
      msa238454.2{401_2603}  TAATGACTCT TTTTAAAAAT CTTCATAAAA AAGGAATGAC TATCGTCTTA
    msa238454.2{401_CJB110}  TAATGACTCT TTTTAAAAAT CTTCATAAAA AAGGAATGAC TATCGTCTTA
      msa238454.2{401_COH1}  TAATGACTCT TTTTAAAAAT CTTCATAAAA AAGGAATGAC TATCGTCTTA
      msa238454.2{401_M732}  TAATGACTCT TTTTAAAAAT CTTCATAAAA AAGGAATGAC TATCGTCTTA
      msa238454.2{401_M781}  TAATGACTCT TTTTAAAAAT CTTCATAAAA AAGGAATGAC TATCGTCTTA
 msa238454.2{401_JM9130013}  TAATGACTCT TTTTAAAAAT CTTCATAAAA AAGGAATGAC TATCGTCTTA
                  Consensus  ********** ********** ********** ********** **********

                             601                                               650
      msa238454.2{401_A909}  GTGACTCACT TAATGGACGA TGTAGCGGAT TATGCTGACT ATGTGTATGT
      msa238454.2{401_H36B}  GTGACTCACT TAATGGACGA TGTAGCGGAT TATGCTGACT ATGTGTATGT
       msa238454.2{401_090}  GTGACTCACT TAATGGACGA TGTAGCGGAT TATGCTGACT ATGTGTATGT
    msa238454.2{401_1169NT}  GTGACTCACT TAATGGACGA TGTAGCGGAT TATGCTGACT ATGTGTATGT
    msa238454.2{401_18RS21}  GTGACTCACT TAATGGACGA TGTAGCGGAT TATGCTGACT ATGTGTATGT
      msa238454.2{401_2603}  GTGACTCACT TAATGGACGA TGTAGCGGAT TATGCTGACT ATGTGTATGT
    msa238454.2{401_CJB110}  GTGACTCACT TAATGGACGA TGTAGCGGAT TATGCTGACT ATGTGTATGT
      msa238454.2{401_COH1}  GTGACTCACT TAATGGACGA TGTAGCGGAT TATGCTGACT ATGTGTATGT
      msa238454.2{401_M732}  GTGACTCACT TAATGGACGA TGTAGCGGAT TATGCTGACT ATGTGTATGT
      msa238454.2{401_M781}  GTGACTCACT TAATGGACGA TGTAGCGGAT TATGCTGACT ATGTGTATGT
 msa238454.2{401_JM9130013}  GTGACTCACT TAATGGACGA TGTAGCGGAT TATGCTGACT ATGTGTATGT
                  Consensus  ********** ********** ********** ********** **********

                             651                                               700
      msa238454.2{401_A909}  TTTAGAAGCA GGGAAAGTAA CCTTATCAGG ACAACCAAAg CAGATTTTTC
      msa238454.2{401_H36B}  TTTAGAAGCA GGGAAAGTAA CCTTATCAGG ACAACCAAAg CAGATTTTTC
       msa238454.2{401_090}  TTTAGAAGCA GGGAAAGTAA CCTTATCAGG ACAACCAAAa CAGATTTTTC
    msa238454.2{401_1169NT}  TTTAGAAGCA GGGAAAGTAA CCTTATCAGG ACAACCAAAa CAGATTTTTC
    msa238454.2{401_18RS21}  TTTAGAAGCA GGGAAAGTAA CCTTATCAGG ACAACCAAAa CAGATTTTTC
```

Table 79: Comparative Sequences relating to SAG2150

```
     msa238454.2{401_2603}  TTTAGAAGCA GGGAAAGTAA CCTTATCAGG ACAACCAAAa CAGATTTTTC
   msa238454.2{401_CJB110}  TTTAGAAGCA GGGAAAGTAA CCTTATCAGG ACAACCAAAa CAGATTTTTC
     msa238454.2{401_COH1}  TTTAGAAGCA GGGAAAGTAA CCTTATCAGG ACAACCAAAa CAGATTTTTC
     msa238454.2{401_M732}  TTTAGAAGCA GGGAAAGTAA CCTTATCAGG ACAACCAAAa CAGATTTTTC
     msa238454.2{401_M781}  TTTAGAAGCA GGGAAAGTAA CCTTATCAGG ACAACCAAAa CAGATTTTTC
msa238454.2{401_JM9130013}  TTTAGAAGCA GGGAAAGTAA CCTTATCAGG ACAACCAAAa CAGATTTTTC
                 Consensus  ********** ********** ********** *********_ **********

                            701                                                750
     msa238454.2{401_A909}  AAGAAGTAGA ACTTTTAGAA AGTAAACAAT TAGGAGTTCC CAAAATCACC
     msa238454.2{401_H36B}  AAGAAGTAGA ACTTTTAGAA AGTAAACAAT TAGGAGTTCC CAAAATCACC
      msa238454.2{401_090}  AAGAAGTAGA ACTTTTAGAA AGTAAACAAT TAGGAGTTCC CAAAATCACC
   msa238454.2{401_1169NT}  AAGAAGTAGA ACTTTTAGAA AGTAAACAAT TAGGAGTTCC CAAAATCACC
   msa238454.2{401_18RS21}  AAGAAGTAGA ACTTTTAGAA AGTAAACAAT TAGGAGTTCC CAAAATCACC
     msa238454.2{401_2603}  AAGAAGTAGA ACTTTTAGAA AGTAAACAAT TAGGAGTTCC CAAAATCACC
   msa238454.2{401_CJB110}  AAGAAGTAGA ACTTTTAGAA AGTAAACAAT TAGGAGTTCC CAAAATCACC
     msa238454.2{401_COH1}  AAGAAGTAGA ACTTTTAGAA AGTAAACAAT TAGGAGTTCC CAAAATCACC
     msa238454.2{401_M732}  AAGAAGTAGA ACTTTTAGAA AGTAAACAAT TAGGAGTTCC CAAAATCACC
     msa238454.2{401_M781}  AAGAAGTAGA ACTTTTAGAA AGTAAACAAT TAGGAGTTCC CAAAATCACC
msa238454.2{401_JM9130013}  AAGAAGTAGA ACTTTTAGAA AGTAAACAAT TAGGAGTTCC CAAAATCACC
                 Consensus  ********** ********** ********** ********** **********

                            751                                                800
     msa238454.2{401_A909}  AAGTTTGCTC AAAGgCTATC TCATAAGGGA TTAAATTTAC CTAGTTTACC
     msa238454.2{401_H36B}  AAGTTTGCTC AAAGgCTATC TCATAAGGGA TTAAATTTAC CTAGTTTACC
      msa238454.2{401_090}  AAGTTTGCTC AAAGaCTATC TCATAAGGGA TTAAATTTAC CTAGTTTACC
   msa238454.2{401_1169NT}  AAGTTTGCTC AAAGaCTATC TCATAAGGGA TTAAATTTAC CTAGTTTACC
   msa238454.2{401_18RS21}  AAGTTTGCTC AAAGaCTATC TCATAAGGGA TTAAATTTAC CTAGTTTACC
     msa238454.2{401_2603}  AAGTTTGCTC AAAGaCTATC TCATAAGGGA TTAAATTTAC CTAGTTTACC
   msa238454.2{401_CJB110}  AAGTTTGCTC AAAGaCTATC TCATAAGGGA TTAAATTTAC CTAGTTTACC
     msa238454.2{401_COH1}  AAGTTTGCTC AAAGaCTATC TCATAAGGGA TTAAATTTAC CTAGTTTACC
     msa238454.2{401_M732}  AAGTTTGCTC AAAGaCTATC TCATAAGGGA TTAAATTTAC CTAGTTTACC
     msa238454.2{401_M781}  AAGTTTGCTC AAAGaCTATC TCATAAGGGA TTAAATTTAC CTAGTTTACC
msa238454.2{401_JM9130013}  AAGTTTGCTC AAAGaCTATC TCATAAGGGA TTAAATTTAC CTAGTTTACC
                 Consensus  ********** ****_***** ********** ********** **********

                            801                                     840
     msa238454.2{401_A909}  AATTACTATT AACGAATTTG TGGAGGCTAT TAAGCATGGA
     msa238454.2{401_H36B}  AATTACTATT AACGAATTTG TGGAGGCTAT TAAGCATGGA
      msa238454.2{401_090}  AATTACTATT AACGAATTTG TGGAGGCTAT TAAGCATGGA
   msa238454.2{401_1169NT}  AATTACTATT AACGAATTTG TGGAGGCTAT TAAGCATGGA
   msa238454.2{401_18RS21}  AATTACTATT AACGAATTTG TGGAGGCTAT TAAGCATGGA
     msa238454.2{401_2603}  AATTACTATT AACGAATTTG TGGAGGCTAT TAAGCATGGA
   msa238454.2{401_CJB110}  AATTACTATT AACGAATTTG TGGAGGCTAT TAAGCATGGA
     msa238454.2{401_COH1}  AATTACTATT AACGAATTTG TGGAGGCTAT TAAGCATGGA
     msa238454.2{401_M732}  AATTACTATT AACGAATTTG TGGAGGCTAT TAAGCATGGA
     msa238454.2{401_M781}  AATTACTATT AACGAATTTG TGGAGGCTAT TAAGCATGGA
msa238454.2{401_JM9130013}  AATTACTATT AACGAATTTG TGGAGGCTAT TAAGCATGGA
                 Consensus  ********** ********** ********** **********
```

SEQ ID NO. 7912
STRAIN 2603 frame: 1
MGIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
ERLAEEKLRLVGISEDLFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7913
STRAIN 090 frame: 1
GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
ERLAEEKLRLVGISEDLFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7914
STRAIN 090 frame: 1
GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
ERLAEEKLRLVGISEDLFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7915
STRAIN H36B frame: 1
GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
ERLAEEKLRLVGISEDLFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7916

Table 79: Comparative Sequences relating to SAG2150

STRAIN 18RS21 frame: 1
GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
ERLAEEKLRLVGISEDLFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7917
STRAIN M732 frame: 1
GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDVSYTAFIGHTGSGKSTIMQLLNGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
ERLAEEKLRLVGISEDLFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7918
STRAIN COH1 frame: 1
GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDVSYTAFIGHTGSGKSTIMQLLNGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
ERLAEEKLRLVGISEDLFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7919
STRAIN M781 frame: 1
GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDVSYTAFIGHTGSGKSTIMQLLNGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
ERLAEEKLRLVGISEDLFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7920
STRAIN CJB110 frame: 1
GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
ERLAEEKLRLVGISEDLFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7921
STRAIN 1169NT frame: 1
GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
ERLAEEKLRLVGISEDLFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

SEQ ID NO. 7922
STRAIN JM9130013 frame: 1
GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
ERLAEEKLRLVGISEDLFDKNPFELSGGQMRRVAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
KQLGVPKITKFAQRLSHKGLNLPSLPITINEFVEAIKHG

```
PRETTY of: /biotmp/msa238553.2{*}   May 14, 2003 06:55  ..

                                1                                                  50
       msa238553.2{401_090}   ~GIEFKNVSY TYQAGTPFEG RALFDVNLKI EDaSYTAFIG HTGSGKSTIM
    msa238553.2{401_1169NT}   ~GIEFKNVSY TYQAGTPFEG RALFDVNLKI EDaSYTAFIG HTGSGKSTIM
    msa238553.2{401_18RS21}   ~GIEFKNVSY TYQAGTPFEG RALFDVNLKI EDaSYTAFIG HTGSGKSTIM
      msa238553.2{401_2603}   mGIEFKNVSY TYQAGTPFEG RALFDVNLKI EDaSYTAFIG HTGSGKSTIM
    msa238553.2{401_CJB110}   ~GIEFKNVSY TYQAGTPFEG RALFDVNLKI EDaSYTAFIG HTGSGKSTIM
      msa238553.2{401_H36B}   ~GIEFKNVSY TYQAGTPFEG RALFDVNLKI EDaSYTAFIG HTGSGKSTIM
 msa238553.2{401_JM9130013}   ~GIEFKNVSY TYQAGTPFEG RALFDVNLKI EDaSYTAFIG HTGSGKSTIM
      msa238553.2{401_COH1}   ~GIEFKNVSY TYQAGTPFEG RALFDVNLKI EDvSYTAFIG HTGSGKSTIM
      msa238553.2{401_M732}   ~GIEFKNVSY TYQAGTPFEG RALFDVNLKI EDvSYTAFIG HTGSGKSTIM
      msa238553.2{401_M781}   ~GIEFKNVSY TYQAGTPFEG RALFDVNLKI EDvSYTAFIG HTGSGKSTIM
                  Consensus   ********** ********** ********** **_******* **********

                                51                                                100
       msa238553.2{401_090}   QLLNGLHIPT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
    msa238553.2{401_1169NT}   QLLNGLHIPT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
    msa238553.2{401_18RS21}   QLLNGLHIPT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
      msa238553.2{401_2603}   QLLNGLHIPT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
    msa238553.2{401_CJB110}   QLLNGLHIPT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
      msa238553.2{401_H36B}   QLLNGLHIPT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
 msa238553.2{401_JM9130013}   QLLNGLHIPT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
      msa238553.2{401_COH1}   QLLNGLHIPT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
      msa238553.2{401_M732}   QLLNGLHIPT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
      msa238553.2{401_M781}   QLLNGLHIPT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
```

Table 79: Comparative Sequences relating to SAG2150

```
                 Consensus  ********** ********** ********** ********** **********

                            101                                               150
         msa238553.2{401_090}  ETVLKDVAFG PQNFGISQIE AERLAEEKLR LVGISEDLFD KNPFELSGGQ
      msa238553.2{401_1169NT}  ETVLKDVAFG PQNFGISQIE AERLAEEKLR LVGISEDLFD KNPFELSGGQ
      msa238553.2{401_18RS21}  ETVLKDVAFG PQNFGISQIE AERLAEEKLR LVGISEDLFD KNPFELSGGQ
        msa238553.2{401_2603}  ETVLKDVAFG PQNFGISQIE AERLAEEKLR LVGISEDLFD KNPFELSGGQ
      msa238553.2{401_CJB110}  ETVLKDVAFG PQNFGISQIE AERLAEEKLR LVGISEDLFD KNPFELSGGQ
        msa238553.2{401_H36B}  ETVLKDVAFG PQNFGISQIE AERLAEEKLR LVGISEDLFD KNPFELSGGQ
    msa238553.2{401_JM9130013}  ETVLKDVAFG PQNFGISQIE AERLAEEKLR LVGISEDLFD KNPFELSGGQ
        msa238553.2{401_COH1}  ETVLKDVAFG PQNFGISQIE AERLAEEKLR LVGISEDLFD KNPFELSGGQ
        msa238553.2{401_M732}  ETVLKDVAFG PQNFGISQIE AERLAEEKLR LVGISEDLFD KNPFELSGGQ
        msa238553.2{401_M781}  ETVLKDVAFG PQNFGISQIE AERLAEEKLR LVGISEDLFD KNPFELSGGQ
                    Consensus  ********** ********** ********** ********** **********

                               151                                               200
         msa238553.2{401_090}  MRRVAIAGIL AMEPKVLVLD EPTAGLDPKG RKELMTLFKN LHKKGMTIVL
      msa238553.2{401_1169NT}  MRRVAIAGIL AMEPKVLVLD EPTAGLDPKG RKELMTLFKN LHKKGMTIVL
      msa238553.2{401_18RS21}  MRRVAIAGIL AMEPKVLVLD EPTAGLDPKG RKELMTLFKN LHKKGMTIVL
        msa238553.2{401_2603}  MRRVAIAGIL AMEPKVLVLD EPTAGLDPKG RKELMTLFKN LHKKGMTIVL
      msa238553.2{401_CJB110}  MRRVAIAGIL AMEPKVLVLD EPTAGLDPKG RKELMTLFKN LHKKGMTIVL
        msa238553.2{401_H36B}  MRRVAIAGIL AMEPKVLVLD EPTAGLDPKG RKELMTLFKN LHKKGMTIVL
    msa238553.2{401_JM9130013}  MRRVAIAGIL AMEPKVLVLD EPTAGLDPKG RKELMTLFKN LHKKGMTIVL
        msa238553.2{401_COH1}  MRRVAIAGIL AMEPKVLVLD EPTAGLDPKG RKELMTLFKN LHKKGMTIVL
        msa238553.2{401_M732}  MRRVAIAGIL AMEPKVLVLD EPTAGLDPKG RKELMTLFKN LHKKGMTIVL
        msa238553.2{401_M781}  MRRVAIAGIL AMEPKVLVLD EPTAGLDPKG RKELMTLFKN LHKKGMTIVL
                    Consensus  ********** ********** ********** ********** **********

                               201                                               250
         msa238553.2{401_090}  VTHLMDDVAD YADYVYVLEA GKVTLSGQPK QIFQEVELLE SKQLGVPKIT
      msa238553.2{401_1169NT}  VTHLMDDVAD YADYVYVLEA GKVTLSGQPK QIFQEVELLE SKQLGVPKIT
      msa238553.2{401_18RS21}  VTHLMDDVAD YADYVYVLEA GKVTLSGQPK QIFQEVELLE SKQLGVPKIT
        msa238553.2{401_2603}  VTHLMDDVAD YADYVYVLEA GKVTLSGQPK QIFQEVELLE SKQLGVPKIT
      msa238553.2{401_CJB110}  VTHLMDDVAD YADYVYVLEA GKVTLSGQPK QIFQEVELLE SKQLGVPKIT
        msa238553.2{401_H36B}  VTHLMDDVAD YADYVYVLEA GKVTLSGQPK QIFQEVELLE SKQLGVPKIT
    msa238553.2{401_JM9130013}  VTHLMDDVAD YADYVYVLEA GKVTLSGQPK QIFQEVELLE SKQLGVPKIT
        msa238553.2{401_COH1}  VTHLMDDVAD YADYVYVLEA GKVTLSGQPK QIFQEVELLE SKQLGVPKIT
        msa238553.2{401_M732}  VTHLMDDVAD YADYVYVLEA GKVTLSGQPK QIFQEVELLE SKQLGVPKIT
        msa238553.2{401_M781}  VTHLMDDVAD YADYVYVLEA GKVTLSGQPK QIFQEVELLE SKQLGVPKIT
                    Consensus  ********** ********** ********** ********** **********

                               251                         280
         msa238553.2{401_090}  KFAQRLSHKG LNLPSLPITI NEFVEAIKHG
      msa238553.2{401_1169NT}  KFAQRLSHKG LNLPSLPITI NEFVEAIKHG
      msa238553.2{401_18RS21}  KFAQRLSHKG LNLPSLPITI NEFVEAIKHG
        msa238553.2{401_2603}  KFAQRLSHKG LNLPSLPITI NEFVEAIKHG
      msa238553.2{401_CJB110}  KFAQRLSHKG LNLPSLPITI NEFVEAIKHG
        msa238553.2{401_H36B}  KFAQRLSHKG LNLPSLPITI NEFVEAIKHG
    msa238553.2{401_JM9130013}  KFAQRLSHKG LNLPSLPITI NEFVEAIKHG
        msa238553.2{401_COH1}  KFAQRLSHKG LNLPSLPITI NEFVEAIKHG
        msa238553.2{401_M732}  KFAQRLSHKG LNLPSLPITI NEFVEAIKHG
        msa238553.2{401_M781}  KFAQRLSHKG LNLPSLPITI NEFVEAIKHG
                    Consensus  ********** ********** **********
```

Table 80: Comparative Sequences relating to SAG1266

SEQ ID NO. 8001
STRAIN 2603
GTGAACCACTTACTTAACCTCAGTAAAGAAAATATAGCTAAAATAGATTTTGACTTTCTT
AATGAGGCACTTAATGCAAATATTCGTTTGAAAGAATTAGTAGATGAACTAAAAATTTCA
AAAGAACTGGACAGTAAAGGTTGGTCCAAAAAAGACTCTCGAACGATAAAAATCTTGTAC
GATGGCCTTATCAATAAACATATAGTTTCCCTAGATCGTGCAGATTATAACATTATCCAA
GTCATTCCATTTGCTAATGTACATGTACTACTGTTTTTAATACCAGAAAGGGAGAATTCT
AAAAATTATAGAATATACAACTACAGTGATTATGAAATGGAGTTAATCAATGAGGATAGG
CAACAATTTTCAAAATATGAAACAGTTGATTTAGACCAATTGATACTTGTTGATATTTTT
AATATTGATGACTACATTTCATCATATTTAACAATA

SEQ ID NO. 8002
STRAIN H36B
AACCACTTACTTAACCTCAGTAAAGAAAATATAGCT
AAAATAGATTTTGACTTTCTTAATGAGGCACTTAATGCAAATATTCGTTT
GAAAGAATTAGTAGATGAACTAAAAATTTCAAAAGAACTGGACAGTAAAG
GTTGGTCCAAAAAAGACTCTCGAACGATAAAAATCTTGTACGATGGCCTT
ATCAATAAACATATAGTTTCCCTAGATCGTGCAGATTATAACATTATCCA
AGTCATTCCATTTGCTAATGTACATGTACTACTGTTTTTAATACCAGAAA
GGGAGAATTCTAAAAATTATAgAATATACAACTACAGTGATTATGAAATG
GAGTTAATCAATGAGGATAGGCAACAATTTTCAAAATATGAAACAGTTGA
TTTAGACCAATTGATACTTGTTGATATTTTTAATATTGATGACTACATTT
CATCATATTTAACAATA

SEQ ID NO. 8003
STRAIN 18RS21
AACCACTTACTTAACCTCAGTAAAGAAAATATAG
CTAAAATAGATTTTGACTTTCTTAATGAGGCACTTAATGCAAATATTCGT
TTGAAAGAATTAGTAGATGAACTAAAAATTTCAAAAGAACTGGACAGTAA
AGGTTGGTCCAAAAAAGACTCTCGAACGATAAAAATCTTGTACGATGGCC
TTATCAATAAACATATAGTTTCCCTAGATCGTGCAGATTATAACATTATC
CAAGTCATTCCATTTGCTAATGTACATGTACTACTGTTTTTAATACCAGA
AAGGGAGAATTCTAAAAATTATAGAATATACAACTACAGTGATTATGAAA
TGGAGTTAATCAATGAGGATAGGCAACAATTTTCAAAATATGAAACAGTT
GATTTAGACCAATTGATACTTGTTGATATTTTTAATATTGATGACTACAT
TTCATCATATTTAACAATA

```
PRETTY of: /biotmp/msa49308.2{*}   February 19, 2003 07:45  ..

                          1                                                     50
msa49308.2{408_18RS21}    ---AACCACT TACTTAACCT CAGTAAAGAA AATATAGCTA AAATAGATTT
  msa49308.2{408_2603}    gtgAACCACT TACTTAACCT CAGTAAAGAA AATATAGCTA AAATAGATTT
  msa49308.2{408_H36B}    ---AACCACT TACTTAACCT CAGTAAAGAA AATATAGCTA AAATAGATTT
             Consensus    ********** ********** ********** ********** **********

                          51                                                   100
msa49308.2{408_18RS21}    TGACTTTCTT AATGAGGCAC TTAATGCAAA TATTCGTTTG AAAGAATTAG
  msa49308.2{408_2603}    TGACTTTCTT AATGAGGCAC TTAATGCAAA TATTCGTTTG AAAGAATTAG
  msa49308.2{408_H36B}    TGACTTTCTT AATGAGGCAC TTAATGCAAA TATTCGTTTG AAAGAATTAG
             Consensus    ********** ********** ********** ********** **********

                          101                                                  150
msa49308.2{408_18RS21}    TAGATGAACT AAAAATTTCA AAAGAACTGG ACAGTAAAGG TTGGTCCAAA
  msa49308.2{408_2603}    TAGATGAACT AAAAATTTCA AAAGAACTGG ACAGTAAAGG TTGGTCCAAA
  msa49308.2{408_H36B}    TAGATGAACT AAAAATTTCA AAAGAACTGG ACAGTAAAGG TTGGTCCAAA
             Consensus    ********** ********** ********** ********** **********

                          151                                                  200
msa49308.2{408_18RS21}    AAAGACTCTC GAACGATAAA AATCTTGTAC GATGGCCTTA TCAATAAACA
  msa49308.2{408_2603}    AAAGACTCTC GAACGATAAA AATCTTGTAC GATGGCCTTA TCAATAAACA
  msa49308.2{408_H36B}    AAAGACTCTC GAACGATAAA AATCTTGTAC GATGGCCTTA TCAATAAACA
             Consensus    ********** ********** ********** ********** **********

                          201                                                  250
msa49308.2{408_18RS21}    TATAGTTTCC CTAGATCGTG CAGATTATAA CATTATCCAA GTCATTCCAT
  msa49308.2{408_2603}    TATAGTTTCC CTAGATCGTG CAGATTATAA CATTATCCAA GTCATTCCAT
  msa49308.2{408_H36B}    TATAGTTTCC CTAGATCGTG CAGATTATAA CATTATCCAA GTCATTCCAT
             Consensus    ********** ********** ********** ********** **********

                          251                                                  300
msa49308.2{408_18RS21}    TTGCTAATGT ACATGTACTA CTGTTTTTAA TACCAGAAAG GGAGAATTCT
  msa49308.2{408_2603}    TTGCTAATGT ACATGTACTA CTGTTTTTAA TACCAGAAAG GGAGAATTCT
  msa49308.2{408_H36B}    TTGCTAATGT ACATGTACTA CTGTTTTTAA TACCAGAAAG GGAGAATTCT
             Consensus    ********** ********** ********** ********** **********

                          301                                                  350
msa49308.2{408_18RS21}    AAAAATTATA GAATATACAA CTACAGTGAT TATGAAATGG AGTTAATCAA
  msa49308.2{408_2603}    AAAAATTATA GAATATACAA CTACAGTGAT TATGAAATGG AGTTAATCAA
  msa49308.2{408_H36B}    AAAAATTATA GAATATACAA CTACAGTGAT TATGAAATGG AGTTAATCAA
             Consensus    ********** ********** ********** ********** **********
```

Table 80: Comparative Sequences relating to SAG1266

```
                       351                                                    400
msa49308.2{408_18RS21} TGAGGATAGG CAACAATTTT CAAAATATGA AACAGTTGAT TTAGACCAAT
  msa49308.2{408_2603} TGAGGATAGG CAACAATTTT CAAAATATGA AACAGTTGAT TTAGACCAAT
  msa49308.2{408_H36B} TGAGGATAGG CAACAATTTT CAAAATATGA AACAGTTGAT TTAGACCAAT
             Consensus ********** ********** ********** ********** **********

                       401                                                    450
msa49308.2{408_18RS21} TGATACTTGT TGATATTTTT AATATTGATG ACTACATTTC ATCATATTTA
  msa49308.2{408_2603} TGATACTTGT TGATATTTTT AATATTGATG ACTACATTTC ATCATATTTA
  msa49308.2{408_H36B} TGATACTTGT TGATATTTTT AATATTGATG ACTACATTTC ATCATATTTA
             Consensus ********** ********** ********** ********** **********

                       451
msa49308.2{408_18RS21} ACAATA
  msa49308.2{408_2603} ACAATA
  msa49308.2{408_H36B} ACAATA
             Consensus ******
```

SEQ ID NO. 8004
STRAIN 2603 frame: 1

```
VNHLLNLSKENIAKIDFDFLNEALNANIRLKELVDELKISKELDSKGWSKKDSRTIKILY
DGLINKHIVSLDRADYNIIQVIPFANVHVLLFLIPERENSKNYRIYNYSDYEMELINEDR
QQFSKYETVDLDQLILVDIFNIDDYISSYLTI
```

SEQ ID NO. 8005
STRAIN H36B frame: 1

```
NHLLNLSKENIAKIDFDFLNEALNANIRLKELVDELKISKELDSKGWSKKDSRTIKILYD
GLINKHIVSLDRADYNIIQVIPFANVHVLLFLIPERENSKNYRIYNYSDYEMELINEDRQ
QFSKYETVDLDQLILVDIFNIDDYISSYLTI
```

SEQ ID NO. 8006
STRAIN 18RS21 frame: 1

```
NHLLNLSKENIAKIDFDFLNEALNANIRLKELVDELKISKELDSKGWSKKDSRTIKILYD
GLINKHIVSLDRADYNIIQVIPFANVHVLLFLIPERENSKNYRIYNYSDYEMELINEDRQ
QFSKYETVDLDQLILVDIFNIDDYISSYLTI
```

```
PRETTY of: /biotmp/msa49418.2{*}    February 19, 2003 07:47  ..

                       1                                                       50
msa49418.2{408_18RS21} -NHLLNLSKE NIAKIDFDFL NEALNANIRL KELVDELKIS KELDSKGWSK
  msa49418.2{408_2603} vNHLLNLSKE NIAKIDFDFL NEALNANIRL KELVDELKIS KELDSKGWSK
  msa49418.2{408_H36B} -NHLLNLSKE NIAKIDFDFL NEALNANIRL KELVDELKIS KELDSKGWSK
             Consensus ********** ********** ********** ********** **********

                       51                                                     100
msa49418.2{408_18RS21} KDSRTIKILY DGLINKHIVS LDRADYNIIQ VIPFANVHVL LFLIPERENS
  msa49418.2{408_2603} KDSRTIKILY DGLINKHIVS LDRADYNIIQ VIPFANVHVL LFLIPERENS
  msa49418.2{408_H36B} KDSRTIKILY DGLINKHIVS LDRADYNIIQ VIPFANVHVL LFLIPERENS
             Consensus ********** ********** ********** ********** **********

                       101                                                    150
msa49418.2{408_18RS21} KNYRIYNYSD YEMELINEDR QQFSKYETVD LDQLILVDIF NIDDYISSYL
  msa49418.2{408_2603} KNYRIYNYSD YEMELINEDR QQFSKYETVD LDQLILVDIF NIDDYISSYL
  msa49418.2{408_H36B} KNYRIYNYSD YEMELINEDR QQFSKYETVD LDQLILVDIF NIDDYISSYL
             Consensus ********** ********** ********** ********** **********

                       151
msa49418.2{408_18RS21} TI
  msa49418.2{408_2603} TI
  msa49418.2{408_H36B} TI
             Consensus **
```

Table 81: Comparative Sequences relating to SAG0011

SEQ ID NO. 8101
STRAIN 090
AGCAAGCCTAATGTTGTTCAGTTAAA
TAATCAATATATTAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGG
AGTTACGCCGAAAAAATCGTTTAATGGGTTGGGTTCTTATTTTTGTCATG
CTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTT
ACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACAT
TAACTAATAGAACTGAGAACCAGAAGTTGCTAGCAAAACAACTAAAAAAT
CCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
CGGCGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8102
STRAIN A909
AGCAAGCCTAATGTTGTTCAGTTAAATAATCAATA
TATTAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGGAGTTACGCCGAAAAAATCG
TTTAATGGGTTGGGTTCTTATTTTTGTCATGCTtttATTTATTTTACCCACTTATAATTT
AGTTAAGAGTTACAGAACTTTACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGA
CTATCAGACATTAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAACTAAAAAA
TCCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGACCGGCGAAAT
GATTTACCCATTACCAGACCT

SEQ ID NO. 8103
STRAIN H36B
AGCAAGCCTAATGTTGTTCAGTTAAA
TAATCAATATATTAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGG
AGTTACGCCGAAAAAATCGTTTAATGGGTTGGGTTCTTATTTTTGTCATG
CTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTT
ACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACAT
TAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAACTAAAAAAT
CCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
CGGCGAAATGATTTACCCATTACCAGACCtTTTACCAAAA

SEQ ID NO. 8104
STRAIN 18RS21
AGCAAGCCTAATGTTGTTCAGTTAAATAATCAATATATTAACGATGAGAATCTAAAAAAA
CGTTACGAAGCTGAGGAGTTACGCCGAAAAAATCGTTTAATGGGTTGGGTTCTTATTTTT
GTCATGCTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTTACAA
GAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACATTAACTAATAGAACT
GAGAACCAGAAGTTGCTAGCAAAACAACTAAAAAATCCAGATTACGTTCAAAAATATGCT
CGAGCTAAGTATTATTTCTCTAAGACCGGCGAAATGATTTACCCATTACCAGACCTTTTA
CCAAAA

SEQ ID NO. 8105
STRAIN M732
AGCAAGCCTAATGTTGTTCAGTTAAA
TAATCAATATATTAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGG
AGTTACGCCGAAAAAATCGTTTAATGGGTTGGGTTCTTATTTTTGTCATG
CTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTT
ACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACAT
TAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAACTAAAAAAT
CCAGATTACGTTCAAAAATATGCTCGAGCGAAGTATTATTTCTCTAAGAC
CGGCGAAATGATTTACCCATTACCAGACCtTTTACCAAAA

SEQ ID NO. 8106
STRAIN COH1
AGCAAGCCTAATGTTGTTCAGTTAAATAATC
AATATATTAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGGAGTTA
CGCCGAAAAAATCGTTTAATGGGTTGGGTTCTTATTTTTGTCATGCTttt
ATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTTACAAG
AACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACATTAACT
AATAGAACTGAGAACCAGAAGTTACTAGCAAAACAACTAAAAAATCCAGA
TTACGTTCAAAAATATGCTCGAGCGAAGTATTATTTCTCTAAGACCGGCG
AAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8107
STRAIN M781
AGCaAGCCTAATGTTGTTCAGTT
AAATAATCAATATaTTAACGATGAGAATCTAAAAAAACGTTACGAAGCTG
AGGAGTTACGCCGAAAAAATCGTTTAATGGGTTGGGTTCTTATTTTTGTC
ATGCTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAAC
TTTACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGA
CATTAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAACTAAAA
AATCCAGATTACGTTCAAAAATATGCTCGAGCGAAGTATTATTTCTCTAA
GACCGGCGAAATGATTTACCCATTACCAGACCtTTTACCAAAA

SEQ ID NO. 8108
STRAIN CJB110
AGCAAGCCTAATGTTGTTCAGTTAAATAATC
AATATATTAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGGAGTTA
CGCCGAAAAAATCGTTTAATGGGTTGGGTTCTTATTTTTGTCATGCTttt
ATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTTACAAG

Table 81: Comparative Sequences relating to SAG0011

AACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACATTAACT
AATAGAACTGAGAACCAGAAGTTGCTAGCAAAACAACTAAAAAATCCAGA
TTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGACCGGCG
AAATGATTTACCCATTACCAGACCtTTTACCAAAA

SEQ ID NO. 8109
STRAIN 1169NT
AGCAAGCCTAATGTTGTTCAGTTAAA
TAATCAATATATTAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGG
AGTTACGCCGAAAAAATCGTTTAATGGGTTGGGTTCTTATTTTTGTCATG
CTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTT
ACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACAT
TAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAACTAAAAAAT
CCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
CGGCGAAATGATTTACCCATTACCAGACCtTTTACCAAAA

SEQ ID NO. 8110
STRAIN JM9130013
AGCaAGCCTAATGTTGTTCAGTTAAA
TAATCAATATATTAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGG
AGTTACGCCGAAAAAATCGTTTAATGGGTTGGGTTCTTATTTTTGTCATG
CTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACTTT
ACAAGAACGTCGTCAAGAAGTTGTAAAATTAACGAAAGACTATCAGACAT
TAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAACTAAAAAAT
CCAGATTACGTTCAAAAATATGCTCGAGCGAAGTATTATTTCTCTAAGAC
TGGCGAAATGATTTACCCATTACCAGACCtTTTACCAAAA

SEQ ID NO. 8111
STRAIN 2603
agcaagcctaatgttgttcagttaaataatcaatatattaacgatgagaa
tctaaaaaaacgttacgaagctgaggagttacgccgaaaaaatcgtttaa
tgggttgggttcttatttttgtcatgcttttatttattttacccacttat
aatttagttaagagttacagaactttacaagaacgtcgtcaagaagttgt
aaaattaacgaaagactatcagacattaactaatagaactgagaaccaga
agttgctagcaaaacaactaaaaaatccagattacgttcaaaaatatgct
cgagctaagtattatttctctaagaccggcgaaatgatttacccattacc
agaccttttaccaaaa

```
PRETTY of: /biotmp/msa25643.2{*} . April 29, 2002 05:59  ..

                               1                                                 50
       msa25643.2{418_COH1}   AGCAAGCCTA ATGTTGTTCA GTTAAATAAT CAATATATTA ACGATGAGAA
       msa25643.2{418_M732}   AGCAAGCCTA ATGTTGTTCA GTTAAATAAT CAATATATTA ACGATGAGAA
       msa25643.2{418_M781}   AGCAAGCCTA ATGTTGTTCA GTTAAATAAT CAATATATTA ACGATGAGAA
  msa25643.2{418_JM9130013}   AGCAAGCCTA ATGTTGTTCA GTTAAATAAT CAATATATTA ACGATGAGAA
        msa25643.2{418_090}   AGCAAGCCTA ATGTTGTTCA GTTAAATAAT CAATATATTA ACGATGAGAA
      msa25643.2{418_18RS21}  AGCAAGCCTA ATGTTGTTCA GTTAAATAAT CAATATATTA ACGATGAGAA
       msa25643.2{418_2603}   AGCAAGCCTA ATGTTGTTCA GTTAAATAAT CAATATATTA ACGATGAGAA
      msa25643.2{418_CJB110}  AGCAAGCCTA ATGTTGTTCA GTTAAATAAT CAATATATTA ACGATGAGAA
      msa25643.2{418_1169NT}  AGCAAGCCTA ATGTTGTTCA GTTAAATAAT CAATATATTA ACGATGAGAA
       msa25643.2{418_A909}   AGCAAGCCTA ATGTTGTTCA GTTAAATAAT CAATATATTA ACGATGAGAA
       msa25643.2{418_H36B}   AGCAAGCCTA ATGTTGTTCA GTTAAATAAT CAATATATTA ACGATGAGAA
                  Consensus   ********** ********** ********** ********** **********

                               51                                               100
       msa25643.2{418_COH1}   TCTAAAAAAA CGTTACGAAG CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
       msa25643.2{418_M732}   TCTAAAAAAA CGTTACGAAG CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
       msa25643.2{418_M781}   TCTAAAAAAA CGTTACGAAG CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
  msa25643.2{418_JM9130013}   TCTAAAAAAA CGTTACGAAG CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
        msa25643.2{418_090}   TCTAAAAAAA CGTTACGAAG CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
      msa25643.2{418_18RS21}  TCTAAAAAAA CGTTACGAAG CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
       msa25643.2{418_2603}   TCTAAAAAAA CGTTACGAAG CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
      msa25643.2{418_CJB110}  TCTAAAAAAA CGTTACGAAG CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
      msa25643.2{418_1169NT}  TCTAAAAAAA CGTTACGAAG CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
       msa25643.2{418_A909}   TCTAAAAAAA CGTTACGAAG CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
       msa25643.2{418_H36B}   TCTAAAAAAA CGTTACGAAG CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
                  Consensus   ********** ********** ********** ********** **********

                               101                                              150
       msa25643.2{418_COH1}   TGGGTTGGGT TCTTATTTTT GTCATGCTTT TATTTATTTT ACCCACTTAT
       msa25643.2{418_M732}   TGGGTTGGGT TCTTATTTTT GTCATGCTTT TATTTATTTT ACCCACTTAT
       msa25643.2{418_M781}   TGGGTTGGGT TCTTATTTTT GTCATGCTTT TATTTATTTT ACCCACTTAT
  msa25643.2{418_JM9130013}   TGGGTTGGGT TCTTATTTTT GTCATGCTTT TATTTATTTT ACCCACTTAT
        msa25643.2{418_090}   TGGGTTGGGT TCTTATTTTT GTCATGCTTT TATTTATTTT ACCCACTTAT
      msa25643.2{418_18RS21}  TGGGTTGGGT TCTTATTTTT GTCATGCTTT TATTTATTTT ACCCACTTAT
       msa25643.2{418_2603}   TGGGTTGGGT TCTTATTTTT GTCATGCTTT TATTTATTTT ACCCACTTAT
      msa25643.2{418_CJB110}  TGGGTTGGGT TCTTATTTTT GTCATGCTTT TATTTATTTT ACCCACTTAT
      msa25643.2{418_1169NT}  TGGGTTGGGT TCTTATTTTT GTCATGCTTT TATTTATTTT ACCCACTTAT
       msa25643.2{418_A909}   TGGGTTGGGT TCTTATTTTT GTCATGCTTT TATTTATTTT ACCCACTTAT
       msa25643.2{418_H36B}   TGGGTTGGGT TCTTATTTTT GTCATGCTTT TATTTATTTT ACCCACTTAT
                  Consensus   ********** ********** ********** ********** **********
```

Table 81: Comparative Sequences relating to SAG0011

```
                          151                                                200
   msa25643.2{418_COH1}   AATTTAGTTA AGAGTTACAG AACTTTACAA GAACGTCGTC AAGAAGTTGT
   msa25643.2{418_M732}   AATTTAGTTA AGAGTTACAG AACTTTACAA GAACGTCGTC AAGAAGTTGT
   msa25643.2{418_M781}   AATTTAGTTA AGAGTTACAG AACTTTACAA GAACGTCGTC AAGAAGTTGT
msa25643.2{418_JM9130013} AATTTAGTTA AGAGTTACAG AACTTTACAA GAACGTCGTC AAGAAGTTGT
    msa25643.2{418_090}   AATTTAGTTA AGAGTTACAG AACTTTACAA GAACGTCGTC AAGAAGTTGT
  msa25643.2{418_18RS21}  AATTTAGTTA AGAGTTACAG AACTTTACAA GAACGTCGTC AAGAAGTTGT
   msa25643.2{418_2603}   AATTTAGTTA AGAGTTACAG AACTTTACAA GAACGTCGTC AAGAAGTTGT
  msa25643.2{418_CJB110}  AATTTAGTTA AGAGTTACAG AACTTTACAA GAACGTCGTC AAGAAGTTGT
  msa25643.2{418_1169NT}  AATTTAGTTA AGAGTTACAG AACTTTACAA GAACGTCGTC AAGAAGTTGT
   msa25643.2{418_A909}   AATTTAGTTA AGAGTTACAG AACTTTACAA GAACGTCGTC AAGAAGTTGT
   msa25643.2{418_H36B}   AATTTAGTTA AGAGTTACAG AACTTTACAA GAACGTCGTC AAGAAGTTGT
              Consensus   ********** ********** ********** ********** **********

                          201                                                250
   msa25643.2{418_COH1}   AAAATTAACG AAAGACTATC AGACATTAAC TAATAGAACT GAGAACCAGA
   msa25643.2{418_M732}   AAAATTAACG AAAGACTATC AGACATTAAC TAATAGAACT GAGAACCAGA
   msa25643.2{418_M781}   AAAATTAACG AAAGACTATC AGACATTAAC TAATAGAACT GAGAACCAGA
msa25643.2{418_JM9130013} AAAATTAACG AAAGACTATC AGACATTAAC TAATAGAACT GAGAACCAGA
    msa25643.2{418_090}   AAAATTAACG AAAGACTATC AGACATTAAC TAATAGAACT GAGAACCAGA
  msa25643.2{418_18RS21}  AAAATTAACG AAAGACTATC AGACATTAAC TAATAGAACT GAGAACCAGA
   msa25643.2{418_2603}   AAAATTAACG AAAGACTATC AGACATTAAC TAATAGAACT GAGAACCAGA
  msa25643.2{418_CJB110}  AAAATTAACG AAAGACTATC AGACATTAAC TAATAGAACT GAGAACCAGA
  msa25643.2{418_1169NT}  AAAATTAACG AAAGACTATC AGACATTAAC TAATAGAACT GAGAACCAGA
   msa25643.2{418_A909}   AAAATTAACG AAAGACTATC AGACATTAAC TAATAGAACT GAGAACCAGA
   msa25643.2{418_H36B}   AAAATTAACG AAAGACTATC AGACATTAAC TAATAGAACT GAGAACCAGA
              Consensus   ********** ********** ********** ********** **********

                          251                                                300
   msa25643.2{418_COH1}   AGTTaCTAGC AAAACAACTA AAAAATCCAG ATTACGTTCA AAAATATGCT
   msa25643.2{418_M732}   AGTTaCTAGC AAAACAACTA AAAAATCCAG ATTACGTTCA AAAATATGCT
   msa25643.2{418_M781}   AGTTaCTAGC AAAACAACTA AAAAATCCAG ATTACGTTCA AAAATATGCT
msa25643.2{418_JM9130013} AGTTaCTAGC AAAACAACTA AAAAATCCAG ATTACGTTCA AAAATATGCT
    msa25643.2{418_090}   AGTTgCTAGC AAAACAACTA AAAAATCCAG ATTACGTTCA AAAATATGCT
  msa25643.2{418_18RS21}  AGTTgCTAGC AAAACAACTA AAAAATCCAG ATTACGTTCA AAAATATGCT
   msa25643.2{418_2603}   AGTTgCTAGC AAAACAACTA AAAAATCCAG ATTACGTTCA AAAATATGCT
  msa25643.2{418_CJB110}  AGTTgCTAGC AAAACAACTA AAAAATCCAG ATTACGTTCA AAAATATGCT
  msa25643.2{418_1169NT}  AGTTaCTAGC AAAACAACTA AAAAATCCAG ATTACGTTCA AAAATATGCT
   msa25643.2{418_A909}   AGTTaCTAGC AAAACAACTA AAAAATCCAG ATTACGTTCA AAAATATGCT
   msa25643.2{418_H36B}   AGTTaCTAGC AAAACAACTA AAAAATCCAG ATTACGTTCA AAAATATGCT
              Consensus   ****-***** ********** ********** ********** **********

                          301                                                350
   msa25643.2{418_COH1}   CGAGCgAAGT ATTATTTCTC TAAGACcGGC GAAATGATTT ACCCATTACC
   msa25643.2{418_M732}   CGAGCgAAGT ATTATTTCTC TAAGACcGGC GAAATGATTT ACCCATTACC
   msa25643.2{418_M781}   CGAGCgAAGT ATTATTTCTC TAAGACcGGC GAAATGATTT ACCCATTACC
msa25643.2{418_JM9130013} CGAGCgAAGT ATTATTTCTC TAAGACtGGC GAAATGATTT ACCCATTACC
    msa25643.2{418_090}   CGAGCtAAGT ATTATTTCTC TAAGACcGGC GAAATGATTT ACCCATTACC
  msa25643.2{418_18RS21}  CGAGCtAAGT ATTATTTCTC TAAGACcGGC GAAATGATTT ACCCATTACC
   msa25643.2{418_2603}   CGAGCtAAGT ATTATTTCTC TAAGACcGGC GAAATGATTT ACCCATTACC
  msa25643.2{418_CJB110}  CGAGCtAAGT ATTATTTCTC TAAGACcGGC GAAATGATTT ACCCATTACC
  msa25643.2{418_1169NT}  CGAGCtAAGT ATTATTTCTC TAAGACcGGC GAAATGATTT ACCCATTACC
   msa25643.2{418_A909}   CGAGCtAAGT ATTATTTCTC TAAGACcGGC GAAATGATTT ACCCATTACC
   msa25643.2{418_H36B}   CGAGCtAAGT ATTATTTCTC TAAGACcGGC GAAATGATTT ACCCATTACC
              Consensus   *****-**** ********** ******-*** ********** **********

                          351        366
   msa25643.2{418_COH1}   AGACCTttta ccaaaa
   msa25643.2{418_M732}   AGACCTttta ccaaaa
   msa25643.2{418_M781}   AGACCTttta ccaaaa
msa25643.2{418_JM9130013} AGACCTttta ccaaaa
    msa25643.2{418_090}   AGACCTttta ccaaaa
  msa25643.2{418_18RS21}  AGACCTttta ccaaaa
   msa25643.2{418_2603}   AGACCTttta ccaaaa
  msa25643.2{418_CJB110}  AGACCTttta ccaaaa
  msa25643.2{418_1169NT}  AGACCTttta ccaaaa
   msa25643.2{418_A909}   AGACCT~~~~ ~~~~~~
   msa25643.2{418_H36B}   AGACCTttta ccaaaa
              Consensus   ******---- ------
```

SEQ ID NO. 8112

STRAIN 090

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNL
VKSYRTLQERRQEVVKLTKDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
IYPLPDLLPK

SEQ ID NO. 8113

STRAIN A909

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNL
VKSYRTLQERRQEVVKLTKDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM

Table 81: Comparative Sequences relating to SAG0011

IYPLPD

SEQ ID NO. 8114

STRAIN H36B

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNL
VKSYRTLQERRQEVVKLTKDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
IYPLPDLLPK

SEQ ID NO. 8115

STRAIN 18RS21

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNLVKSYRTLQ
ERRQEVVKLTKDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEMIYPLPDLL
PK

SEQ ID NO. 8116

STRAIN M732

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNL
VKSYRTLQERRQEVVKLTKDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
IYPLPDLLPK

SEQ ID NO. 8117

STRAIN COH1

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNLVK
SYRTLQERRQEVVKLTKDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEMIY
PLPDLLPK

SEQ ID NO. 8118

STRAIN M781

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYN
LVKSYRTLQERRQEVVKLTKDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGE
MIYPLPDLLPK

SEQ ID NO. 8119

STRAIN CJB110

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNLVK
SYRTLQERRQEVVKLTKDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEMIY
PLPDLLPK

SEQ ID NO. 8120

STRAIN 1169NT

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNL
VKSYRTLQERRQEVVKLTKDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
IYPLPDLLPK

SEQ ID NO. 8121

STRAIN JM9130013

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNL
VKSYRTLQERRQEVVKLTKDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
IYPLPDLLPK

SEQ ID NO. 8122

STRAIN 2603

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNLVKSYRTLQ
ERRQEVVKLTKDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEMIYPLPDLL
PK

```
MSA Alignment Results: Pretty output
PRETTY of: /biotmp/msa20122.2{*}   April 29, 2002 06:08  ..

                             1                                                  50
       msa20122.2{418_090}   SKPNVVQLNN QYINDENLKK RYEAEELRRK NRLMGWVLIF VMLLFILPTY
       msa20122.2{418_A909}  SKPNVVQLNN QYINDENLKK RYEAEELRRK NRLMGWVLIF VMLLFILPTY
     msa20122.2{418_1169NT}  SKPNVVQLNN QYINDENLKK RYEAEELRRK NRLMGWVLIF VMLLFILPTY
     msa20122.2{418_18RS21}  SKPNVVQLNN QYINDENLKK RYEAEELRRK NRLMGWVLIF VMLLFILPTY
       msa20122.2{418_2603}  SKPNVVQLNN QYINDENLKK RYEAEELRRK NRLMGWVLIF VMLLFILPTY
     msa20122.2{418_CJB110}  SKPNVVQLNN QYINDENLKK RYEAEELRRK NRLMGWVLIF VMLLFILPTY
       msa20122.2{418_COH1}  SKPNVVQLNN QYINDENLKK RYEAEELRRK NRLMGWVLIF VMLLFILPTY
       msa20122.2{418_H36B}  SKPNVVQLNN QYINDENLKK RYEAEELRRK NRLMGWVLIF VMLLFILPTY
   msa20122.2{418_JM9130013} SKPNVVQLNN QYINDENLKK RYEAEELRRK NRLMGWVLIF VMLLFILPTY
       msa20122.2{418_M732}  SKPNVVQLNN QYINDENLKK RYEAEELRRK NRLMGWVLIF VMLLFILPTY
       msa20122.2{418_M781}  SKPNVVQLNN QYINDENLKK RYEAEELRRK NRLMGWVLIF VMLLFILPTY
                  Consensus  ********** ********** ********** ********** **********

                             51                                                100
       msa20122.2{418_090}   NLVKSYRTLQ ERRQEVVKLT KDYQTLTNRT ENQKLLAKQL KNPDYVQKYA
       msa20122.2{418_A909}  NLVKSYRTLQ ERRQEVVKLT KDYQTLTNRT ENQKLLAKQL KNPDYVQKYA
```

Table 81: Comparative Sequences relating to SAG0011

```
  msa20122.2{418_1169NT}  NLVKSYRTLQ ERRQEVVKLT KDYQTLTNRT ENQKLLAKQL KNPDYVQKYA
  msa20122.2{418_18RS21}  NLVKSYRTLQ ERRQEVVKLT KDYQTLTNRT ENQKLLAKQL KNPDYVQKYA
    msa20122.2{418_2603}  NLVKSYRTLQ ERRQEVVKLT KDYQTLTNRT ENQKLLAKQL KNPDYVQKYA
  msa20122.2{418_CJB110}  NLVKSYRTLQ ERRQEVVKLT KDYQTLTNRT ENQKLLAKQL KNPDYVQKYA
    msa20122.2{418_COH1}  NLVKSYRTLQ ERRQEVVKLT KDYQTLTNRT ENQKLLAKQL KNPDYVQKYA
    msa20122.2{418_H36B}  NLVKSYRTLQ ERRQEVVKLT KDYQTLTNRT ENQKLLAKQL KNPDYVQKYA
msa20122.2{418_JM9130013} NLVKSYRTLQ ERRQEVVKLT KDYQTLTNRT ENQKLLAKQL KNPDYVQKYA
    msa20122.2{418_M732}  NLVKSYRTLQ ERRQEVVKLT KDYQTLTNRT ENQKLLAKQL KNPDYVQKYA
    msa20122.2{418_M781}  NLVKSYRTLQ ERRQEVVKLT KDYQTLTNRT ENQKLLAKQL KNPDYVQKYA
               Consensus  ********** ********** ********** ********** **********

                          101                  122
     msa20122.2{418_090}  RAKYYFSKTG EMIYPLPDll pk
     msa20122.2{418_A909}  RAKYYFSKTG EMIYPLPD~~ ~~
  msa20122.2{418_1169NT}  RAKYYFSKTG EMIYPLPDll pk
  msa20122.2{418_18RS21}  RAKYYFSKTG EMIYPLPDll pk
    msa20122.2{418_2603}  RAKYYFSKTG EMIYPLPDll pk
  msa20122.2{418_CJB110}  RAKYYFSKTG EMIYPLPDll pk
    msa20122.2{418_COH1}  RAKYYFSKTG EMIYPLPDll pk
    msa20122.2{418_H36B}  RAKYYFSKTG EMIYPLPDll pk
msa20122.2{418_JM9130013} RAKYYFSKTG EMIYPLPDll pk
    msa20122.2{418_M732}  RAKYYFSKTG EMIYPLPDll pk
    msa20122.2{418_M781}  RAKYYFSKTG EMIYPLPDll pk
               Consensus  ********** ********-- --
```

Table 82: Comparative Sequences relating to SAG0165

SEQ ID NO. 8201
STRAIN 2603
ATGAAAAATTTATTGTTAAAATGTAAGGATAAGAAGGTTAAAGCATTTACACTTTTAGAA
TGTTTGGTAGCATTGGTTACAATCACAGGAGCTTTACTAGTTTATCAAGGACTGACAAAA
TTGTTGGCTCAACAGATAGTAGTGATGTCTTCTTCCAGTCAGTCTGAATGGGTGTTATTA
AcTCAGCAACTAAATGCAGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAAA
CTTTATTTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATTTC
CGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGGTTAGACAATTGT
CAAATGAGTCAGACCAAAAGTATGGTAAAACTTGTTTTTTATTTTAAGGACGGGTTAAAA
AGGACATTTTACTATGATTTTAAAGAAGAAACTTAA

SEQ ID NO. 8202
STRAIN 090
AATTCGAAGGCGCTCACTTGGAATATTTAAGACAGAACAAACTTTATTTA
CGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATTT
CCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGGT
TAGACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAAACTTGTTTTT
TATTTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAGA
AACT

SEQ ID NO. 8203
STRAIN A909
CAGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAAACTTTAT
TTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGA
TTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATG
GGTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTGTT
TTTTATTTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGA
AGAAACT

SEQ ID NO. 8204
STRAIN H36B
ATGCAGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAAACTT
TATTTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGA
TGATTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTT
ATGGGTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTT
GTTTTTTATTTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAA
AGAAGAAACT

SEQ ID NO. 8205
STRAIN 18RS21
AGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAAACTTTATT
TACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAT
TTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGG
GTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTGTTT
TTTATTTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAA
GAAACT

SEQ ID NO. 8206
STRAIN M732
CAGAATTCGAAGGCGCTCACTTGGAATATTTAAGACAGAACAAACTTTAT
TTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGA
TTTCCGTAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTTATG
GGTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTGTT
TTTTATTTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGA
AGAAACT

SEQ ID NO. 8207
STRAIN COH1
GAATTCGAAGGCGCTCACTTGGAATATTTAAGACAGAACAAACTTTATTT
ACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATT
TCCGTAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTTATGGG
TTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTGTTTT
TTATTTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAG
AAACT

SEQ ID NO. 8208
STRAIN M781
AGAATTCGAAGGCGCTCACTTGGAATATTTAAGACAGAACAAACTTTATT
TACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAT
TTCCGTAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTTATGG
GTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTGTTT
TTTATTTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAA
GAAACT

SEQ ID NO. 8209
STRAIN CJB110
GAATTCGAAGGCGCTCACTTGGAATATTTAAGACAGAACAAACTTTATTT
ACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATT
TCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGG
TTAGACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAAACTTGTTTT
TTATTTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAG
AAACT

Table 82: Comparative Sequences relating to SAG0165

SEQ ID NO. 8210
STRAIN 1169NT
TCGAAGGCGCTCACTTGGAATATTTAAGACAGAACAAACTTTATTTACGT
AAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATTTTCG
TAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGGTTAG
ACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAAACTTGTTTTTTAT
TTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAGAAAC
T

SEQ ID NO. 8211
STRAIN JM9130013
TGCAGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAAACTTT
ATTTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGAT
GATTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTA
TGGGTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTG
TTTTTTATTTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAA
GAAGAAACT

```
PRETTY of: /biotmp/msa128189.2{*}   February 7, 2003 08:19  ..

                         1                                                   50
   msa128189.2{6_18RS21} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa128189.2{6_2603} atgaaaaatt tattgttaaa atgtaaggat aagaaggtta aagcatttac
     msa128189.2{6_A909} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa128189.2{6_H36B} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa128189.2{6_JM9130013} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa128189.2{6_COH1} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa128189.2{6_M732} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa128189.2{6_M781} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa128189.2{6_090} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa128189.2{6_CJB110} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa128189.2{6_1169NT} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
               Consensus ********** ********** ********** ********** **********

                         51                                                 100
   msa128189.2{6_18RS21} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa128189.2{6_2603} acttttagaa tgtttggtag cattggttac aatcacagga gctttactag
     msa128189.2{6_A909} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa128189.2{6_H36B} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa128189.2{6_JM9130013} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa128189.2{6_COH1} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa128189.2{6_M732} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa128189.2{6_M781} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa128189.2{6_090} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa128189.2{6_CJB110} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa128189.2{6_1169NT} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
               Consensus ********** ********** ********** ********** **********

                         101                                                150
   msa128189.2{6_18RS21} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa128189.2{6_2603} tttatcaagg actgacaaaa ttgttggctc aacagatagt agtgatgtct
     msa128189.2{6_A909} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa128189.2{6_H36B} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa128189.2{6_JM9130013} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa128189.2{6_COH1} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa128189.2{6_M732} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa128189.2{6_M781} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa128189.2{6_090} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa128189.2{6_CJB110} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa128189.2{6_1169NT} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
               Consensus ********** ********** ********** ********** **********

                         151                                                200
   msa128189.2{6_18RS21} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~aga
     msa128189.2{6_2603} tcttccagtc agtctgaatg ggtgttatta actcagcaac taaATGCaga
     msa128189.2{6_A909} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~Caga
     msa128189.2{6_H36B} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~ATGCaga
msa128189.2{6_JM9130013} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~TGCaga
     msa128189.2{6_COH1} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~ga
     msa128189.2{6_M732} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~Caga
     msa128189.2{6_M781} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~aga
      msa128189.2{6_090} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~a
   msa128189.2{6_CJB110} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~ga
   msa128189.2{6_1169NT} ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
               Consensus ********** ********** ********** ********** *******---

                         201                                                250
   msa128189.2{6_18RS21} atTtGAAGGC GCTCAtcTGG AATATTTAAG ACAGAACAAA CTTTATTTAC
     msa128189.2{6_2603} atTtGAAGGC GCTCAtcTGG AATATTTAAG ACAGAACAAA CTTTATTTAC
     msa128189.2{6_A909} atTtGAAGGC GCTCAtcTGG AATATTTAAG ACAGAACAAA CTTTATTTAC
     msa128189.2{6_H36B} atTtGAAGGC GCTCAtcTGG AATATTTAAG ACAGAACAAA CTTTATTTAC
```

Table 82: Comparative Sequences relating to SAG0165

```
msa128189.2{6_JM9130013}  atTtGAAGGC GCTCAtcTGG AATATTTAAG ACAGAACAAA CTTTATTTAC
     msa128189.2{6_COH1}  atTcGAAGGC GCTCActTGG AATATTTAAG ACAGAACAAA CTTTATTTAC
     msa128189.2{6_M732}  atTcGAAGGC GCTCActTGG AATATTTAAG ACAGAACAAA CTTTATTTAC
     msa128189.2{6_M781}  atTcGAAGGC GCTCActTGG AATATTTAAG ACAGAACAAA CTTTATTTAC
      msa128189.2{6_090}  atTcGAAGGC GCTCActTGG AATATTTAAG ACAGAACAAA CTTTATTTAC
   msa128189.2{6_CJB110}  atTcGAAGGC GCTCActTGG AATATTTAAG ACAGAACAAA CTTTATTTAC
  msa128189.2{6_1169NT}   --TcGAAGGC GCTCActTGG AATATTTAAG ACAGAACAAA CTTTATTTAC
               Consensus  --*-****** *****--*** ********** ********** **********

                          251                                                300
   msa128189.2{6_18RS21}  GTAAGCAAGA TAAGATTGTA ACCTTTGGCA AATCTAATAA AGATGATTTc
     msa128189.2{6_2603}  GTAAGCAAGA TAAGATTGTA ACCTTTGGCA AATCTAATAA AGATGATTTc
     msa128189.2{6_A909}  GTAAGCAAGA TAAGATTGTA ACCTTTGGCA AATCTAATAA AGATGATTTc
     msa128189.2{6_H36B}  GTAAGCAAGA TAAGATTGTA ACCTTTGGCA AATCTAATAA AGATGATTTc
msa128189.2{6_JM9130013}  GTAAGCAAGA TAAGATTGTA ACCTTTGGCA AATCTAATAA AGATGATTTc
     msa128189.2{6_COH1}  GTAAGCAAGA TAAGATTGTA ACCTTTGGCA AATCTAATAA AGATGATTTc
     msa128189.2{6_M732}  GTAAGCAAGA TAAGATTGTA ACCTTTGGCA AATCTAATAA AGATGATTTc
     msa128189.2{6_M781}  GTAAGCAAGA TAAGATTGTA ACCTTTGGCA AATCTAATAA AGATGATTTc
      msa128189.2{6_090}  GTAAGCAAGA TAAGATTGTA ACCTTTGGCA AATCTAATAA AGATGATTTc
   msa128189.2{6_CJB110}  GTAAGCAAGA TAAGATTGTA ACCTTTGGCA AATCTAATAA AGATGATTTc
  msa128189.2{6_1169NT}   GTAAGCAAGA TAAGATTGTA ACCTTTGGCA AATCTAATAA AGATGATTTt
               Consensus  ********** ********** ********** ********** *********-

                          301                                                350
   msa128189.2{6_18RS21}  CGTAAGACAG GTTATgATGG TCGAGGTTAT CAACCAATGG TTTATGGGTT
     msa128189.2{6_2603}  CGTAAGACAG GTTATgATGG TCGAGGTTAT CAACCAATGG TTTATGGGTT
     msa128189.2{6_A909}  CGTAAGACAG GTTATgATGG TCGAGGTTAT CAACCAATGG TTTATGGGTT
     msa128189.2{6_H36B}  CGTAAGACAG GTTATgATGG TCGAGGTTAT CAACCAATGG TTTATGGGTT
msa128189.2{6_JM9130013}  CGTAAGACAG GTTATgATGG TCGAGGTTAT CAACCAATGG TTTATGGGTT
     msa128189.2{6_COH1}  CGTAAGACAG GTTATaATGG TCGAGGTTAT CAACCAATGG TTTATGGGTT
     msa128189.2{6_M732}  CGTAAGACAG GTTATaATGG TCGAGGTTAT CAACCAATGG TTTATGGGTT
     msa128189.2{6_M781}  CGTAAGACAG GTTATaATGG TCGAGGTTAT CAACCAATGG TTTATGGGTT
      msa128189.2{6_090}  CGTAAGACAG GTTATgATGG TCGAGGTTAT CAACCAATGG TTTATGGGTT
   msa128189.2{6_CJB110}  CGTAAGACAG GTTATgATGG TCGAGGTTAT CAACCAATGG TTTATGGGTT
  msa128189.2{6_1169NT}   CGTAAGACAG GTTATgATGG TCGAGGTTAT CAACCAATGG TTTATGGGTT
               Consensus  ********** *****-**** ********** ********** **********

                          351                                                400
   msa128189.2{6_18RS21}  AGACAATTGT CAAATGAGTC AgACCAAAAG TATGGTAAAA CTTGTTTTTT
     msa128189.2{6_2603}  AGACAATTGT CAAATGAGTC AgACCAAAAG TATGGTAAAA CTTGTTTTTT
     msa128189.2{6_A909}  AGACAATTGT CAAATGAGTC AgACCAAAAG TATGGTAAAA CTTGTTTTTT
     msa128189.2{6_H36B}  AGACAATTGT CAAATGAGTC AgACCAAAAG TATGGTAAAA CTTGTTTTTT
msa128189.2{6_JM9130013}  AGACAATTGT CAAATGAGTC AgACCAAAAG TATGGTAAAA CTTGTTTTTT
     msa128189.2{6_COH1}  AGACAATTGT CAAATGAGTC AgACCAAAAG TATGGTAAAA CTTGTTTTTT
     msa128189.2{6_M732}  AGACAATTGT CAAATGAGTC AgACCAAAAG TATGGTAAAA CTTGTTTTTT
     msa128189.2{6_M781}  AGACAATTGT CAAATGAGTC AgACCAAAAG TATGGTAAAA CTTGTTTTTT
      msa128189.2{6_090}  AGACAATTGT CAAATGAGTC AaACCAAAAG TATGGTAAAA CTTGTTTTTT
   msa128189.2{6_CJB110}  AGACAATTGT CAAATGAGTC AaACCAAAAG TATGGTAAAA CTTGTTTTTT
  msa128189.2{6_1169NT}   AGACAATTGT CAAATGAGTC AaACCAAAAG TATGGTAAAA CTTGTTTTTT
               Consensus  ********** ********** *-******** ********** **********

                          401                                                450
   msa128189.2{6_18RS21}  ATTTTAAGGA CGGGTTAAAA AGGACATTTT ACTATGATTT TAAAGAAGAA
     msa128189.2{6_2603}  ATTTTAAGGA CGGGTTAAAA AGGACATTTT ACTATGATTT TAAAGAAGAA
     msa128189.2{6_A909}  ATTTTAAGGA CGGGTTAAAA AGGACATTTT ACTATGATTT TAAAGAAGAA
     msa128189.2{6_H36B}  ATTTTAAGGA CGGGTTAAAA AGGACATTTT ACTATGATTT TAAAGAAGAA
msa128189.2{6_JM9130013}  ATTTTAAGGA CGGGTTAAAA AGGACATTTT ACTATGATTT TAAAGAAGAA
     msa128189.2{6_COH1}  ATTTTAAGGA CGGGTTAAAA AGGACATTTT ACTATGATTT TAAAGAAGAA
     msa128189.2{6_M732}  ATTTTAAGGA CGGGTTAAAA AGGACATTTT ACTATGATTT TAAAGAAGAA
     msa128189.2{6_M781}  ATTTTAAGGA CGGGTTAAAA AGGACATTTT ACTATGATTT TAAAGAAGAA
      msa128189.2{6_090}  ATTTTAAGGA CGGGTTAAAA AGGACATTTT ACTATGATTT TAAAGAAGAA
   msa128189.2{6_CJB110}  ATTTTAAGGA CGGGTTAAAA AGGACATTTT ACTATGATTT TAAAGAAGAA
  msa128189.2{6_1169NT}   ATTTTAAGGA CGGGTTAAAA AGGACATTTT ACTATGATTT TAAAGAAGAA
               Consensus  ********** ********** ********** ********** **********

                          451
   msa128189.2{6_18RS21}  ACT---
     msa128189.2{6_2603}  ACTtaa
     msa128189.2{6_A909}  ACT---
     msa128189.2{6_H36B}  ACT---
msa128189.2{6_JM9130013}  ACT---
     msa128189.2{6_COH1}  ACT---
     msa128189.2{6_M732}  ACT---
     msa128189.2{6_M781}  ACT---
      msa128189.2{6_090}  ACT---
   msa128189.2{6_CJB110}  ACT---
  msa128189.2{6_1169NT}   ACT---
               Consensus  ******
```

SEQ ID NO. 8212
STRAIN 2603 frame: 1
MKNLLLKCKDKKVKAFTLLECLVALVTITGALLVYQGLTKLLAQQIVVMSSSSQSEWVLL
TQQLNAEFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNC

Table 82: Comparative Sequences relating to SAG0165

QMSQTKSMVKLVFYFKDGLKRTFYYDFKEET.

SEQ ID NO. 8213
STRAIN 090 frame: 3
FEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTKS
MVKLVFYFKDGLKRTFYYDFKEET

SEQ ID NO. 8214
STRAIN A909 frame: 3
EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYYDFKEET

SEQ ID NO. 8215
STRAIN H36B frame: 3
AEFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQT
KSMVKLVFYFKDGLKRTFYYDFKEET

SEQ ID NO. 8216
STRAIN 18RS21 frame: 2
EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYYDFKEET

SEQ ID NO. 8217
STRAIN M732 frame: 3
EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYYDFKEET

SEQ ID NO. 8218
STRAIN COH1 frame: 1
EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYYDFKEET

SEQ ID NO. 8219
STRAIN M781 frame: 2
EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYYDFKEET

SEQ ID NO. 8220
STRAIN CJB110 frame: 1
EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFYYDFKEET

SEQ ID NO. 8221
STRAIN 1169NT frame: 3
EGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTKSM
VKLVFYFKDGLKRTFYYDFKEET

SEQ ID NO. 8222
STRAIN JM9130013 frame: 2
AEFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQT
KSMVKLVFYFKDGLKRTFYYDFKEET

```
PRETTY of: /biotmp/msa128319.2{*}   February 7, 2003 08:27  ..

                                1                                                   50
       msa128319.2{6_090}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa128319.2{6_1169NT}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa128319.2{6_18RS21}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa128319.2{6_2603}    mknlllkckd kkvkaftlle clvalvtitg allvyqgltk llaqqivvms
      msa128319.2{6_H36B}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
 msa128319.2{6_JM9130013}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa128319.2{6_A909}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa128319.2{6_CJB110}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa128319.2{6_COH1}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa128319.2{6_M732}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa128319.2{6_M781}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                Consensus    ********** ********** ********** ********** **********

                             51                                                  100
       msa128319.2{6_090}    ~~~~~~~~~~ ~~~~~~~fEG AHLEYLRQNK LYLRKQDKIV TFGKSNKDDF
    msa128319.2{6_1169NT}    ~~~~~~~~~~ ~~~~~~~~EG AHLEYLRQNK LYLRKQDKIV TFGKSNKDDF
    msa128319.2{6_18RS21}    ~~~~~~~~~~ ~~~~~~EfEG AHLEYLRQNK LYLRKQDKIV TFGKSNKDDF
      msa128319.2{6_2603}    sssqsewvll tqqlnAEfEG AHLEYLRQNK LYLRKQDKIV TFGKSNKDDF
      msa128319.2{6_H36B}    ~~~~~~~~~~ ~~~~~AEfEG AHLEYLRQNK LYLRKQDKIV TFGKSNKDDF
 msa128319.2{6_JM9130013}    ~~~~~~~~~~ ~~~~~AEfEG AHLEYLRQNK LYLRKQDKIV TFGKSNKDDF
      msa128319.2{6_A909}    ~~~~~~~~~~ ~~~~~~EfEG AHLEYLRQNK LYLRKQDKIV TFGKSNKDDF
    msa128319.2{6_CJB110}    ~~~~~~~~~~ ~~~~~~EfEG AHLEYLRQNK LYLRKQDKIV TFGKSNKDDF
      msa128319.2{6_COH1}    ~~~~~~~~~~ ~~~~~~EfEG AHLEYLRQNK LYLRKQDKIV TFGKSNKDDF
      msa128319.2{6_M732}    ~~~~~~~~~~ ~~~~~~EfEG AHLEYLRQNK LYLRKQDKIV TFGKSNKDDF
      msa128319.2{6_M781}    ~~~~~~~~~~ ~~~~~~EfEG AHLEYLRQNK LYLRKQDKIV TFGKSNKDDF
                Consensus    ********** *******-** ********** ********** **********
```

Table 82: Comparative Sequences relating to SAG0165

```
                            101                                                150
      msa128319.2{6_090}    RKTGYdGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKEE
   msa128319.2{6_1169NT}    RKTGYdGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKEE
   msa128319.2{6_18RS21}    RKTGYdGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKEE
     msa128319.2{6_2603}    RKTGYdGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKEE
     msa128319.2{6_H36B}    RKTGYdGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKEE
 msa128319.2{6_JM9130013}   RKTGYdGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKEE
     msa128319.2{6_A909}    RKTGYdGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKEE
   msa128319.2{6_CJB110}    RKTGYdGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKEE
     msa128319.2{6_COH1}    RKTGYnGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKEE
     msa128319.2{6_M732}    RKTGYnGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKEE
     msa128319.2{6_M781}    RKTGYnGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKEE
               Consensus    *****-**** ********** ********** ********** **********

                            151
      msa128319.2{6_090}    T~
   msa128319.2{6_1169NT}    T~
   msa128319.2{6_18RS21}    T~
     msa128319.2{6_2603}    T~
     msa128319.2{6_H36B}    T~
 msa128319.2{6_JM9130013}   T~
     msa128319.2{6_A909}    T~
   msa128319.2{6_CJB110}    T~
     msa128319.2{6_COH1}    T~
     msa128319.2{6_M732}    T~
     msa128319.2{6_M781}    T~
               Consensus    **
```

Table 83: Comparative Sequences relating to SAG0108

SEQ ID NO. 8301
STRAIN 2603
atgaaaaagattcgattatcaaagtttattaaaatgattgttgttattttgtttttaatt
agtgtagcagctagtttttatttttttccacgttgcccaagttcgagatgataaatccttt
atttcaaatggtcaacgtaagcctggaaactctttatatgcttatgataaatcctttgat
aagctattaaagcaaaaaatagaaatgacaaaccaaaatataaagcaagttgcttggtat
gttcctgctgttaagaaaactcataagacagctgttgtcgttcatggttttgcgaatagc
aaagagaatatgaaggcatatggttggctgtttcataagttaggatacaatgttcttatg
cctgacaatattgcacatggtgaaagtcatgggcagttgataggctatggctggaacgac
cgcgagaacattatcaaatggacagaaatgatagttgataagaatccatcaagccaaatt
actttatttggtgtttcaatgggtggagcaacagtcatgatggctagtggtgaaaaatta
cctagtcaggttgttaatatcattgaagattgcggttattctagtgtttgggatgaatta
aaatttcaggctaaagagatgtatggtttaccagccttcccactcttatatgaagtttca
acaatttctaaaatcagagcaggtttttcgtatggacaagcaagtagtgtcgaacaattg
aaaaagaataatttaccagccctctttattcatggtgataaggataattttgttccaaca
agtatggtttatgacaactataaagctacagcaggtaagaaagagctttatattgtaaaa
ggggcaaaacatgcgaaatcttttgaaacagagccagaaaaatatgagaaacgtatctct
agtttttttgaaaaaatatgaaaaa

SEQ ID NO. 8302
STRAIN 090
GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCG
AGATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTT
TATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAA
ATGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCCTGCTGCTAA
GAAAACTCATAAGACAGCTGTTGTCGTTCATGGTTTTGCGAATAgCAAAG
AGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTT
cTTATGCCTGACAATATTGCACATGGtGAAAGTCATGGGCAGTTGATAGG
CTATGGCTGGAACGACCGCGAGAACATTATCaAATGGACAGAAATGATAG
TTGATAAGAATCCATCAAGCCAAATTACTTtaTTTGGTGTTTCAATGGGT
GGAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGT
TAATATCATTGAAGATTGCGGTTATTCTAGTGTTTGGGATGAATTAAAAT
TTCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAA
GTTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAG
TAGTGTCGAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCATG
GTGATAAGGATAATTTTGTTCCAACAAGTATGGTTTATGACAACTATAAA
GCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGC
GAAATCTTTTGAAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTT
TTTTGAAAAAATATGAAAAA

SEQ ID NO. 8303
STRAIN A909
AATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTTATATGCT
TATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAATGACAAA
CCAAAATATAAAGCAAGTTGCTTGGTATGTTCCTGCTGCTAAGAAAACTC
ATAAGACAGCTGTTGTCGTTCATGGTTTTGCGAATAGCAAAGAGAATATG
AAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTCTTATGCC
TGACAACATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGCTATGGCT
GGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGTTGATAAG
AATTCATCAAGCCAAATTACTTTATTTGGTGTTTCAATGGGTGGAGCAAC
AGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTTAATATCA
TTGAAGAtTGCGGTTATTCTGGTGTTTGGGATGAATTAAAATTTCAGGCT
AAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAGTTTCAAC
AATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAgCAAGTAGTGTCG
AACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCATGGTGATAAG
GATAATTTTGTTCCAACAaGTATGGTTTATGACAACTATAAAGCTACAGC
AGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGCGAAATCTT
TTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTTTTTGAAA
AAATATGAAAAA

SEQ ID NO. 8304
STRAIN H36B
AGTTTTTATTTTTTCCACGTTGCCCAAGTTCGAGATGATAAATCCTTTAT
TTCAAATGGTCAACGTAAGCCTGGAAACTCTTTATATGCTTATGATAAAT
CCTTTGATAAGCTATTAAAGCAAAAAATAGAAATGACAAACCAAAATATA
AAGCAAGTTGCTTGGTATGTTCCTGCTGCTAAGAAAACTCATAAGACAGC
TGTTGTCGTTCATGGTTTTGCGAATAGCAAAGAGAATATGAAGGCATATG
GTTGGCTGTTTCATAAGTTAGGATACAATGTTcTTATGCCTGACAACATT
GCACATGGTGAAAGTCATGGGCAGTTGATAGGCTATGGCTGGAACGACCG
CGAGAACATTATCAAATGGACAGAAATGATAGTTGATAAGAATTCATCAA
GCCAAATTACTTTATTTGGTGTTTCAATGGGTGGAGCAACAGTCATGATG
GCTAGTGGTGAAAAATTACCTAGTCAGGTTGTTAATATCATTGAAGATTG
CGGTTATTCtGGTGTTTGGGATGAATTAAAATTTCAGGCTAAAGAGATGT
ATGGTTTACCAGCCTTCCCACTCTTATATGAAGTTTCAACAATTTCTAAA
ATCAGAGCAGGTTTTTCGTATGGACAAgCAAGTAGTGTCGAACAATTGAA
AAAGAATAATTTACCAGCCCTCTTTATTCATGGTGATAAGGATAATTTTG
TTCCAACAAGTATGGTTTATGACAACTATAAAGCTACAGCAGGTAAGAAA
GAGCTTTATATTGTAAAAGGGGCAAAACATGCGAAATCTTTTGAAACAGA
GCCAGAAAAATATGAGAAACGTATCTCTAGTTTTTTGAAAAAaTATgAAA
AA

SEQ ID NO. 8305
STRAIN 18RS21

Table 83: Comparative Sequences relating to SAG0108

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCGA
GATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTT
ATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAA
TGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCCTGCTGTTAAG
AAAACTCATAAGACAGCTGTTGTCGTTCATGGTTTTGCGAATAGCAAAGA
GAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTC
TTATGCCTGACAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGC
TATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
TGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTTCAATGGGTG
GAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTT
AATATCATTGAAGATTGCGGTTATTcTAGTGTTTGGGATgAATTAAAATT
TCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAG
TTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAgCAAGT
AGTGTCGAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCATGG
TGATAAGGATAATTTTGTTCCAACAAGTATGGTTTATGACAACTATAAAG
CTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGCG
AAATCTTTTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTT
TTTGAAAAAATATGAAAAA

SEQ ID NO. 8306
STRAIN M732
GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCGA
GATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTT
ATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAA
TGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCCTGCTGCTAAG
AAAACTCATAAGACAGTTGTTGTCGTTCATGGTTTTGCGAATAGCAAAGA
GAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTC
TTATGCCTGACAACATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGC
TATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
GGATAAGAATCCATCAAGCCAAATTaCTTTATTTGGTGTTTCAATGGGTG
GAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTT
AATATCATTGAAGATTGTGGTTATTCTAGTGTTTGGGATGAATTAAAATT
TCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAG
TTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAgCAAGT
AGTGTCGAACAATTGAAAAAGAATAATTTACCAGCCCTcTTTATTCATGG
TGATAAGGATAATTTTGTTCCAACAAGTATGGTTTATGACAACTATAAAG
CTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGCG
AAATCTTTTGAAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTT
TTTGAAAAAATATGAAAAA

SEQ ID NO. 8307
STRAIN COH1
GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTC
GAGATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCT
TTATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGA
AATGaCAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCCTGCTGCTA
AGAAAACTCATAAGACAGTTGTTGTCGTTCATGGTTTTGCGAATAGCAAA
GAGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGT
TCTTATGCCTGACAACATTGCACATGGTGAAAGTCATGGGCAGTTGATAG
GCTATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATA
GTGGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTTCAATGGG
TGGAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTG
TTAATATCATTGAAGATTGTGGTTATTcTAGTGTTTGGGATgAATTAAAA
TTTCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGA
AGTTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAA
GTAGTGTCGAACAATTGAAAAAGAATAATTTACCAGCCCTcTTTATTCAT
GGTGATAAGGATAATTTTGTTCCAACAaGTATGGTTTATGACAACTATAA
AGCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATG
CGAAATCTTTTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGT
TTTTTGAAAAAATATGAAAAA

SEQ ID NO. 8308
STRAIN M781
GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCG
AGATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTT
TATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAA
ATGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCCTGCTGCTAA
GAAAACTCATAAGACAGTTGTTGTCGTTCATGGTTTTGCGAATAGCAAAG
AGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTT
CTTATGCCTGACAACATTGCACATGGTGAAAGTCATGGGCAGTTGATAGG
CTATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAG
TGGATAAGAATCCATCAAGCCAAATTaCTTTATTTGGTGTTTCAATGGGT
GGAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGT
TAATATCATTGAAGATTGTGGTTATTcTAGTGTTTGGGATgAATTAAAAT
TTCAGGcTAAAGAGATGTATGGTTTACCAGCCTTCCCACTcTTATATGaA
GTTTCAacAATTTcTAAAATcAgAGCAGGTTTTTCGTATGGACaAgCAAG
TAgTGTCGAACAATtGAAAAAGAATAATTTACCAGCCCTcTTTATTCATG
GTGATAAGGATAATTTTGTTCCAACAaGTATGGTTTATGaCAaCTATAAA
GCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGC
GAAATCTTTTGAAaCAGAGCCAGAaaAATATGAGAAACGTATCTCTAGTT
TTTTGAAAAAATATGAAAAA

SEQ ID NO. 8309

Table 83: Comparative Sequences relating to SAG0108

STRAIN CJB110
GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCGAG
ATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTTA
TATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAAT
GACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCCTGCTGCTAAGA
AAACTCATAAGACAGCTGTTGTCGTTCATGGTTTTGCGAATAGCAAAGAG
AATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTcT
TATGCCTGACAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGCT
ATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGTT
GATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTTCAATGGGTGG
AGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTTA
ATATCATTGAAGATTGCGGTTATTcTAGTGTTTGGGATgAATTAAAATTT
CAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAGT
TTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAgCAAGTA
gTGTCGAACAATTGAAAAAGAATAATTTACCAGCCCTcTTTATTCATGGT
GATAAGGATAATTTTGTTCCAACAAGTATGGTTTATGACAACTATAAAGC
TACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGCGA
AATCTTTTGAAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTTT
TTGAAAAAATATGAAAAA

SEQ ID NO. 8310
STRAIN 1169NT
GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCGA
GATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTT
ATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAA
TGACAAACCaAAATATAAAGCAAGTTGCTTGGTATGTTCCTGCTGCTAAG
AAAACTCATAAGACAGCTGTTGTCGTTCATGGTTTTGCGAAtAGCAAAGA
gAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTc
TTATACCTGACAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGC
TATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
TGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTTCAATGGGTG
GAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTT
AATATCATTGAAGATTgCGGTTATTcTAGTGTTTGGGATgAATTAAAATT
TCAGGCTAaAGAGATGTATGGTTTaCCAGCCTTCCCACTcTTATATGAAG
TTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGT
AGTGTAGAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCATGG
TGATAAGGATAATTTTGTTCCAACAAGTATGGTTTATGACAACTATAAAG
CTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGCG
AAATCTTTTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTT
TTTGAAAAAATATGAAAAA

SEQ ID NO. 8311
STRAIN JM9130013
GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCG
AGATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTT
TATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAA
ATGaCAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCCTGCTGTTAA
GAAAACTCATAAGACAGCTGTTGTCGTTCATGGTTTTGCGAATAGCAAAG
AGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTT
CTTATGCCTGACAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGG
CTATGGCTGGAACGACCGCGAGAACATTATCaAATGGACAGAAATGATAG
TTGATAAGAATCCATCAAGCCAAATTaCTTTATTTGGTGTTTCAATGGGT
GGAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGT
TAATATCATTGAAGATTGCGGTTATTcTAGTGTTTGGGATgAATTAAAAT
TTCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAA
GTTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAG
TAGTGTCGAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCATG
GTGATAAGGATAATTTTGTTCCAACAAGTATGGTTTATGACAACTATAAA
GCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGC
GAAATCTTTTGAAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTT
TTTTGAAAAAATATGAAAAA

```
PRETTY of: /biotmp/msa286608.2{*}   February 24, 2003 06:26  ..

                                  1                                                50
       msa286608.2{662_COH1}      ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
       msa286608.2{662_M732}      ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
       msa286608.2{662_M781}      ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
       msa286608.2{662_A909}      ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
       msa286608.2{662_H36B}      ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
        msa286608.2{662_090}      ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa286608.2{662_CJB110}      ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa286608.2{662_18RS21}      ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
       msa286608.2{662_2603}      atgaaaaaga ttcgattatc aaagtttatt aaaatgattg ttgttatttt
  msa286608.2{662_JM9130013}      ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa286608.2{662_1169NT}      ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                   Consensus      ********** ********** ********** ********** **********

                                  51                                              100
       msa286608.2{662_COH1}      ~~~~~~~~~~ ~~~~~~~~~g ctagttttta tttttccac gttgcccaag
       msa286608.2{662_M732}      ~~~~~~~~~~ ~~~~~~~~~g ctagttttta tttttccac gttgcccaag
       msa286608.2{662_M781}      ~~~~~~~~~~ ~~~~~~~~~g ctagttttta tttttccac gttgcccaag
```

Table 83: Comparative Sequences relating to SAG0108

```
     msa286608.2{662_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa286608.2{662_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~agttttta tttttttccac gttgcccaag
      msa286608.2{662_090}  ~~~~~~~~~~ ~~~~~~~~~g ctagttttta tttttttccac gttgcccaag
   msa286608.2{662_CJB110}  ~~~~~~~~~~ ~~~~~~~~~g ctagttttta tttttttccac gttgcccaag
   msa286608.2{662_18RS21}  ~~~~~~~~~~ ~~~~~~~~~g ctagttttta tttttttccac gttgcccaag
     msa286608.2{662_2603}  gtttttaatt agtgtagcag ctagttttta tttttttccac gttgcccaag
msa286608.2{662_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~g ctagttttta tttttttccac gttgcccaag
   msa286608.2{662_1169NT}  ~~~~~~~~~~ ~~~~~~~~~g ctagttttta tttttttccac gttgcccaag
                 Consensus  ********** *********_ ---------- ---------- ----------

                            101                                              150
     msa286608.2{662_COH1}  ttcgagatga taAATCCTTT ATTTCAAATG GTCAACGTAA GCCTGGAAAC
     msa286608.2{662_M732}  ttcgagatga taAATCCTTT ATTTCAAATG GTCAACGTAA GCCTGGAAAC
     msa286608.2{662_M781}  ttcgagatga taAATCCTTT ATTTCAAATG GTCAACGTAA GCCTGGAAAC
     msa286608.2{662_A909}  ~~~~~~~~~~ ~~AATCCTTT ATTTCAAATG GTCAACGTAA GCCTGGAAAC
     msa286608.2{662_H36B}  ttcgagatga taAATCCTTT ATTTCAAATG GTCAACGTAA GCCTGGAAAC
      msa286608.2{662_090}  ttcgagatga taAATCCTTT ATTTCAAATG GTCAACGTAA GCCTGGAAAC
   msa286608.2{662_CJB110}  ttcgagatga taAATCCTTT ATTTCAAATG GTCAACGTAA GCCTGGAAAC
   msa286608.2{662_18RS21}  ttcgagatga taAATCCTTT ATTTCAAATG GTCAACGTAA GCCTGGAAAC
     msa286608.2{662_2603}  ttcgagatga taAATCCTTT ATTTCAAATG GTCAACGTAA GCCTGGAAAC
msa286608.2{662_JM9130013}  ttcgagatga taAATCCTTT ATTTCAAATG GTCAACGTAA GCCTGGAAAC
   msa286608.2{662_1169NT}  ttcgagatga taAATCCTTT ATTTCAAATG GTCAACGTAA GCCTGGAAAC
                 Consensus  ---------- --******** ********** ********** **********

                            151                                              200
     msa286608.2{662_COH1}  TCTTTATATG CTTATGATAA ATCCTTTGAT AAGCTATTAA AGCAAAAAAT
     msa286608.2{662_M732}  TCTTTATATG CTTATGATAA ATCCTTTGAT AAGCTATTAA AGCAAAAAAT
     msa286608.2{662_M781}  TCTTTATATG CTTATGATAA ATCCTTTGAT AAGCTATTAA AGCAAAAAAT
     msa286608.2{662_A909}  TCTTTATATG CTTATGATAA ATCCTTTGAT AAGCTATTAA AGCAAAAAAT
     msa286608.2{662_H36B}  TCTTTATATG CTTATGATAA ATCCTTTGAT AAGCTATTAA AGCAAAAAAT
      msa286608.2{662_090}  TCTTTATATG CTTATGATAA ATCCTTTGAT AAGCTATTAA AGCAAAAAAT
   msa286608.2{662_CJB110}  TCTTTATATG CTTATGATAA ATCCTTTGAT AAGCTATTAA AGCAAAAAAT
   msa286608.2{662_18RS21}  TCTTTATATG CTTATGATAA ATCCTTTGAT AAGCTATTAA AGCAAAAAAT
     msa286608.2{662_2603}  TCTTTATATG CTTATGATAA ATCCTTTGAT AAGCTATTAA AGCAAAAAAT
msa286608.2{662_JM9130013}  TCTTTATATG CTTATGATAA ATCCTTTGAT AAGCTATTAA AGCAAAAAAT
   msa286608.2{662_1169NT}  TCTTTATATG CTTATGATAA ATCCTTTGAT AAGCTATTAA AGCAAAAAAT
                 Consensus  ********** ********** ********** ********** **********

                            201                                              250
     msa286608.2{662_COH1}  AGAAATGACA AACCAAAATA TAAAGCAAGT TGCTTGGTAT GTTCCTGCTG
     msa286608.2{662_M732}  AGAAATGACA AACCAAAATA TAAAGCAAGT TGCTTGGTAT GTTCCTGCTG
     msa286608.2{662_M781}  AGAAATGACA AACCAAAATA TAAAGCAAGT TGCTTGGTAT GTTCCTGCTG
     msa286608.2{662_A909}  AGAAATGACA AACCAAAATA TAAAGCAAGT TGCTTGGTAT GTTCCTGCTG
     msa286608.2{662_H36B}  AGAAATGACA AACCAAAATA TAAAGCAAGT TGCTTGGTAT GTTCCTGCTG
      msa286608.2{662_090}  AGAAATGACA AACCAAAATA TAAAGCAAGT TGCTTGGTAT GTTCCTGCTG
   msa286608.2{662_CJB110}  AGAAATGACA AACCAAAATA TAAAGCAAGT TGCTTGGTAT GTTCCTGCTG
   msa286608.2{662_18RS21}  AGAAATGACA AACCAAAATA TAAAGCAAGT TGCTTGGTAT GTTCCTGCTG
     msa286608.2{662_2603}  AGAAATGACA AACCAAAATA TAAAGCAAGT TGCTTGGTAT GTTCCTGCTG
msa286608.2{662_JM9130013}  AGAAATGACA AACCAAAATA TAAAGCAAGT TGCTTGGTAT GTTCCTGCTG
   msa286608.2{662_1169NT}  AGAAATGACA AACCAAAATA TAAAGCAAGT TGCTTGGTAT GTTCCTGCTG
                 Consensus  ********** ********** ********** ********** **********

                            251                                              300
     msa286608.2{662_COH1}  cTAAGAAAAC TCATAAGACA GtTGTTGTCG TTCATGGTTT TGCGAATAGC
     msa286608.2{662_M732}  cTAAGAAAAC TCATAAGACA GtTGTTGTCG TTCATGGTTT TGCGAATAGC
     msa286608.2{662_M781}  cTAAGAAAAC TCATAAGACA GtTGTTGTCG TTCATGGTTT TGCGAATAGC
     msa286608.2{662_A909}  cTAAGAAAAC TCATAAGACA GcTGTTGTCG TTCATGGTTT TGCGAATAGC
     msa286608.2{662_H36B}  cTAAGAAAAC TCATAAGACA GcTGTTGTCG TTCATGGTTT TGCGAATAGC
      msa286608.2{662_090}  cTAAGAAAAC TCATAAGACA GcTGTTGTCG TTCATGGTTT TGCGAATAGC
   msa286608.2{662_CJB110}  cTAAGAAAAC TCATAAGACA GcTGTTGTCG TTCATGGTTT TGCGAATAGC
   msa286608.2{662_18RS21}  tTAAGAAAAC TCATAAGACA GcTGTTGTCG TTCATGGTTT TGCGAATAGC
     msa286608.2{662_2603}  tTAAGAAAAC TCATAAGACA GcTGTTGTCG TTCATGGTTT TGCGAATAGC
msa286608.2{662_JM9130013}  tTAAGAAAAC TCATAAGACA GcTGTTGTCG TTCATGGTTT TGCGAATAGC
   msa286608.2{662_1169NT}  cTAAGAAAAC TCATAAGACA GcTGTTGTCG TTCATGGTTT TGCGAATAGC
                 Consensus  -********* ********** *_******** ********** **********

                            301                                              350
     msa286608.2{662_COH1}  AAAGAGAATA TGAAGGCATA TGGTTGGCTG TTTCATAAGT TAGGATACAA
     msa286608.2{662_M732}  AAAGAGAATA TGAAGGCATA TGGTTGGCTG TTTCATAAGT TAGGATACAA
     msa286608.2{662_M781}  AAAGAGAATA TGAAGGCATA TGGTTGGCTG TTTCATAAGT TAGGATACAA
     msa286608.2{662_A909}  AAAGAGAATA TGAAGGCATA TGGTTGGCTG TTTCATAAGT TAGGATACAA
     msa286608.2{662_H36B}  AAAGAGAATA TGAAGGCATA TGGTTGGCTG TTTCATAAGT TAGGATACAA
      msa286608.2{662_090}  AAAGAGAATA TGAAGGCATA TGGTTGGCTG TTTCATAAGT TAGGATACAA
   msa286608.2{662_CJB110}  AAAGAGAATA TGAAGGCATA TGGTTGGCTG TTTCATAAGT TAGGATACAA
   msa286608.2{662_18RS21}  AAAGAGAATA TGAAGGCATA TGGTTGGCTG TTTCATAAGT TAGGATACAA
     msa286608.2{662_2603}  AAAGAGAATA TGAAGGCATA TGGTTGGCTG TTTCATAAGT TAGGATACAA
msa286608.2{662_JM9130013}  AAAGAGAATA TGAAGGCATA TGGTTGGCTG TTTCATAAGT TAGGATACAA
   msa286608.2{662_1169NT}  AAAGAGAATA TGAAGGCATA TGGTTGGCTG TTTCATAAGT TAGGATACAA
                 Consensus  ********** ********** ********** ********** **********

                            351                                              400
     msa286608.2{662_COH1}  TGTTCTTATg CCTGACAAcA TTGCACATGG TGAAAGTCAT GGGCAGTTGA
     msa286608.2{662_M732}  TGTTCTTATg CCTGACAAcA TTGCACATGG TGAAAGTCAT GGGCAGTTGA
```

Table 83: Comparative Sequences relating to SAG0108

```
   msa286608.2{662_M781}  TGTTCTTATg CCTGACAAcA TTGCACATGG TGAAAGTCAT GGGCAGTTGA
   msa286608.2{662_A909}  TGTTCTTATg CCTGACAAcA TTGCACATGG TGAAAGTCAT GGGCAGTTGA
   msa286608.2{662_H36B}  TGTTCTTATg CCTGACAAcA TTGCACATGG TGAAAGTCAT GGGCAGTTGA
    msa286608.2{662_090}  TGTTCTTATg CCTGACAAtA TTGCACATGG TGAAAGTCAT GGGCAGTTGA
  msa286608.2{662_CJB110}  TGTTCTTATg CCTGACAAtA TTGCACATGG TGAAAGTCAT GGGCAGTTGA
  msa286608.2{662_18RS21}  TGTTCTTATg CCTGACAAtA TTGCACATGG TGAAAGTCAT GGGCAGTTGA
   msa286608.2{662_2603}  TGTTCTTATg CCTGACAAtA TTGCACATGG TGAAAGTCAT GGGCAGTTGA
msa286608.2{662_JM9130013}  TGTTCTTATg CCTGACAAtA TTGCACATGG TGAAAGTCAT GGGCAGTTGA
  msa286608.2{662_1169NT}  TGTTCTTATa CCTGACAAtA TTGCACATGG TGAAAGTCAT GGGCAGTTGA
               Consensus  *********_ ********_* ********** ********** **********

                          401                                               450
   msa286608.2{662_COH1}  TAGGCTATGG CTGGAACGAC CGCGAGAACA TTATCAAATG GACAGAAATG
   msa286608.2{662_M732}  TAGGCTATGG CTGGAACGAC CGCGAGAACA TTATCAAATG GACAGAAATG
   msa286608.2{662_M781}  TAGGCTATGG CTGGAACGAC CGCGAGAACA TTATCAAATG GACAGAAATG
   msa286608.2{662_A909}  TAGGCTATGG CTGGAACGAC CGCGAGAACA TTATCAAATG GACAGAAATG
   msa286608.2{662_H36B}  TAGGCTATGG CTGGAACGAC CGCGAGAACA TTATCAAATG GACAGAAATG
    msa286608.2{662_090}  TAGGCTATGG CTGGAACGAC CGCGAGAACA TTATCAAATG GACAGAAATG
  msa286608.2{662_CJB110}  TAGGCTATGG CTGGAACGAC CGCGAGAACA TTATCAAATG GACAGAAATG
  msa286608.2{662_18RS21}  TAGGCTATGG CTGGAACGAC CGCGAGAACA TTATCAAATG GACAGAAATG
   msa286608.2{662_2603}  TAGGCTATGG CTGGAACGAC CGCGAGAACA TTATCAAATG GACAGAAATG
msa286608.2{662_JM9130013}  TAGGCTATGG CTGGAACGAC CGCGAGAACA TTATCAAATG GACAGAAATG
  msa286608.2{662_1169NT}  TAGGCTATGG CTGGAACGAC CGCGAGAACA TTATCAAATG GACAGAAATG
               Consensus  ********** ********** ********** ********** **********

                          451                                               500
   msa286608.2{662_COH1}  ATAGTgGATA AGAATcCATC AAGCCAAATT ACTTTATTTG GTGTTTCAAT
   msa286608.2{662_M732}  ATAGTgGATA AGAATcCATC AAGCCAAATT ACTTTATTTG GTGTTTCAAT
   msa286608.2{662_M781}  ATAGTgGATA AGAATcCATC AAGCCAAATT ACTTTATTTG GTGTTTCAAT
   msa286608.2{662_A909}  ATAGTtGATA AGAATtCATC AAGCCAAATT ACTTTATTTG GTGTTTCAAT
   msa286608.2{662_H36B}  ATAGTtGATA AGAATtCATC AAGCCAAATT ACTTTATTTG GTGTTTCAAT
    msa286608.2{662_090}  ATAGTtGATA AGAATcCATC AAGCCAAATT ACTTTATTTG GTGTTTCAAT
  msa286608.2{662_CJB110}  ATAGTtGATA AGAATcCATC AAGCCAAATT ACTTTATTTG GTGTTTCAAT
  msa286608.2{662_18RS21}  ATAGTtGATA AGAATcCATC AAGCCAAATT ACTTTATTTG GTGTTTCAAT
   msa286608.2{662_2603}  ATAGTtGATA AGAATcCATC AAGCCAAATT ACTTTATTTG GTGTTTCAAT
msa286608.2{662_JM9130013}  ATAGTtGATA AGAATcCATC AAGCCAAATT ACTTTATTTG GTGTTTCAAT
  msa286608.2{662_1169NT}  ATAGTtGATA AGAATcCATC AAGCCAAATT ACTTTATTTG GTGTTTCAAT
               Consensus  *****_**** *****_**** ********** ********** **********

                          501                                               550
   msa286608.2{662_COH1}  GGGTGGAGCA ACAGTCATGA TGGCTAGTGG TGAAAAATTA CCTAGTCAGG
   msa286608.2{662_M732}  GGGTGGAGCA ACAGTCATGA TGGCTAGTGG TGAAAAATTA CCTAGTCAGG
   msa286608.2{662_M781}  GGGTGGAGCA ACAGTCATGA TGGCTAGTGG TGAAAAATTA CCTAGTCAGG
   msa286608.2{662_A909}  GGGTGGAGCA ACAGTCATGA TGGCTAGTGG TGAAAAATTA CCTAGTCAGG
   msa286608.2{662_H36B}  GGGTGGAGCA ACAGTCATGA TGGCTAGTGG TGAAAAATTA CCTAGTCAGG
    msa286608.2{662_090}  GGGTGGAGCA ACAGTCATGA TGGCTAGTGG TGAAAAATTA CCTAGTCAGG
  msa286608.2{662_CJB110}  GGGTGGAGCA ACAGTCATGA TGGCTAGTGG TGAAAAATTA CCTAGTCAGG
  msa286608.2{662_18RS21}  GGGTGGAGCA ACAGTCATGA TGGCTAGTGG TGAAAAATTA CCTAGTCAGG
   msa286608.2{662_2603}  GGGTGGAGCA ACAGTCATGA TGGCTAGTGG TGAAAAATTA CCTAGTCAGG
msa286608.2{662_JM9130013}  GGGTGGAGCA ACAGTCATGA TGGCTAGTGG TGAAAAATTA CCTAGTCAGG
  msa286608.2{662_1169NT}  GGGTGGAGCA ACAGTCATGA TGGCTAGTGG TGAAAAATTA CCTAGTCAGG
               Consensus  ********** ********** ********** ********** **********

                          551                                               600
   msa286608.2{662_COH1}  TTGTTAATAT CATTGAAGAT TGtGGTTATT CTaGTGTTTG GGATGAATTA
   msa286608.2{662_M732}  TTGTTAATAT CATTGAAGAT TGtGGTTATT CTaGTGTTTG GGATGAATTA
   msa286608.2{662_M781}  TTGTTAATAT CATTGAAGAT TGtGGTTATT CTaGTGTTTG GGATGAATTA
   msa286608.2{662_A909}  TTGTTAATAT CATTGAAGAT TGcGGTTATT CTgGTGTTTG GGATGAATTA
   msa286608.2{662_H36B}  TTGTTAATAT CATTGAAGAT TGcGGTTATT CTgGTGTTTG GGATGAATTA
    msa286608.2{662_090}  TTGTTAATAT CATTGAAGAT TGcGGTTATT CTaGTGTTTG GGATGAATTA
  msa286608.2{662_CJB110}  TTGTTAATAT CATTGAAGAT TGcGGTTATT CTaGTGTTTG GGATGAATTA
  msa286608.2{662_18RS21}  TTGTTAATAT CATTGAAGAT TGcGGTTATT CTaGTGTTTG GGATGAATTA
   msa286608.2{662_2603}  TTGTTAATAT CATTGAAGAT TGcGGTTATT CTaGTGTTTG GGATGAATTA
msa286608.2{662_JM9130013}  TTGTTAATAT CATTGAAGAT TGcGGTTATT CTaGTGTTTG GGATGAATTA
  msa286608.2{662_1169NT}  TTGTTAATAT CATTGAAGAT TGcGGTTATT CTaGTGTTTG GGATGAATTA
               Consensus  ********** ********** **_******* **_******* **********

                          601                                               650
   msa286608.2{662_COH1}  AAATTTCAGG CTAAAGAGAT GTATGGTTTA CCAGCCTTCC CACTCTTATA
   msa286608.2{662_M732}  AAATTTCAGG CTAAAGAGAT GTATGGTTTA CCAGCCTTCC CACTCTTATA
   msa286608.2{662_M781}  AAATTTCAGG CTAAAGAGAT GTATGGTTTA CCAGCCTTCC CACTCTTATA
   msa286608.2{662_A909}  AAATTTCAGG CTAAAGAGAT GTATGGTTTA CCAGCCTTCC CACTCTTATA
   msa286608.2{662_H36B}  AAATTTCAGG CTAAAGAGAT GTATGGTTTA CCAGCCTTCC CACTCTTATA
    msa286608.2{662_090}  AAATTTCAGG CTAAAGAGAT GTATGGTTTA CCAGCCTTCC CACTCTTATA
  msa286608.2{662_CJB110}  AAATTTCAGG CTAAAGAGAT GTATGGTTTA CCAGCCTTCC CACTCTTATA
  msa286608.2{662_18RS21}  AAATTTCAGG CTAAAGAGAT GTATGGTTTA CCAGCCTTCC CACTCTTATA
   msa286608.2{662_2603}  AAATTTCAGG CTAAAGAGAT GTATGGTTTA CCAGCCTTCC CACTCTTATA
msa286608.2{662_JM9130013}  AAATTTCAGG CTAAAGAGAT GTATGGTTTA CCAGCCTTCC CACTCTTATA
  msa286608.2{662_1169NT}  AAATTTCAGG CTAAAGAGAT GTATGGTTTA CCAGCCTTCC CACTCTTATA
               Consensus  ********** ********** ********** ********** **********

                          651                                               700
   msa286608.2{662_COH1}  TGAAGTTTCA ACAATTTCTA AAATCAGAGC AGGTTTTTCG TATGGACAAG
```

Table 83: Comparative Sequences relating to SAG0108

```
     msa286608.2{662_M732}  TGAAGTTTCA ACAATTTCTA AAATCAGAGC AGGTTTTTCG TATGGACAAG
     msa286608.2{662_M781}  TGAAGTTTCA ACAATTTCTA AAATCAGAGC AGGTTTTTCG TATGGACAAG
     msa286608.2{662_A909}  TGAAGTTTCA ACAATTTCTA AAATCAGAGC AGGTTTTTCG TATGGACAAG
     msa286608.2{662_H36B}  TGAAGTTTCA ACAATTTCTA AAATCAGAGC AGGTTTTTCG TATGGACAAG
      msa286608.2{662_090}  TGAAGTTTCA ACAATTTCTA AAATCAGAGC AGGTTTTTCG TATGGACAAG
   msa286608.2{662_CJB110}  TGAAGTTTCA ACAATTTCTA AAATCAGAGC AGGTTTTTCG TATGGACAAG
   msa286608.2{662_18RS21}  TGAAGTTTCA ACAATTTCTA AAATCAGAGC AGGTTTTTCG TATGGACAAG
     msa286608.2{662_2603}  TGAAGTTTCA ACAATTTCTA AAATCAGAGC AGGTTTTTCG TATGGACAAG
msa286608.2{662_JM9130013}  TGAAGTTTCA ACAATTTCTA AAATCAGAGC AGGTTTTTCG TATGGACAAG
  msa286608.2{662_1169NT}   TGAAGTTTCA ACAATTTCTA AAATCAGAGC AGGTTTTTCG TATGGACAAG
                Consensus   ********** ********** ********** ********** **********

                            701                                                750
     msa286608.2{662_COH1}  CAAGTAGTGT cGAACAATTG AAAAAGAATA ATTTACCAGC CCTCTTTATT
     msa286608.2{662_M732}  CAAGTAGTGT cGAACAATTG AAAAAGAATA ATTTACCAGC CCTCTTTATT
     msa286608.2{662_M781}  CAAGTAGTGT cGAACAATTG AAAAAGAATA ATTTACCAGC CCTCTTTATT
     msa286608.2{662_A909}  CAAGTAGTGT cGAACAATTG AAAAAGAATA ATTTACCAGC CCTCTTTATT
     msa286608.2{662_H36B}  CAAGTAGTGT cGAACAATTG AAAAAGAATA ATTTACCAGC CCTCTTTATT
      msa286608.2{662_090}  CAAGTAGTGT cGAACAATTG AAAAAGAATA ATTTACCAGC CCTCTTTATT
   msa286608.2{662_CJB110}  CAAGTAGTGT cGAACAATTG AAAAAGAATA ATTTACCAGC CCTCTTTATT
   msa286608.2{662_18RS21}  CAAGTAGTGT cGAACAATTG AAAAAGAATA ATTTACCAGC CCTCTTTATT
     msa286608.2{662_2603}  CAAGTAGTGT cGAACAATTG AAAAAGAATA ATTTACCAGC CCTCTTTATT
msa286608.2{662_JM9130013}  CAAGTAGTGT cGAACAATTG AAAAAGAATA ATTTACCAGC CCTCTTTATT
  msa286608.2{662_1169NT}   CAAGTAGTGT aGAACAATTG AAAAAGAATA ATTTACCAGC CCTCTTTATT
                Consensus   ********** -********* ********** ********** **********

                            751                                                800
     msa286608.2{662_COH1}  CATGGTGATA AGGATAATTT TGTTCCAACA AGTATGGTTT ATGACAACTA
     msa286608.2{662_M732}  CATGGTGATA AGGATAATTT TGTTCCAACA AGTATGGTTT ATGACAACTA
     msa286608.2{662_M781}  CATGGTGATA AGGATAATTT TGTTCCAACA AGTATGGTTT ATGACAACTA
     msa286608.2{662_A909}  CATGGTGATA AGGATAATTT TGTTCCAACA AGTATGGTTT ATGACAACTA
     msa286608.2{662_H36B}  CATGGTGATA AGGATAATTT TGTTCCAACA AGTATGGTTT ATGACAACTA
      msa286608.2{662_090}  CATGGTGATA AGGATAATTT TGTTCCAACA AGTATGGTTT ATGACAACTA
   msa286608.2{662_CJB110}  CATGGTGATA AGGATAATTT TGTTCCAACA AGTATGGTTT ATGACAACTA
   msa286608.2{662_18RS21}  CATGGTGATA AGGATAATTT TGTTCCAACA AGTATGGTTT ATGACAACTA
     msa286608.2{662_2603}  CATGGTGATA AGGATAATTT TGTTCCAACA AGTATGGTTT ATGACAACTA
msa286608.2{662_JM9130013}  CATGGTGATA AGGATAATTT TGTTCCAACA AGTATGGTTT ATGACAACTA
  msa286608.2{662_1169NT}   CATGGTGATA AGGATAATTT TGTTCCAACA AGTATGGTTT ATGACAACTA
                Consensus   ********** ********** ********** ********** **********

                            801                                                850
     msa286608.2{662_COH1}  TAAAGCTACA GCAGGTAAGA AAGAGCTTTA TATTGTAAAA GGGGCAAAAC
     msa286608.2{662_M732}  TAAAGCTACA GCAGGTAAGA AAGAGCTTTA TATTGTAAAA GGGGCAAAAC
     msa286608.2{662_M781}  TAAAGCTACA GCAGGTAAGA AAGAGCTTTA TATTGTAAAA GGGGCAAAAC
     msa286608.2{662_A909}  TAAAGCTACA GCAGGTAAGA AAGAGCTTTA TATTGTAAAA GGGGCAAAAC
     msa286608.2{662_H36B}  TAAAGCTACA GCAGGTAAGA AAGAGCTTTA TATTGTAAAA GGGGCAAAAC
      msa286608.2{662_090}  TAAAGCTACA GCAGGTAAGA AAGAGCTTTA TATTGTAAAA GGGGCAAAAC
   msa286608.2{662_CJB110}  TAAAGCTACA GCAGGTAAGA AAGAGCTTTA TATTGTAAAA GGGGCAAAAC
   msa286608.2{662_18RS21}  TAAAGCTACA GCAGGTAAGA AAGAGCTTTA TATTGTAAAA GGGGCAAAAC
     msa286608.2{662_2603}  TAAAGCTACA GCAGGTAAGA AAGAGCTTTA TATTGTAAAA GGGGCAAAAC
msa286608.2{662_JM9130013}  TAAAGCTACA GCAGGTAAGA AAGAGCTTTA TATTGTAAAA GGGGCAAAAC
  msa286608.2{662_1169NT}   TAAAGCTACA GCAGGTAAGA AAGAGCTTTA TATTGTAAAA GGGGCAAAAC
                Consensus   ********** ********** ********** ********** **********

                            851                                                900
     msa286608.2{662_COH1}  ATGCGAAATC TTTTGAAACA GAGCCAGAAA AATATGAGAA ACGTATCTCT
     msa286608.2{662_M732}  ATGCGAAATC TTTTGAAACA GAGCCAGAAA AATATGAGAA ACGTATCTCT
     msa286608.2{662_M781}  ATGCGAAATC TTTTGAAACA GAGCCAGAAA AATATGAGAA ACGTATCTCT
     msa286608.2{662_A909}  ATGCGAAATC TTTTGAAACA GAGCCAGAAA AATATGAGAA ACGTATCTCT
     msa286608.2{662_H36B}  ATGCGAAATC TTTTGAAACA GAGCCAGAAA AATATGAGAA ACGTATCTCT
      msa286608.2{662_090}  ATGCGAAATC TTTTGAAACA GAGCCAGAAA AATATGAGAA ACGTATCTCT
   msa286608.2{662_CJB110}  ATGCGAAATC TTTTGAAACA GAGCCAGAAA AATATGAGAA ACGTATCTCT
   msa286608.2{662_18RS21}  ATGCGAAATC TTTTGAAACA GAGCCAGAAA AATATGAGAA ACGTATCTCT
     msa286608.2{662_2603}  ATGCGAAATC TTTTGAAACA GAGCCAGAAA AATATGAGAA ACGTATCTCT
msa286608.2{662_JM9130013}  ATGCGAAATC TTTTGAAACA GAGCCAGAAA AATATGAGAA ACGTATCTCT
  msa286608.2{662_1169NT}   ATGCGAAATC TTTTGAAACA GAGCCAGAAA AATATGAGAA ACGTATCTCT
                Consensus   ********** ********** ********** ********** **********

                            901                  924
     msa286608.2{662_COH1}  AGTTTTTTGA AAAAATATGA AAAA
     msa286608.2{662_M732}  AGTTTTTTGA AAAAATATGA AAAA
     msa286608.2{662_M781}  AGTTTTTTGA AAAAATATGA AAAA
     msa286608.2{662_A909}  AGTTTTTTGA AAAAATATGA AAAA
     msa286608.2{662_H36B}  AGTTTTTTGA AAAAATATGA AAAA
      msa286608.2{662_090}  AGTTTTTTGA AAAAATATGA AAAA
   msa286608.2{662_CJB110}  AGTTTTTTGA AAAAATATGA AAAA
   msa286608.2{662_18RS21}  AGTTTTTTGA AAAAATATGA AAAA
     msa286608.2{662_2603}  AGTTTTTTGA AAAAATATGA AAAA
msa286608.2{662_JM9130013}  AGTTTTTTGA AAAAATATGA AAAA
  msa286608.2{662_1169NT}   AGTTTTTTGA AAAAATATGA AAAA
                Consensus   ********** ********** ****
```

SEQ ID NO. 8312

Table 83: Comparative Sequences relating to SAG0108

STRAIN 2603 frame: 1
MKKIRLSKFIKMIVVILFLISVAASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFD
KLLKQKIEMTNQNIKQVAWYVPAVKKTHKTAVVVHGFANSKENMKAYGWLFHKLGYNVLM
PDNIAHGESHGQLIGYGWNDRENIIKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKL
PSQVVNIIEDCGYSSVWDELKFQAKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQL
KKNNLPALFIHGDKDNFVPTSMVYDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRIS
SFLKKYEK

SEQ ID NO. 8313
STRAIN 090 frame: 1
ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
AKKTHKTAVVVHGFANSKENMKAYGWLFHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
IIKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNIIEDCGYSSVWDELKFQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNNLPALFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8314
STRAIN A909 frame: 3
SFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPAAKKTHKTAVVVHGFA
NSKENMKAYGWLFHKLGYNVLMPDNIAHGESHGQLIGYGWNDRENIIKWTEMIVDKNSSS
QITLFGVSMGGATVMMASGEKLPSQVVNIIEDCGYSGVWDELKFQAKEMYGLPAFPLLYE
VSTISKIRAGFSYGQASSVEQLKKNNLPALFIHGDKDNFVPTSMVYDNYKATAGKKELYI
VKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8315
STRAIN H36B frame: 1
SFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPAA
KKTHKTAVVVHGFANSKENMKAYGWLFHKLGYNVLMPDNIAHGESHGQLIGYGWNDRENI
IKWTEMIVDKNSSSQITLFGVSMGGATVMMASGEKLPSQVVNIIEDCGYSGVWDELKFQA
KEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNNLPALFIHGDKDNFVPTSMVY
DNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8316
STRAIN 18RS21 frame: 1
ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
VKKTHKTAVVVHGFANSKENMKAYGWLFHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
IIKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNIIEDCGYSSVWDELKFQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNNLPALFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8317
STRAIN M732 frame: 1
ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
AKKTHKTVVVVHGFANSKENMKAYGWLFHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
IIKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNIIEDCGYSSVWDELKFQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNNLPALFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8318
STRAIN COH1 frame: 1
ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
AKKTHKTVVVVHGFANSKENMKAYGWLFHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
IIKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNIIEDCGYSSVWDELKFQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNNLPALFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8319
STRAIN M781 frame: 1
ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
AKKTHKTVVVVHGFANSKENMKAYGWLFHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
IIKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNIIEDCGYSSVWDELKFQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNNLPALFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8320
STRAIN CJB110 frame: 1
ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
AKKTHKTAVVVHGFANSKENMKAYGWLFHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
IIKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNIIEDCGYSSVWDELKFQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNNLPALFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8321
STRAIN 1169NT frame: 1
ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
AKKTHKTAVVVHGFANSKENMKAYGWLFHKLGYNVLIPDNIAHGESHGQLIGYGWNDREN
IIKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNIIEDCGYSSVWDELKFQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNNLPALFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8322

Table 83: Comparative Sequences relating to SAG0108

STRAIN JM9130013 frame: 1
ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
VKKTHKTAVVVHGFANSKENMKAYGWLFHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
IIKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNIIEDCGYSSVWDELKFQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYGQASSVEQLKKNNLPALFIHGDKDNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

```
PRETTY of: /biotmp/msa286876.2{*}   February 24, 2003 06:46  ..

                            1                                                   50
     msa286876.2{662_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~SF ISNGQRKPGN
     msa286876.2{662_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~SFYFFH VAQVRDDKSF ISNGQRKPGN
     msa286876.2{662_COH1}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~ASFYFFH VAQVRDDKSF ISNGQRKPGN
     msa286876.2{662_M732}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~ASFYFFH VAQVRDDKSF ISNGQRKPGN
     msa286876.2{662_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~ASFYFFH VAQVRDDKSF ISNGQRKPGN
   msa286876.2{662_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~ASFYFFH VAQVRDDKSF ISNGQRKPGN
     msa286876.2{662_2603}  mkkirlskfi kmivvilfli svaASFYFFH VAQVRDDKSF ISNGQRKPGN
msa286876.2{662_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~ASFYFFH VAQVRDDKSF ISNGQRKPGN
      msa286876.2{662_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~ASFYFFH VAQVRDDKSF ISNGQRKPGN
   msa286876.2{662_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~ASFYFFH VAQVRDDKSF ISNGQRKPGN
   msa286876.2{662_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~ASFYFFH VAQVRDDKSF ISNGQRKPGN
                 Consensus  ********** ********** ********** ********** **********

                            51                                                 100
     msa286876.2{662_A909}  SLYAYDKSFD KLLKQKIEMT NQNIKQVAWY VPAaKKTHKT aVVVHGFANS
     msa286876.2{662_H36B}  SLYAYDKSFD KLLKQKIEMT NQNIKQVAWY VPAaKKTHKT aVVVHGFANS
     msa286876.2{662_COH1}  SLYAYDKSFD KLLKQKIEMT NQNIKQVAWY VPAaKKTHKT vVVVHGFANS
     msa286876.2{662_M732}  SLYAYDKSFD KLLKQKIEMT NQNIKQVAWY VPAaKKTHKT vVVVHGFANS
     msa286876.2{662_M781}  SLYAYDKSFD KLLKQKIEMT NQNIKQVAWY VPAaKKTHKT vVVVHGFANS
   msa286876.2{662_18RS21}  SLYAYDKSFD KLLKQKIEMT NQNIKQVAWY VPAvKKTHKT aVVVHGFANS
     msa286876.2{662_2603}  SLYAYDKSFD KLLKQKIEMT NQNIKQVAWY VPAvKKTHKT aVVVHGFANS
msa286876.2{662_JM9130013}  SLYAYDKSFD KLLKQKIEMT NQNIKQVAWY VPAvKKTHKT aVVVHGFANS
      msa286876.2{662_090}  SLYAYDKSFD KLLKQKIEMT NQNIKQVAWY VPAaKKTHKT aVVVHGFANS
   msa286876.2{662_CJB110}  SLYAYDKSFD KLLKQKIEMT NQNIKQVAWY VPAaKKTHKT aVVVHGFANS
   msa286876.2{662_1169NT}  SLYAYDKSFD KLLKQKIEMT NQNIKQVAWY VPAaKKTHKT aVVVHGFANS
                 Consensus  ********** ********** ********** ***_****** _*********

                            101                                                150
     msa286876.2{662_A909}  KENMKAYGWL FHKLGYNVLm PDNIAHGESH GQLIGYGWND RENIIKWTEM
     msa286876.2{662_H36B}  KENMKAYGWL FHKLGYNVLm PDNIAHGESH GQLIGYGWND RENIIKWTEM
     msa286876.2{662_COH1}  KENMKAYGWL FHKLGYNVLm PDNIAHGESH GQLIGYGWND RENIIKWTEM
     msa286876.2{662_M732}  KENMKAYGWL FHKLGYNVLm PDNIAHGESH GQLIGYGWND RENIIKWTEM
     msa286876.2{662_M781}  KENMKAYGWL FHKLGYNVLm PDNIAHGESH GQLIGYGWND RENIIKWTEM
   msa286876.2{662_18RS21}  KENMKAYGWL FHKLGYNVLm PDNIAHGESH GQLIGYGWND RENIIKWTEM
     msa286876.2{662_2603}  KENMKAYGWL FHKLGYNVLm PDNIAHGESH GQLIGYGWND RENIIKWTEM
msa286876.2{662_JM9130013}  KENMKAYGWL FHKLGYNVLm PDNIAHGESH GQLIGYGWND RENIIKWTEM
      msa286876.2{662_090}  KENMKAYGWL FHKLGYNVLm PDNIAHGESH GQLIGYGWND RENIIKWTEM
   msa286876.2{662_CJB110}  KENMKAYGWL FHKLGYNVLm PDNIAHGESH GQLIGYGWND RENIIKWTEM
   msa286876.2{662_1169NT}  KENMKAYGWL FHKLGYNVLi PDNIAHGESH GQLIGYGWND RENIIKWTEM
                 Consensus  ********** *********_ ********** ********** **********

                            151                                                200
     msa286876.2{662_A909}  IVDKNsSSQI TLFGVSMGGA TVMMASGEKL PSQVVNIIED CGYSgVWDEL
     msa286876.2{662_H36B}  IVDKNsSSQI TLFGVSMGGA TVMMASGEKL PSQVVNIIED CGYSgVWDEL
     msa286876.2{662_COH1}  IVDKNpSSQI TLFGVSMGGA TVMMASGEKL PSQVVNIIED CGYSsVWDEL
     msa286876.2{662_M732}  IVDKNpSSQI TLFGVSMGGA TVMMASGEKL PSQVVNIIED CGYSsVWDEL
     msa286876.2{662_M781}  IVDKNpSSQI TLFGVSMGGA TVMMASGEKL PSQVVNIIED CGYSsVWDEL
   msa286876.2{662_18RS21}  IVDKNpSSQI TLFGVSMGGA TVMMASGEKL PSQVVNIIED CGYSsVWDEL
     msa286876.2{662_2603}  IVDKNpSSQI TLFGVSMGGA TVMMASGEKL PSQVVNIIED CGYSsVWDEL
msa286876.2{662_JM9130013}  IVDKNpSSQI TLFGVSMGGA TVMMASGEKL PSQVVNIIED CGYSsVWDEL
      msa286876.2{662_090}  IVDKNpSSQI TLFGVSMGGA TVMMASGEKL PSQVVNIIED CGYSsVWDEL
   msa286876.2{662_CJB110}  IVDKNpSSQI TLFGVSMGGA TVMMASGEKL PSQVVNIIED CGYSsVWDEL
   msa286876.2{662_1169NT}  IVDKNpSSQI TLFGVSMGGA TVMMASGEKL PSQVVNIIED CGYSsVWDEL
                 Consensus  *****_**** ********** ********** ********** ****_*****

                            201                                                250
     msa286876.2{662_A909}  KFQAKEMYGL PAFPLLYEVS TISKIRAGFS YGQASSVEQL KKNNLPALFI
     msa286876.2{662_H36B}  KFQAKEMYGL PAFPLLYEVS TISKIRAGFS YGQASSVEQL KKNNLPALFI
     msa286876.2{662_COH1}  KFQAKEMYGL PAFPLLYEVS TISKIRAGFS YGQASSVEQL KKNNLPALFI
     msa286876.2{662_M732}  KFQAKEMYGL PAFPLLYEVS TISKIRAGFS YGQASSVEQL KKNNLPALFI
     msa286876.2{662_M781}  KFQAKEMYGL PAFPLLYEVS TISKIRAGFS YGQASSVEQL KKNNLPALFI
   msa286876.2{662_18RS21}  KFQAKEMYGL PAFPLLYEVS TISKIRAGFS YGQASSVEQL KKNNLPALFI
     msa286876.2{662_2603}  KFQAKEMYGL PAFPLLYEVS TISKIRAGFS YGQASSVEQL KKNNLPALFI
msa286876.2{662_JM9130013}  KFQAKEMYGL PAFPLLYEVS TISKIRAGFS YGQASSVEQL KKNNLPALFI
      msa286876.2{662_090}  KFQAKEMYGL PAFPLLYEVS TISKIRAGFS YGQASSVEQL KKNNLPALFI
   msa286876.2{662_CJB110}  KFQAKEMYGL PAFPLLYEVS TISKIRAGFS YGQASSVEQL KKNNLPALFI
   msa286876.2{662_1169NT}  KFQAKEMYGL PAFPLLYEVS TISKIRAGFS YGQASSVEQL KKNNLPALFI
                 Consensus  ********** ********** ********** ********** **********

                            251                                                300
     msa286876.2{662_A909}  HGDKDNFVPT SMVYDNYKAT AGKKELYIVK GAKHAKSFET EPEKYEKRIS
     msa286876.2{662_H36B}  HGDKDNFVPT SMVYDNYKAT AGKKELYIVK GAKHAKSFET EPEKYEKRIS
     msa286876.2{662_COH1}  HGDKDNFVPT SMVYDNYKAT AGKKELYIVK GAKHAKSFET EPEKYEKRIS
```

Table 83: Comparative Sequences relating to SAG0108

```
      msa286876.2{662_M732}  HGDKDNFVPT SMVYDNYKAT AGKKELYIVK GAKHAKSFET EPEKYEKRIS
      msa286876.2{662_M781}  HGDKDNFVPT SMVYDNYKAT AGKKELYIVK GAKHAKSFET EPEKYEKRIS
    msa286876.2{662_18RS21}  HGDKDNFVPT SMVYDNYKAT AGKKELYIVK GAKHAKSFET EPEKYEKRIS
      msa286876.2{662_2603}  HGDKDNFVPT SMVYDNYKAT AGKKELYIVK GAKHAKSFET EPEKYEKRIS
 msa286876.2{662_JM9130013}  HGDKDNFVPT SMVYDNYKAT AGKKELYIVK GAKHAKSFET EPEKYEKRIS
       msa286876.2{662_090}  HGDKDNFVPT SMVYDNYKAT AGKKELYIVK GAKHAKSFET EPEKYEKRIS
    msa286876.2{662_CJB110}  HGDKDNFVPT SMVYDNYKAT AGKKELYIVK GAKHAKSFET EPEKYEKRIS
    msa286876.2{662_1169NT}  HGDKDNFVPT SMVYDNYKAT AGKKELYIVK GAKHAKSFET EPEKYEKRIS
                  Consensus  ********** ********** ********** ********** **********

                             301
      msa286876.2{662_A909}  SFLKKYEK
      msa286876.2{662_H36B}  SFLKKYEK
      msa286876.2{662_COH1}  SFLKKYEK
      msa286876.2{662_M732}  SFLKKYEK
      msa286876.2{662_M781}  SFLKKYEK
    msa286876.2{662_18RS21}  SFLKKYEK
      msa286876.2{662_2603}  SFLKKYEK
 msa286876.2{662_JM9130013}  SFLKKYEK
       msa286876.2{662_090}  SFLKKYEK
    msa286876.2{662_CJB110}  SFLKKYEK
    msa286876.2{662_1169NT}  SFLKKYEK
                  Consensus  ********
```

Table 84: Comparative Sequences relating to SAG0267

SEQ ID NO. 8401
STRAIN 2603
ATGATGAAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTATCAGTGGCTGTACTAAAC
AATATGGAATGTTTAGCGACTGTCACTATCAATATCAAAAAGAATCATAGCATTAATTTG
ATGCCAGCCATTGATTTTTTAATGCAATCAATTGATTTAGAACCTCAAGATTTGGACCGT
ATCGTAGTAGCAGAGGGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCA
AAAATGCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACGCTTTA
ACAAATGGATTTTCAGAAAATGATTTATTGGTACCACTTATAGATGCACGACGTAATAAT
GTTTATGTTGGTTTCTATCAAAATGGTGATACTGTTAAACCAGACTGTCACACTTCTCTT
GAAGAAGTCTTACAAGAGGTGGGGAATAAAGCCAATGTTCATTTTGTCGGAGAGGTTGCA
GCATTTTTTGATCAGATTAAGAAAGCCTTACCACATGCTAAAATTACAGAAACTTTACCT
TGTGCAGTAGCAATTGGGCGCAAAGGACAAAAAATGAAAAGCGTTAATGTAGATGCGTTT
GTTCCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTAAAAAACCACTGTGAA
ACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8402
STRAIN 090
AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTATCAGTGGCTGTACT
AAACAATATGGAATGTTTAGCGACTGTCACTaTCAATATCAAAAAGAATC
ATAGCATTAATTTGATGCCAGCCATTGATTTTTTAATGCAATCAATTGAT
TTAGAACCTCAAGATTTGGACCGTATCGTAGTGGCAGAGGGTCCAGGATC
TTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAATGCTAGCTTATA
CGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACGCTTTAACAAAT
GGATTTTCAGAAAATGATTTGTTGGTACCACTTATAGATGCACGACGTAA
CAATGTTTATGTTGGTTTCTATCAAAATGGTGATACTGTTAAACCAgACT
GTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGAATAAAGCCAAT
GTTCATTTTGTCGGAGAGGTTGCAGCATTTTTTGATCAGATTAAgAAAGC
CTTACCACATGCTAAAATTACAGAAACTTTACCTTGTGCAGTGGCAATTG
GGCGCAAAGGACAAAAAATGGAAAGCGTTAATGTAGATGCGTTTGTTCCA
CGATACTTAAAACGAGTTGAAGCTGAGGAAAATTGGTTAAAAAACCACTG
TGAAACGAAT

SEQ ID NO. 8403
STRAIN A909
AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTATCAG
TGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATATC
AAAAAGAATCATAGCATTAATTTGATGCCAGCCATTGATTTTTTAATGCA
ATCAATTGATTTAGAACCTCAAGATTTGGACCGTATCGTAGTAGCAGAGG
GTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAATG
CTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACGC
TTTAACAAATGGATTTTCAGAAAATGATTTATTGGTACCACTTATAGATG
CACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGTT
AAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGAA
TAAAGCCAATGTTCATTTTGTCGGAgAGGTTGCAgCATTTGTTGACCAGA
tTAAgAAAGTTTTACCACATGCTAAAATTACAGAAACTTTACCTTGTGCA
GtGGCAATTGGGCGCAAAGGACAAAAAATGAAAAGCGTTAATGTAGATGC
GTTTGTTCCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTAA
GAAACCACTGTGAAACGAAT

SEQ ID NO. 8404
STRAIN H36B
AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTATCA
GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
CAAAAAGAATCATAGCATTAATTTGATGCCAGCCATTGATTTTTTAATGC
AATCAATTGATTTAGAACCTCAAGATTTGGACCGTATCGTAGTAGCAGAG
GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
CTTTAACAAATGGATTTTCAGAAAATGATTTATTGGTACCACTTATAGAT
GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGT
TAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
ATAAAGCCAATGTTCATTTTGTCGGAGAGGTTGCAGCATTTGTTGACCAG
ATTAAGAAAGTTTTACCACATGCTAAAATTACAGAAACTTTACCTTGTGC
AGTGGCAATTGGGCGCAAAGGACAAAAAATGAAAAGCGTTAATGTAGATG
CGTTTGTTCCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTA
AGAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8405
STRAIN 18RS21
AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTATCA
GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
CAAAAAGAATCATAGCATTAATTTGATGCCAGCCATTGATTTTTTAATGC
AATCAATTGATTTAGAACCTCAAGATTTGGACCGTATCGTAGTAGCAGAG
GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
CTTTAACAAATGGATTTTCAGAAAATGATTTATTGGTACCACTTATAGAT
GCACGACGTAATAATGTTTATGTTGGTTTCTATCAAAATGGTGATACTGT
TAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
ATAAAGCCAATGTTCATTTTGTCGGAGAGGtTGCAGCATTTTTTGATCAg
ATTAAgAAAGCCTTACCACATGCTAAAATTACAGAAACTTTACCTTGTGC
AGTAGCAATTGGGCGCAAAGGACAAAAAATGAAAAGCGTTAATGTAGATG
CGTTTGTTCCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTA
AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

Table 84: Comparative Sequences relating to SAG0267

SEQ ID NO. 8406
STRAIN M732
AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTATCA
GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
CAAAAAGAATCATAGCATTAATTTGATGCCAGCCATTGATTTTTTAATGC
AATCAATTGATTTAGAACCTCAAGATTTGGACCGTATCGTAGTAGCAGAG
GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
CTTTAACAAATGGATTTTCAGAAAATGATTTATTGGTACCACTTATAGAT
GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGATACTGT
TAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
ATAAAGCCAATGTTCATTTTGTCGGAGAGGTTGCAGCATTTTTTGATCAG
ATTAAGAAAGCCTTACCACATGCTAAAATTACAGAAACTTTACCTTGTGC
AGTAGCAATTGGGCGCAAAGGACAAAAAATGAAAAGCGTTAATGTAGAnn
CGTTTGTTCCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTA
AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8407
STRAIN COH1
AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCAC
TATCAGTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATC
AATATCAAAAAGAATCATAGCATTAATTTGATGCCAGCCATTGATTTTTT
AATGCAATCAATTGATTTAGAACCTCAAGATTTGGACCGTATCGTAGTAG
CAGAGGGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCA
AAAATGCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCT
GTACGCTTTAACAAATGGATTTTCAGAAAATGATTTATTGGTACCACTTA
TAGATGCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGAT
ACTGTTAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGT
GGGGAATAAAGCCAATGTTCATTTTGTCGGAGAGGTTGCAGCATTTTTTG
ATCAGATTAAGAAAGCCTTACCACATGCTAAAATTACAGAAACTTTACCT
TGTGCAGTAGCAATTGGGCGCAAAGGACAAAAAATGAAAAGCGTTAATGT
AGATGCGTTTGTTCCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATT
GGTTAAAAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8408
STRAIN M781
AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTA
TCAGTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAA
TATCAAAAAGAATCATAGCATTAATTTGATGCCAGCCATTGATTTTTTAA
TGCAATCAATTGATTTAGAACCTCAAGATTTGGACCGTATCGTAGTATCA
GAGGGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAA
AATGCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGT
ACGCTTTAACAAATGGATTTTCAGAAAATGATTTATTGGTACCACTTATA
GATGCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGATAC
TGTTAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGG
GGAATAAAGCCAATGTTCATTTTGTCGGAGAGGTTGCAGCATTTTTTGAT
CAGATTAAGAAAGCCTTACCACATGCTAAAATTACAGAAACTTTACCTTG
TGCAGTAGCAATTGGGCGCAAAGGACAAAAAATGAAAAGCGTTAATGTAG
ATGCGTTTGTTCCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGG
TTAAAAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8409
STRAIN CJB110
AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTATCA
GTGGCTGtaCTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
CAAAAAGAATCATAGCATTAATTTGATGCCAGCCATTGATTTTTTAATGC
AATCAATTGATTTAGAACCTCAAGATTTGGACCGTATCGTAGTGGCAGAG
GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
CTTTAACAAATGGATTTTCAGAAAATGATTTGTTGGTACCACTTATAGAT
GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGATACTGT
TAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
ATAAAGCCAATGTTCATTTTGTCGGAGAGGTTGCAGCATTTTTtgATCAG
ATTAAGAAAGCCTTACCACATGCTAAAATTACAGAAACTTTACCTTGTGC
AGTGGCAATTGGGCGCAAAGGACAAAAAATGGAAAGCGTTAATGTAgATG
CGTTTGTTCCACGATACTTAAAACGAGTTGAAGCTGAGGAAAATTGGTTA
AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8410
STRAIN 1169NT
AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTATCA
GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
CAAAAAGAATCATAGCATTAATTTGATGCCAGCCaTTGATTTTTTAATGC
AATCAATTGATTTAGAACCTCAAGATTTGGACCGTATCGTAGTAGCAGAG
GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
CTTTAACAAATGGATTTTCAGAAAATGATTTATTGGTACCACTTATAGAT
GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGATACTGT
TAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
ATAAAGCCAATGTTCATTTTGTCGGAgAGGTTGCAGCATTTGTTGACCAG
ATTAAGAAAGCTTTACCACAtGCTAAAATTACAGAAACTTTACCTTGTGC

Table 84: Comparative Sequences relating to SAG0267

AGTGGCAATTGGGCGCAAAGGACAAAAAATGGAAAGCGTTAATGTAgATG
CGTTTGTTCCACGATACTTAAAACGTGTTGAAGCTGAgGAAAATTGGTTA
AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO.: 8411
STRAIN JM9130013
AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTATCA
GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
CAAAAAGAATCATAGCATTAATTTGATGCCAGCCATTGATTTTTTAATGC
AATCAATTGATTTAGAACCTCAAGATTTGGACCGTATCGTAGTAGCAGAG
GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
gCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
CTTTAACAAATGGATTTTCAGAAAATGATTTATTGGTACCACTTATAGAT
GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGT
TAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
ATAAAGCCAATGTTCATTTTGTCGGAGAGGTTGCAGCATTTGTTGACCAG
ATTAAGAAAGTTTTACCACATGCTAAAATTACAGAAACTTTACCTTGTGC
AGTGGCAATTGGGCGCAAAGGACAAAAAATGAAAAGCGTTAATGTAGATG
CGTTTGTTCCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTA
AGAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

```
PRETTY of: /biotmp/msa521675.2{*}   March 10, 2003 08:34  ..

                           1                                                50
     msa521675.2{69_A909}  ~~~~~~AAAG TTTTAGCCTT TGATACTTCA AGCAAAGCAC TATCAGTGGC
     msa521675.2{69_H36B}  ~~~~~~AAAG TTTTAGCCTT TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_JM9130013}  ~~~~~~AAAG TTTTAGCCTT TGATACTTCA AGCAAAGCAC TATCAGTGGC
   msa521675.2{69_1169NT}  ~~~~~~AAAG TTTTAGCCTT TGATACTTCA AGCAAAGCAC TATCAGTGGC
      msa521675.2{69_090}  ~~~~~~AAAG TTTTAGCCTT TGATACTTCA AGCAAAGCAC TATCAGTGGC
   msa521675.2{69_CJB110}  ~~~~~~AAAG TTTTAGCCTT TGATACTTCA AGCAAAGCAC TATCAGTGGC
   msa521675.2{69_18RS21}  ~~~~~~AAAG TTTTAGCCTT TGATACTTCA AGCAAAGCAC TATCAGTGGC
     msa521675.2{69_2603}  atgatgAAAG TTTTAGCCTT TGATACTTCA AGCAAAGCAC TATCAGTGGC
     msa521675.2{69_COH1}  ~~~~~~AAAG TTTTAGCCTT TGATACTTCA AGCAAAGCAC TATCAGTGGC
     msa521675.2{69_M732}  ~~~~~~AAAG TTTTAGCCTT TGATACTTCA AGCAAAGCAC TATCAGTGGC
     msa521675.2{69_M781}  ~~~~~~AAAG TTTTAGCCTT TGATACTTCA AGCAAAGCAC TATCAGTGGC
                Consensus  ********** ********** ********** ********** **********

                           51                                              100
     msa521675.2{69_A909}  TGTACTAAAC AATATGGAAT GTTTAGCGAC TGTCACTATC AATATCAAAA
     msa521675.2{69_H36B}  TGTACTAAAC AATATGGAAT GTTTAGCGAC TGTCACTATC AATATCAAAA
msa521675.2{69_JM9130013}  TGTACTAAAC AATATGGAAT GTTTAGCGAC TGTCACTATC AATATCAAAA
   msa521675.2{69_1169NT}  TGTACTAAAC AATATGGAAT GTTTAGCGAC TGTCACTATC AATATCAAAA
      msa521675.2{69_090}  TGTACTAAAC AATATGGAAT GTTTAGCGAC TGTCACTATC AATATCAAAA
   msa521675.2{69_CJB110}  TGTACTAAAC AATATGGAAT GTTTAGCGAC TGTCACTATC AATATCAAAA
   msa521675.2{69_18RS21}  TGTACTAAAC AATATGGAAT GTTTAGCGAC TGTCACTATC AATATCAAAA
     msa521675.2{69_2603}  TGTACTAAAC AATATGGAAT GTTTAGCGAC TGTCACTATC AATATCAAAA
     msa521675.2{69_COH1}  TGTACTAAAC AATATGGAAT GTTTAGCGAC TGTCACTATC AATATCAAAA
     msa521675.2{69_M732}  TGTACTAAAC AATATGGAAT GTTTAGCGAC TGTCACTATC AATATCAAAA
     msa521675.2{69_M781}  TGTACTAAAC AATATGGAAT GTTTAGCGAC TGTCACTATC AATATCAAAA
                Consensus  ********** ********** ********** ********** **********

                           101                                             150
     msa521675.2{69_A909}  AGAATCATAG CATTAATTTG ATGCCAGCCA TTGATTTTTT AATGCAATCA
     msa521675.2{69_H36B}  AGAATCATAG CATTAATTTG ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_JM9130013}  AGAATCATAG CATTAATTTG ATGCCAGCCA TTGATTTTTT AATGCAATCA
   msa521675.2{69_1169NT}  AGAATCATAG CATTAATTTG ATGCCAGCCA TTGATTTTTT AATGCAATCA
      msa521675.2{69_090}  AGAATCATAG CATTAATTTG ATGCCAGCCA TTGATTTTTT AATGCAATCA
   msa521675.2{69_CJB110}  AGAATCATAG CATTAATTTG ATGCCAGCCA TTGATTTTTT AATGCAATCA
   msa521675.2{69_18RS21}  AGAATCATAG CATTAATTTG ATGCCAGCCA TTGATTTTTT AATGCAATCA
     msa521675.2{69_2603}  AGAATCATAG CATTAATTTG ATGCCAGCCA TTGATTTTTT AATGCAATCA
     msa521675.2{69_COH1}  AGAATCATAG CATTAATTTG ATGCCAGCCA TTGATTTTTT AATGCAATCA
     msa521675.2{69_M732}  AGAATCATAG CATTAATTTG ATGCCAGCCA TTGATTTTTT AATGCAATCA
     msa521675.2{69_M781}  AGAATCATAG CATTAATTTG ATGCCAGCCA TTGATTTTTT AATGCAATCA
                Consensus  ********** ********** ********** ********** **********

                           151                                             200
     msa521675.2{69_A909}  ATTGATTTAG AACCTCAAGA TTTGGACCGT ATCGTAGTag CAGAGGGTCC
     msa521675.2{69_H36B}  ATTGATTTAG AACCTCAAGA TTTGGACCGT ATCGTAGTag CAGAGGGTCC
msa521675.2{69_JM9130013}  ATTGATTTAG AACCTCAAGA TTTGGACCGT ATCGTAGTag CAGAGGGTCC
   msa521675.2{69_1169NT}  ATTGATTTAG AACCTCAAGA TTTGGACCGT ATCGTAGTag CAGAGGGTCC
      msa521675.2{69_090}  ATTGATTTAG AACCTCAAGA TTTGGACCGT ATCGTAGTgg CAGAGGGTCC
   msa521675.2{69_CJB110}  ATTGATTTAG AACCTCAAGA TTTGGACCGT ATCGTAGTgg CAGAGGGTCC
   msa521675.2{69_18RS21}  ATTGATTTAG AACCTCAAGA TTTGGACCGT ATCGTAGTag CAGAGGGTCC
     msa521675.2{69_2603}  ATTGATTTAG AACCTCAAGA TTTGGACCGT ATCGTAGTag CAGAGGGTCC
     msa521675.2{69_COH1}  ATTGATTTAG AACCTCAAGA TTTGGACCGT ATCGTAGTag CAGAGGGTCC
     msa521675.2{69_M732}  ATTGATTTAG AACCTCAAGA TTTGGACCGT ATCGTAGTag CAGAGGGTCC
     msa521675.2{69_M781}  ATTGATTTAG AACCTCAAGA TTTGGACCGT ATCGTAGTat CAGAGGGTCC
                Consensus  ********** ********** ********** ********-- **********

                           201                                             250
     msa521675.2{69_A909}  AGGATCTTAT ACGGGCTTAC GTGTAGCTGT TGCTACAGCA AAAATGCTAG
     msa521675.2{69_H36B}  AGGATCTTAT ACGGGCTTAC GTGTAGCTGT TGCTACAGCA AAAATGCTAG
```

Table 84: Comparative Sequences relating to SAG0267

```
msa521675.2{69_JM9130013}  AGGATCTTAT ACGGGCTTAC GTGTAGCTGT TGCTACAGCA AAAATGCTAG
   msa521675.2{69_1169NT}  AGGATCTTAT ACGGGCTTAC GTGTAGCTGT TGCTACAGCA AAAATGCTAG
      msa521675.2{69_090}  AGGATCTTAT ACGGGCTTAC GTGTAGCTGT TGCTACAGCA AAAATGCTAG
   msa521675.2{69_CJB110}  AGGATCTTAT ACGGGCTTAC GTGTAGCTGT TGCTACAGCA AAAATGCTAG
   msa521675.2{69_18RS21}  AGGATCTTAT ACGGGCTTAC GTGTAGCTGT TGCTACAGCA AAAATGCTAG
     msa521675.2{69_2603}  AGGATCTTAT ACGGGCTTAC GTGTAGCTGT TGCTACAGCA AAAATGCTAG
     msa521675.2{69_COH1}  AGGATCTTAT ACGGGCTTAC GTGTAGCTGT TGCTACAGCA AAAATGCTAG
     msa521675.2{69_M732}  AGGATCTTAT ACGGGCTTAC GTGTAGCTGT TGCTACAGCA AAAATGCTAG
     msa521675.2{69_M781}  AGGATCTTAT ACGGGCTTAC GTGTAGCTGT TGCTACAGCA AAAATGCTAG
                Consensus  ********** ********** ********** ********** **********

                           251                                                300
     msa521675.2{69_A909}  CTTATACGCT TAAGATTGAC TTAGTTGGAG TATCTAGCCT GTACGCTTTA
     msa521675.2{69_H36B}  CTTATACGCT TAAGATTGAC TTAGTTGGAG TATCTAGCCT GTACGCTTTA
msa521675.2{69_JM9130013}  CTTATACGCT TAAGATTGAC TTAGTTGGAG TATCTAGCCT GTACGCTTTA
   msa521675.2{69_1169NT}  CTTATACGCT TAAGATTGAC TTAGTTGGAG TATCTAGCCT GTACGCTTTA
      msa521675.2{69_090}  CTTATACGCT TAAGATTGAC TTAGTTGGAG TATCTAGCCT GTACGCTTTA
   msa521675.2{69_CJB110}  CTTATACGCT TAAGATTGAC TTAGTTGGAG TATCTAGCCT GTACGCTTTA
   msa521675.2{69_18RS21}  CTTATACGCT TAAGATTGAC TTAGTTGGAG TATCTAGCCT GTACGCTTTA
     msa521675.2{69_2603}  CTTATACGCT TAAGATTGAC TTAGTTGGAG TATCTAGCCT GTACGCTTTA
     msa521675.2{69_COH1}  CTTATACGCT TAAGATTGAC TTAGTTGGAG TATCTAGCCT GTACGCTTTA
     msa521675.2{69_M732}  CTTATACGCT TAAGATTGAC TTAGTTGGAG TATCTAGCCT GTACGCTTTA
     msa521675.2{69_M781}  CTTATACGCT TAAGATTGAC TTAGTTGGAG TATCTAGCCT GTACGCTTTA
                Consensus  ********** ********** ********** ********** **********

                           301                                                350
     msa521675.2{69_A909}  ACAAATGGAT TTTCAGAAAA TGATTTaTTG GTACCACTTA TAGATGCACG
     msa521675.2{69_H36B}  ACAAATGGAT TTTCAGAAAA TGATTTaTTG GTACCACTTA TAGATGCACG
msa521675.2{69_JM9130013}  ACAAATGGAT TTTCAGAAAA TGATTTaTTG GTACCACTTA TAGATGCACG
   msa521675.2{69_1169NT}  ACAAATGGAT TTTCAGAAAA TGATTTaTTG GTACCACTTA TAGATGCACG
      msa521675.2{69_090}  ACAAATGGAT TTTCAGAAAA TGATTTgTTG GTACCACTTA TAGATGCACG
   msa521675.2{69_CJB110}  ACAAATGGAT TTTCAGAAAA TGATTTgTTG GTACCACTTA TAGATGCACG
   msa521675.2{69_18RS21}  ACAAATGGAT TTTCAGAAAA TGATTTaTTG GTACCACTTA TAGATGCACG
     msa521675.2{69_2603}  ACAAATGGAT TTTCAGAAAA TGATTTaTTG GTACCACTTA TAGATGCACG
     msa521675.2{69_COH1}  ACAAATGGAT TTTCAGAAAA TGATTTaTTG GTACCACTTA TAGATGCACG
     msa521675.2{69_M732}  ACAAATGGAT TTTCAGAAAA TGATTTaTTG GTACCACTTA TAGATGCACG
     msa521675.2{69_M781}  ACAAATGGAT TTTCAGAAAA TGATTTaTTG GTACCACTTA TAGATGCACG
                Consensus  ********** ********** ******_*** ********** **********

                           351                                                400
     msa521675.2{69_A909}  ACGTAAcAAT GTTTATGTTG GTTTCTATCA AAATGGaGAT ACTGTTAAAC
     msa521675.2{69_H36B}  ACGTAAcAAT GTTTATGTTG GTTTCTATCA AAATGGaGAT ACTGTTAAAC
msa521675.2{69_JM9130013}  ACGTAAcAAT GTTTATGTTG GTTTCTATCA AAATGGaGAT ACTGTTAAAC
   msa521675.2{69_1169NT}  ACGTAAcAAT GTTTATGTTG GTTTCTATCA AAATGGtGAT ACTGTTAAAC
      msa521675.2{69_090}  ACGTAAcAAT GTTTATGTTG GTTTCTATCA AAATGGtGAT ACTGTTAAAC
   msa521675.2{69_CJB110}  ACGTAAcAAT GTTTATGTTG GTTTCTATCA AAATGGtGAT ACTGTTAAAC
   msa521675.2{69_18RS21}  ACGTAAtAAT GTTTATGTTG GTTTCTATCA AAATGGtGAT ACTGTTAAAC
     msa521675.2{69_2603}  ACGTAAtAAT GTTTATGTTG GTTTCTATCA AAATGGtGAT ACTGTTAAAC
     msa521675.2{69_COH1}  ACGTAAcAAT GTTTATGTTG GTTTCTATCA AAATGGtGAT ACTGTTAAAC
     msa521675.2{69_M732}  ACGTAAcAAT GTTTATGTTG GTTTCTATCA AAATGGtGAT ACTGTTAAAC
     msa521675.2{69_M781}  ACGTAAcAAT GTTTATGTTG GTTTCTATCA AAATGGtGAT ACTGTTAAAC
                Consensus  ******_*** ********** ********** ******_*** **********

                           401                                                450
     msa521675.2{69_A909}  CAGACTGTCA CACTTCTCTT GAAGAAGTCT TACAAGAGGT GGGGAATAAA
     msa521675.2{69_H36B}  CAGACTGTCA CACTTCTCTT GAAGAAGTCT TACAAGAGGT GGGGAATAAA
msa521675.2{69_JM9130013}  CAGACTGTCA CACTTCTCTT GAAGAAGTCT TACAAGAGGT GGGGAATAAA
   msa521675.2{69_1169NT}  CAGACTGTCA CACTTCTCTT GAAGAAGTCT TACAAGAGGT GGGGAATAAA
      msa521675.2{69_090}  CAGACTGTCA CACTTCTCTT GAAGAAGTCT TACAAGAGGT GGGGAATAAA
   msa521675.2{69_CJB110}  CAGACTGTCA CACTTCTCTT GAAGAAGTCT TACAAGAGGT GGGGAATAAA
   msa521675.2{69_18RS21}  CAGACTGTCA CACTTCTCTT GAAGAAGTCT TACAAGAGGT GGGGAATAAA
     msa521675.2{69_2603}  CAGACTGTCA CACTTCTCTT GAAGAAGTCT TACAAGAGGT GGGGAATAAA
     msa521675.2{69_COH1}  CAGACTGTCA CACTTCTCTT GAAGAAGTCT TACAAGAGGT GGGGAATAAA
     msa521675.2{69_M732}  CAGACTGTCA CACTTCTCTT GAAGAAGTCT TACAAGAGGT GGGGAATAAA
     msa521675.2{69_M781}  CAGACTGTCA CACTTCTCTT GAAGAAGTCT TACAAGAGGT GGGGAATAAA
                Consensus  ********** ********** ********** ********** **********

                           451                                                500
     msa521675.2{69_A909}  GCCAATGTTC ATTTTGTCGG AGAGGTTGCA GCATTTgTTG AcCAGATTAA
     msa521675.2{69_H36B}  GCCAATGTTC ATTTTGTCGG AGAGGTTGCA GCATTTgTTG AcCAGATTAA
msa521675.2{69_JM9130013}  GCCAATGTTC ATTTTGTCGG AGAGGTTGCA GCATTTgTTG AcCAGATTAA
   msa521675.2{69_1169NT}  GCCAATGTTC ATTTTGTCGG AGAGGTTGCA GCATTTgTTG AcCAGATTAA
      msa521675.2{69_090}  GCCAATGTTC ATTTTGTCGG AGAGGTTGCA GCATTTtTTG AtCAGATTAA
   msa521675.2{69_CJB110}  GCCAATGTTC ATTTTGTCGG AGAGGTTGCA GCATTTtTTG AtCAGATTAA
   msa521675.2{69_18RS21}  GCCAATGTTC ATTTTGTCGG AGAGGTTGCA GCATTTtTTG AtCAGATTAA
     msa521675.2{69_2603}  GCCAATGTTC ATTTTGTCGG AGAGGTTGCA GCATTTtTTG AtCAGATTAA
     msa521675.2{69_COH1}  GCCAATGTTC ATTTTGTCGG AGAGGTTGCA GCATTTtTTG AtCAGATTAA
     msa521675.2{69_M732}  GCCAATGTTC ATTTTGTCGG AGAGGTTGCA GCATTTtTTG AtCAGATTAA
     msa521675.2{69_M781}  GCCAATGTTC ATTTTGTCGG AGAGGTTGCA GCATTTtTTG AtCAGATTAA
                Consensus  ********** ********** ********** ******_*** *_********

                           501                                                550
     msa521675.2{69_A909}  GAAAGttTTA CCACATGCTA AAATTACAGA AACTTTACCT TGTGCAGTgG
```

Table 84: Comparative Sequences relating to SAG0267

```
        msa521675.2{69_H36B}  GAAAGttTTA CCACATGCTA AAATTACAGA AACTTTACCT TGTGCAGTgG
    msa521675.2{69_JM9130013}  GAAAGttTTA CCACATGCTA AAATTACAGA AACTTTACCT TGTGCAGTgG
      msa521675.2{69_1169NT}  GAAAGctTTA CCACATGCTA AAATTACAGA AACTTTACCT TGTGCAGTgG
         msa521675.2{69_090}  GAAAGccTTA CCACATGCTA AAATTACAGA AACTTTACCT TGTGCAGTgG
      msa521675.2{69_CJB110}  GAAAGccTTA CCACATGCTA AAATTACAGA AACTTTACCT TGTGCAGTgG
      msa521675.2{69_18RS21}  GAAAGccTTA CCACATGCTA AAATTACAGA AACTTTACCT TGTGCAGTaG
        msa521675.2{69_2603}  GAAAGccTTA CCACATGCTA AAATTACAGA AACTTTACCT TGTGCAGTaG
        msa521675.2{69_COH1}  GAAAGccTTA CCACATGCTA AAATTACAGA AACTTTACCT TGTGCAGTaG
        msa521675.2{69_M732}  GAAAGccTTA CCACATGCTA AAATTACAGA AACTTTACCT TGTGCAGTaG
        msa521675.2{69_M781}  GAAAGccTTA CCACATGCTA AAATTACAGA AACTTTACCT TGTGCAGTaG
                   Consensus  *****--*** ********** ********** ********** ********-*

                              551                                                600
        msa521675.2{69_A909}  CAATTGGGCG CAAAGGACAA AAAATGaAAA GCGTTAATGT AGAtgCGTTT
        msa521675.2{69_H36B}  CAATTGGGCG CAAAGGACAA AAAATGaAAA GCGTTAATGT AGAtgCGTTT
    msa521675.2{69_JM9130013}  CAATTGGGCG CAAAGGACAA AAAATGaAAA GCGTTAATGT AGAtgCGTTT
      msa521675.2{69_1169NT}  CAATTGGGCG CAAAGGACAA AAAATGgAAA GCGTTAATGT AGAtgCGTTT
         msa521675.2{69_090}  CAATTGGGCG CAAAGGACAA AAAATGgAAA GCGTTAATGT AGAtgCGTTT
      msa521675.2{69_CJB110}  CAATTGGGCG CAAAGGACAA AAAATGgAAA GCGTTAATGT AGAtgCGTTT
      msa521675.2{69_18RS21}  CAATTGGGCG CAAAGGACAA AAAATGaAAA GCGTTAATGT AGAtgCGTTT
        msa521675.2{69_2603}  CAATTGGGCG CAAAGGACAA AAAATGaAAA GCGTTAATGT AGAtgCGTTT
        msa521675.2{69_COH1}  CAATTGGGCG CAAAGGACAA AAAATGaAAA GCGTTAATGT AGAtgCGTTT
        msa521675.2{69_M732}  CAATTGGGCG CAAAGGACAA AAAATGaAAA GCGTTAATGT AGAnnCGTTT
        msa521675.2{69_M781}  CAATTGGGCG CAAAGGACAA AAAATGaAAA GCGTTAATGT AGAtgCGTTT
                   Consensus  ********** ********** ******-*** ********** ***--*****

                              601                                                650
        msa521675.2{69_A909}  GTTCCACGAT ACTTAAAACG tGTTGAAGCT GAGGAAAATT GGTTAAgAAA
        msa521675.2{69_H36B}  GTTCCACGAT ACTTAAAACG tGTTGAAGCT GAGGAAAATT GGTTAAgAAA
    msa521675.2{69_JM9130013}  GTTCCACGAT ACTTAAAACG tGTTGAAGCT GAGGAAAATT GGTTAAgAAA
      msa521675.2{69_1169NT}  GTTCCACGAT ACTTAAAACG tGTTGAAGCT GAGGAAAATT GGTTAAaAAA
         msa521675.2{69_090}  GTTCCACGAT ACTTAAAACG aGTTGAAGCT GAGGAAAATT GGTTAAaAAA
      msa521675.2{69_CJB110}  GTTCCACGAT ACTTAAAACG aGTTGAAGCT GAGGAAAATT GGTTAAaAAA
      msa521675.2{69_18RS21}  GTTCCACGAT ACTTAAAACG tGTTGAAGCT GAGGAAAATT GGTTAAaAAA
        msa521675.2{69_2603}  GTTCCACGAT ACTTAAAACG tGTTGAAGCT GAGGAAAATT GGTTAAaAAA
        msa521675.2{69_COH1}  GTTCCACGAT ACTTAAAACG tGTTGAAGCT GAGGAAAATT GGTTAAaAAA
        msa521675.2{69_M732}  GTTCCACGAT ACTTAAAACG tGTTGAAGCT GAGGAAAATT GGTTAAaAAA
        msa521675.2{69_M781}  GTTCCACGAT ACTTAAAACG tGTTGAAGCT GAGGAAAATT GGTTAAaAAA
                   Consensus  ********** ********** -********* ********** ******-***

                              651                                    690
        msa521675.2{69_A909}  CCACTGTGAA ACGAAT~~~~ ~~~~~~~~~~ ~~~~~~~~~~
        msa521675.2{69_H36B}  CCACTGTGAA ACGAATACAG AAGAATATAT TAAGAGAGTT
    msa521675.2{69_JM9130013}  CCACTGTGAA ACGAATACAG AAGAATATAT TAAGAGAGTT
      msa521675.2{69_1169NT}  CCACTGTGAA ACGAATACAG AAGAATATAT TAAGAGAGTT
         msa521675.2{69_090}  CCACTGTGAA ACGAAT~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa521675.2{69_CJB110}  CCACTGTGAA ACGAATACAG AAGAATATAT TAAGAGAGTT
      msa521675.2{69_18RS21}  CCACTGTGAA ACGAATACAG AAGAATATAT TAAGAGAGTT
        msa521675.2{69_2603}  CCACTGTGAA ACGAATACAG AAGAATATAT TAAGAGAGTT
        msa521675.2{69_COH1}  CCACTGTGAA ACGAATACAG AAGAATATAT TAAGAGAGTT
        msa521675.2{69_M732}  CCACTGTGAA ACGAATACAG AAGAATATAT TAAGAGAGTT
        msa521675.2{69_M781}  CCACTGTGAA ACGAATACAG AAGAATATAT TAAGAGAGTT
                   Consensus  ********** ********** ********** **********
```

SEQ ID NO. 8412

STRAIN 2603 frame: 1

MMKVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDR
IVVAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNN
VYVGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLP
CAVAIGRKGQKMKSVNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8413

STRAIN 090 frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
VAIGRKGQKMESVNVDAFVPRYLKRVEAEENWLKNHCETN

SEQ ID NO. 8414

STRAIN A909 frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFVDQIKKVLPHAKITETLPCA
VAIGRKGQKMKSVNVDAFVPRYLKRVEAEENWLRNHCETN

SEQ ID NO. 8415

STRAIN H36B frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFVDQIKKVLPHAKITETLPCA
VAIGRKGQKMKSVNVDAFVPRYLKRVEAEENWLRNHCETNTEEYIKRV

SEQ ID NO. 8416

Table 84: Comparative Sequences relating to SAG0267

STRAIN 18RS21 frame: 1
KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
VAIGRKGQKMKSVNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8417
STRAIN M732 frame: 1
KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
VAIGRKGQKMKSVNVXXFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8418
STRAIN COH1 frame: 1
KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
VAIGRKGQKMKSVNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8419
STRAIN M781 frame: 1
KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
VSEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
VAIGRKGQKMKSVNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8420
STRAIN CJB110 frame: 1
KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFFDQIKKALPHAKITETLPCA
VAIGRKGQKMESVNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8421
STRAIN 1169NT frame: 1
KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFVDQIKKALPHAKITETLPCA
VAIGRKGQKMESVNVDAFVPRYLKRVEAEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8422
STRAIN JM9130013 frame: 1
KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFVDQIKKVLPHAKITETLPCA
VAIGRKGQKMKSVNVDAFVPRYLKRVEAEENWLRNHCETNTEEYIKRV

```
PRETTY of: /biotmp/msa521982.2{*}   March 10, 2003 08:40  ..

                                1                                                   50
      msa521982.2{69_A909}   --KVLAFDTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
      msa521982.2{69_H36B}   --KVLAFDTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
 msa521982.2{69_JM9130013}   --KVLAFDTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
       msa521982.2{69_090}   --KVLAFDTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
    msa521982.2{69_CJB110}   --KVLAFDTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
    msa521982.2{69_18RS21}   --KVLAFDTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
      msa521982.2{69_2603}   mmKVLAFDTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
      msa521982.2{69_COH1}   --KVLAFDTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
      msa521982.2{69_M781}   --KVLAFDTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
    msa521982.2{69_1169NT}   --KVLAFDTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
      msa521982.2{69_M732}   --KVLAFDTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
                 Consensus   ********** ********** ********** ********** **********

                             51                                                  100
      msa521982.2{69_A909}   IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
      msa521982.2{69_H36B}   IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
 msa521982.2{69_JM9130013}   IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
       msa521982.2{69_090}   IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
    msa521982.2{69_CJB110}   IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
    msa521982.2{69_18RS21}   IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
      msa521982.2{69_2603}   IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
      msa521982.2{69_COH1}   IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
      msa521982.2{69_M781}   IDLEPQDLDR IVVsEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
    msa521982.2{69_1169NT}   IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
      msa521982.2{69_M732}   IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
                 Consensus   ********** ***_****** ********** ********** **********

                             101                                                 150
      msa521982.2{69_A909}   TNGFSENDLL VPLIDARRNN VYVGFYQNGD TVKPDCHTSL EEVLQEVGNK
      msa521982.2{69_H36B}   TNGFSENDLL VPLIDARRNN VYVGFYQNGD TVKPDCHTSL EEVLQEVGNK
```

Table 84: Comparative Sequences relating to SAG0267

```
msa521982.2{69_JM9130013}  TNGFSENDLL VPLIDARRNN VYVGFYQNGD TVKPDCHTSL EEVLQEVGNK
      msa521982.2{69_090}  TNGFSENDLL VPLIDARRNN VYVGFYQNGD TVKPDCHTSL EEVLQEVGNK
    msa521982.2{69_CJB110}  TNGFSENDLL VPLIDARRNN VYVGFYQNGD TVKPDCHTSL EEVLQEVGNK
    msa521982.2{69_18RS21}  TNGFSENDLL VPLIDARRNN VYVGFYQNGD TVKPDCHTSL EEVLQEVGNK
      msa521982.2{69_2603}  TNGFSENDLL VPLIDARRNN VYVGFYQNGD TVKPDCHTSL EEVLQEVGNK
      msa521982.2{69_COH1}  TNGFSENDLL VPLIDARRNN VYVGFYQNGD TVKPDCHTSL EEVLQEVGNK
      msa521982.2{69_M781}  TNGFSENDLL VPLIDARRNN VYVGFYQNGD TVKPDCHTSL EEVLQEVGNK
   msa521982.2{69_1169NT}  TNGFSENDLL VPLIDARRNN VYVGFYQNGD TVKPDCHTSL EEVLQEVGNK
      msa521982.2{69_M732}  TNGFSENDLL VPLIDARRNN VYVGFYQNGD TVKPDCHTSL EEVLQEVGNK
                Consensus  ********** ********** ********** ********** **********

                           151                                               200
      msa521982.2{69_A909}  ANVHFVGEVA AFvDQIKKvL PHAKITETLP CAVAIGRKGQ KMkSVNVdaF
      msa521982.2{69_H36B}  ANVHFVGEVA AFvDQIKKvL PHAKITETLP CAVAIGRKGQ KMkSVNVdaF
msa521982.2{69_JM9130013}  ANVHFVGEVA AFvDQIKKvL PHAKITETLP CAVAIGRKGQ KMkSVNVdaF
      msa521982.2{69_090}  ANVHFVGEVA AFfDQIKKaL PHAKITETLP CAVAIGRKGQ KMeSVNVdaF
    msa521982.2{69_CJB110}  ANVHFVGEVA AFfDQIKKaL PHAKITETLP CAVAIGRKGQ KMeSVNVdaF
    msa521982.2{69_18RS21}  ANVHFVGEVA AFfDQIKKaL PHAKITETLP CAVAIGRKGQ KMkSVNVdaF
      msa521982.2{69_2603}  ANVHFVGEVA AFfDQIKKaL PHAKITETLP CAVAIGRKGQ KMkSVNVdaF
      msa521982.2{69_COH1}  ANVHFVGEVA AFfDQIKKaL PHAKITETLP CAVAIGRKGQ KMkSVNVdaF
      msa521982.2{69_M781}  ANVHFVGEVA AFfDQIKKaL PHAKITETLP CAVAIGRKGQ KMkSVNVdaF
   msa521982.2{69_1169NT}  ANVHFVGEVA AFvDQIKKaL PHAKITETLP CAVAIGRKGQ KMeSVNVdaF
      msa521982.2{69_M732}  ANVHFVGEVA AFfDQIKKaL PHAKITETLP CAVAIGRKGQ KMkSVNVxxF
                Consensus  ********** **_*****_* ********** ********** **_****__*

                           201                            230
      msa521982.2{69_A909}  VPRYLKRVEA EENWLrNHCE TN~~~~~~~~
      msa521982.2{69_H36B}  VPRYLKRVEA EENWLrNHCE TNTEEYIKRV
msa521982.2{69_JM9130013}  VPRYLKRVEA EENWLrNHCE TNTEEYIKRV
      msa521982.2{69_090}  VPRYLKRVEA EENWLkNHCE TN~~~~~~~~
    msa521982.2{69_CJB110}  VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
    msa521982.2{69_18RS21}  VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
      msa521982.2{69_2603}  VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
      msa521982.2{69_COH1}  VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
      msa521982.2{69_M781}  VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
   msa521982.2{69_1169NT}  VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
      msa521982.2{69_M732}  VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
                Consensus  ********** *****_**** **********
```

Table 85: Comparative Sequences relating to SAG1361

SEQ ID NO. 8501
STRAIN 2603
atgagtaaacgacaaaatttaggaattagtaaaaaaggagcaattatatcagggctctca
gtggcactaattgtagtaataggtggctttttatgggtacaatctcaacctaataagagt
gcagtaaaaactaactacaaagtttttaatgttagagaaggaagtgtttcgtcctcaact
cttttgacaggaaaagctaaggctaatcaagaacagtatgtgtattttgatgctaataaa
ggtaatcgagcaactgtcacagttaaagtgggtgataaaatcacagctggtcagcagtta
gttcaatatgatacaacaactgcacaagcagcctacgacactgctaatcgtcaattaaat
aaagtagcgcgtcagattaataatctaaagacaacaggaagtcttccagctatggaatca
agtgatcaatcttcttcatcatcacaaggacaagggactcaatcgactagtggtgcgacg
aatcgtctacagcaaaattatcaaagtcaagctaatgcttcatacaaccaacaacttcaa
gatttgaatgatgcttatgcagatgcacaggcagaagtaaataaagcacaaaaagcattg
aatgatactgttattacaagtgacgtatcagggacagttgttgaagttaatagtgatatt
gatccagcttcaaaaactagtcaagtacttgtccatgtagcaactgaaggtaaactccaa
gtacaaggaacgatgagtgagtatgatttggctaatgttaaaaaagaccaggctgttaaa
ataaaatctaaggtctatcctgacaaggaatgggaaggtaaaatttcatatatctcaaat
tatccagaagcagaagcaaacaacaatgactctaataacggctctagtgctgtaaattat
aaatataaagtagatattactagccctctcgatgcattaaaacaaggttttaccgtatca
gttgaagtagttaatggagataagcaccttattgtccctacaagttctgtgataaacaaa
gataataaacactttgtttgggtatacaatgattctaatcgtaaaatttccaaagttgaa
gtcaaaattggtaaagctgatgctaagacacaagaaattttatcaggtttgaaagcagga
caaatcgtggttactaatccaagtaaaaccttcaaggatgggcaaaaaattgataatatt
gaatcaatcgatcttaactctaataagaaatcagaggtgaaa

SEQ ID NO. 8502
STRAIN 090
TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAAACTAACTA
CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTTCGTCCTCAACTCTTTTGA
CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
AAAGGTAATCGAGCAACTGTCACAGTTAAAGTGGGTGATAAAATCACAGC
TGGTCAGCAGTTAGTTCAATATGATACAACAACTGCACAAGCAGCCTACG
ACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
AAGACAACAGGAAGTCTTCCAGCTATGGAATTAAGTGATCAATCTTCTTC
ATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGAATCGTC
TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACTT
CAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
ACAAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAACTAGTCAAGTA
CTTGTCCATGTAGCAACTGAAGGTAAACTCCAAGTACAAGGAACGATGAG
TGAGTATGATTTGGCTAATGTTAAAAAAGACCAGGCTGTTAAAATAAAAT
CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAATTTCATATATCTCA
AATTATCCAGAAGCAGAAGCAAACAACAATGACTCTAATAACGGCTCTAG
TGCTGTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAT
TAAAACAAGGTTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
CTTATTGTCCCTACAAGTTCTGTGATAAACAAAGATAATAAACACTTTGT
TTGGGTATACAATGATTCTAATCGTAAAATTTCCAAAGTTGAAGTCAAAA
TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
GGACAAATCGTGGTTACTAATCCAAGTAAAACCTTCAAGGATGGGCAAAA
AATTGATAATATTGAATCAATCGATCTTAACTCTAATAAGAAATCAGAGG

SEQ ID NO. 8503
STRAIN A909
TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAAACTAA
CTACAAAGTTTTTAATGTTAGAGAAGGAAGTGTTTCGTCCTCAACTCTTT
TGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCT
AATAAAGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCAC
AGCTGGTCAGCAGTTAGTTCAATATGATACAACAACTGCACAAGCAGCCT
ACGACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAAT
CTAAAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTC
ATCATCATCACAAGGACAAGGGGCTCAATCGACTAGTGGTGCGACGAATC
GTCTACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAA
CTTCAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAA
AGCACAAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGA
CAGTTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAACTAGTCAA
GTACTTGTCCATGTAGCAACTGAGGGTAAACTCCAAGTACAAGGAACGAT
GAGTGAGTATGATTTGGCTAATGTTAAAAAAGACCAGTCTGTTAAAATAA
AATCTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAATTTCATATATC
TCAAATTATCCAGAAGCAGAAGCAAACAACAATGACTCTAATAACGGCTC
TAGTGCTGTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCGATG
CATTAAAACAAGGTTTTACTGTATCAGTTGAAGTAGTTAATGGAGATAAG
CACCTTATTGTTCCTACAAGTTCTGTGACAAACAAAGATAATAAACACTT
TGTTTGGGTATACAATGATTCTAATCGTAAAATTTCCAAAGTTGAAGTCA
AAATTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAA
GCAGGACAAATCGTGGTTACTAATCCAAGCAAAACTTTCAAGGATGGGCA
AAAAATTGATAATATTGAATCAATAGATCTTAAGTCTAATAAGAAATCAG
AGGTGAAA

SEQ ID NO. 8504
STRAIN H36B
TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAAACTAATTA
CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTTCGTCCTCAACTCTTTTGA
CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
AAGGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCACAGC

Table 85: Comparative Sequences relating to SAG1361

TGGTCAGCAGTTAGTTCAATATGATACAACAACTGCACAAGCAGCCTACG
ACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
AAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTCATC
ATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGAATCGTC
TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACTT
CAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
ACAAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAACTAGTCAAGTA
CTTGTCCATGTAGCAACTGAAGGTAAACTCCAAGTACAAGGAACGATGAG
TGAGTATGATTTGGCTAATGTAAAAAAAGACCAGGCTGTTAAAATAAAAT
CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAATTTCATATATCTCA
AATTATCCAGAAGCAGAAGCAAACAACAATGACTCTAATAACGGCTCTAG
TGCTGTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAT
TAAAACAAGGTTTTACTGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
CTTATTGTTCCTACAAGTTCTGTGACAAACAAAGATAATAAACACTTTGT
TTGGGTATACAATGATTCTAATCGTAAAATTTCCAAAGTTGAAGTCAAAA
TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
GGACAAATCGTAGTTACTAATCCAAGTAAAGCTTTCAAGGATGGGCAAAA
AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
TG

SEQ ID NO. 8505
STRAIN 18RS21
TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAAACTAACTA
CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTTCGTCCTCAACTCTTTTGA
CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
AAAGGTAATCGAGCAACTGTCACAGTTAAAGTGGGTGATAAAATCACAGC
TGGTCAGCAGTTAGTTCAATATGATACAACAACTGCACAAGCAGCCTACG
ACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
AAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTCTTC
ATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGAATCGTC
TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACTT
CAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
ACAAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAACTAGTCAAGTA
CTTGTCCATGTAGCAACTGAAGGTAAACTCCAAGTACAAGGAACGATGAG
TGAGTATGATTTGGCTAATGTTAAAAAAGACCAGGCTGTTAAAATAAAAT
CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAATTTCATATATCTCA
AATTATCCAGAAGCAGAAGCAAACAACAATGACTCTAATAACGGCTCTAG
TGCTGTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAT
TAAAACAAGGTTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
CTTATTGTCCCTACAAGTTCTGTGATAAACAAAGATAATAAACACTTTGT
TTGGGTATACAATGATTCTAATCGTAAAATTTCCAAAGTTGAAGTCAAAA
TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
GGACAAATCGTGGTTACTAATCCAAGTAAAACCTTCAAGGATGGGCAAAA
AATTGATAATATTGAATCAATCGATCTTAACTCTAATAAGAAATCAGAG

SEQ ID NO. 8506
STRAIN M732
TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAAACTAATTA
CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTTCGTCCTCAACTCTTTTGA
CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
AAAGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCACAGC
TGGTCAGCAGTTAGTTCAATATGATACAACAACTGCACAAGCAGCCTACG
ACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
AAGACAACAGGGAGTTTTCCAGCTATGGAATCAAGTGATCAATCTTCATC
ATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGAATCGTC
TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACTT
CAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
ACAAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAACTAGTCAAGTA
CTTGTCCATGTAGCAACTGAAGGTAAACTCCAAGTACAAGGAACGATGAG
TGAGTATGATTTGGCTAATGTTAAAAAAGATCAGGCTGTTAAAATAAAAT
CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAATTTCATATATCTCA
AATTATCCAGAAGCAGAAGCAAACAACAATGACTCTAATAACGGCTCTAG
TGCTGTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAT
TAAAACAAGGTTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
CTTATTGTCCCTACAAGTTCTGTGATAAACAAAGATAATAAACACTTTGT
TTGGGTATACAATGATTCTAATCGTAAAATTTCCAAAGTTGAAGTCAAAA
TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
GGACAAATCGTGGTTACTAATCCAAGCAAAACTTTCAAGGATGGGCAAAA
AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
TGAA

SEQ ID NO. 8507
STRAIN COH1
TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAAAC
TAATTACAAAGTTTTTAATGTTAGAGAAGGAAGTGTTTCGTCCTCAACTC
TTTTGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGAT
GCTAATAAAGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAAT
CACAGCTGGTCAGCAGTTAGTTCAATATGATACAACAACTGCACAAGCAG
CCTACGACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAAT
AATCTAAAGACAACAGGGAGTTTTCCAGCTATGGAATCAAGTGATCAATC

Table 85: Comparative Sequences relating to SAG1361

TTCATCATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGA
ATCGTCTACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAA
CAACTTCAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAGTAAA
TAAAGCACAAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAG
GGACAGTTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAACTAGT
CAAGTACTTGTCCATGTAGCAACTGAAGGTAAACTCCAAGTACAAGGAAC
GATGAGTGAGTATGATTTGGCTAATGTTAAAAAAGATCAGGCTGTTAAAA
TAAAATCTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAATTTCATAT
ATCTCAAATTATCCAGAAGCAGAAGCAAACAACAATGACTCTAATAACGG
CTCTAGTGCTGTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCG
ATGCATTAAAACAAGGTTTTACCGTATCAGTTGAAGTAGTTAATGGAGAT
AAGCACCTTATTGTCCCTACAAGTTCTGTGATAAACAAAGATAATAAACA
CTTTGTTTGGGTATACAATGATTCTAATCGTAAAATTTCCAAAGTTGAAG
TCAAAATTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTG
AAAGCAGGACAAATCGTGGTTACTAATCCAAGCAAAACTTTCAAGGATGG
GCAAAAAATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAAT
CAGAGGTGAA

SEQ ID NO. 8507
STRAIN M781
TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAAACTAATTA
CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTTCGTCCTCAACTCTTTTGA
CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
AAAGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCACAGC
TGGTCAGCAGTTAGTTCAATATGATACAACAACTGCACAAGCAGCCTACG
ACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
AAGACAACAGGGAGTTTTCCAGCTATGGAATCAAGTGATCAATCTTCATC
ATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGAATCGTC
TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACTT
CAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
ACAAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAACTAGTCAAGTA
CTTGTCCATGTAGCAACTGAAGGTAAACTCCAAGTACAAGGAACGATGAG
TGAGTATGATTTGGCTAATGTTAAAAAAGATCAGGCTGTTAAAATAAAAT
CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAATTTCATATATCTCA
AATTATCCAGAAGCAGAAGCAAACAACAATGACTCTAATAACGGCTCTAG
TGCTGTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAT
TAAAACAAGGTTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
CTTATTGTCCCTACAAGTTCTGTGATAAACAAAGATAATAAACACTTTGT
TTGGGTATACAATGATTCTAATCGTAAAATTTCCAAAGTTGAAGTCAAAA
TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
GGACAAATCGTGGTTACTAATCCAAGCAAAACTTTCAAGGATGGGCAAAA
AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
TGAA

SEQ ID NO. 8508
STRAIN CJB110
TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAAACTAACTA
CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTTCGTCCTCAACTCTTTTGA
CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
AAAGGTAATCGAGCAACTGTCACAGTTAAAGTGGGTGATAAAATCACAGC
TGGTCAGCAGTTAGTTCAATATGATACAACAACTGCACAAGCAGCCTACG
ACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
AAGACAACAGGAAGTCTTCCAGCTATGGAATTAAGTGATCAATCTTCTTC
ATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGAATCGTC
TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACTT
CAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
ACAAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAACTAGTCAAGTA
CTTGTCCATGTAGCAACTGAAGGTAAACTCCAAGTACAAGGAACGATGAG
TGAGTATGATTTGGCTAATGTTAAAAAAGACCAGGCTGTTAAAATAAAAT
CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAATTTCATATATCTCA
AATTATCCAGAAGCAGAAGCAAACAACAATGACTCTAATAACGGCTCTAG
TGCTGTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAT
TAAAACAAGGTTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
CTTATTGTCCCTACAAGTTCTGTGATAAACAAAGATAATAAACACTTTGT
TTGGGTATACAATGATTCTAATCGTAAAATTTCCAAAGTTGAAGTCAAAA
TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
GGACAAATCGTGGTTACTAATCCAAGTAAAACCTTCAAGGATGGGCAAAA
AATTGATAATATTGAATCAATCGATCTTAACTCTAATAAGAAATCAGAGG
TGA

SEQ ID NO. 8509
STRAIN 1169NT
TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAAACT
AACTACAAAGTTTTTAATGTTAGAGAAGGAAGTGTTTCGTCCTCAACTCT
TTTGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATG
CTAATAAAGGTAATCGAGCAACTGTCACAGTTAAAGTGGGTGATAAAATC
ACAGCTGGTCAGCAGTTAGTTCAATATGATACAACAACTGCACAAGCAGC
CTACGACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATA
ATCTAAAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCT
TCTTCATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGAA
TCGTCTACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAAC

Table 85: Comparative Sequences relating to SAG1361

AACTTCAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAGTAAAT
AAAGCACAAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGG
GACAGTTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAACTAGTC
AAGTACTTGTCCATGTAGCAACTGAAGGTAAACTCCAAGTACAAGGAACG
ATGAGTGAGTATGATTTGGCTAATGTTAAAAAAGACCAGGCTGTTAAAAT
AAAATCTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAATTTCATATA
TCTCAAATTATCCAGAAGCAGAAGCAAACAACAATGACTCTAATAACGGC
TCTAGTGCTGTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCGA
TGCATTAAAACAAGGTTTTACCGTATCAGTTGAAGTAGTTAATGGAGATA
AGCACCTTATTGTCCCTACAAGTTCTGTGATAAACAAAGATAATAAACAC
TTTGTTTGGGTATACAATGATTCTAATCGTAAAATTTCCAAAGTTGAAGT
CAAAATTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGA
AAGCAGGACAAATCGTGGTTACTAATCCAAGTAAAACCTTCAAGGATGGG
CAAAAAATTGATAATATTGAATCAATCGATCTTAACTCTAATAAGAAATC
AGAGGTGAA

SEQ ID NO. 8510
STRAIN JM9130013
TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAAACTAACTA
CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTTCGTCCTCAACTCTTTTGA
CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
AAAGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCACAGC
TGGTCAGCAGTTAGTTCAATATGATACAACAACTGCACAAGCAGCCTACG
ACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
AAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTCATC
ATCATCACAAGGACAAGGGGCTCAATCGACTAGTGGTGCGACGAATCGTC
TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACTT
CAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
ACAAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAACTAGTCAAGTA
CTTGTCCATGTAGCAACTGAGGGTAAACTCCAAGTACAAGGAACGATGAG
TGAGTATGATTTGGCTAATGTTAAAAAAGACCAGTCTGTTAAAATAAAAT
CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAATTTCATATATCTCA
AATTATCCAGAAGCAGAAGCAAACAACAATGACTCTAATAACGGCTCTAG
TGCTGTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAT
TAAAACAAGGTTTTACTGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
CTTATTGTTCCTACAAGTTCTGTGACAAACAAAGATAATAAACACTTTGT
TTGGGTATACAATGATTCTAATCGTAAAATTTCCAAAGTTGAAGTCAAAA
TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
GGACAAATCGTGGTTACTAATCCAAGCAAAACTTTCAAGGATGGGCAAAA
AATTGATAATATTGAATCAATAGATCTTAAGTCTAATAAGAAATCAGAGG
TGAAA

```
PRETTY of: /biotmp/msa363690.2{*}   March 31, 2003 07:01  ..

                            1                                                     50
   msa363690.2{690_COH1}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa363690.2{690_M732}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa363690.2{690_M781}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa363690.2{690_090}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa363690.2{690_CJB110}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa363690.2{690_1169NT}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa363690.2{690_18RS21}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa363690.2{690_2603}    atgagtaaac gacaaaattt aggaattagt aaaaaaggag caattatatc
   msa363690.2{690_A909}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa363690.2{690_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa363690.2{690_H36B}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
               Consensus    ********** ********** ********** ********** **********

                            51                                                   100
   msa363690.2{690_COH1}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~TTT TTATGGGTAC
   msa363690.2{690_M732}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~TTT TTATGGGTAC
   msa363690.2{690_M781}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~TTT TTATGGGTAC
    msa363690.2{690_090}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~TTT TTATGGGTAC
  msa363690.2{690_CJB110}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~TTT TTATGGGTAC
  msa363690.2{690_1169NT}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~TTT TTATGGGTAC
  msa363690.2{690_18RS21}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~TTT TTATGGGTAC
   msa363690.2{690_2603}    agggctctca gtggcactaa ttgtagtaat aggtggcTTT TTATGGGTAC
   msa363690.2{690_A909}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~TTT TTATGGGTAC
msa363690.2{690_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~TTT TTATGGGTAC
   msa363690.2{690_H36B}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~TTT TTATGGGTAC
               Consensus    ********** ********** ********** ********** **********

                            101                                                  150
   msa363690.2{690_COH1}    AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAAtTACAA AGTTTTTAAT
   msa363690.2{690_M732}    AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAAtTACAA AGTTTTTAAT
   msa363690.2{690_M781}    AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAAtTACAA AGTTTTTAAT
    msa363690.2{690_090}    AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAAcTACAA AGTTTTTAAT
  msa363690.2{690_CJB110}   AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAAcTACAA AGTTTTTAAT
  msa363690.2{690_1169NT}   AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAAcTACAA AGTTTTTAAT
  msa363690.2{690_18RS21}   AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAAcTACAA AGTTTTTAAT
   msa363690.2{690_2603}    AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAAcTACAA AGTTTTTAAT
```

Table 85: Comparative Sequences relating to SAG1361

```
      msa363690.2{690_A909}  AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAAcTACAA AGTTTTTAAT
 msa363690.2{690_JM9130013}  AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAAcTACAA AGTTTTTAAT
      msa363690.2{690_H36B}  AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAAtTACAA AGTTTTTAAT
                  Consensus  ********** ********** ********** ****_***** **********

                             151                                               200
      msa363690.2{690_COH1}  GTTAGAGAAG GAAGTGTTTC GTCCTCAACT CTTTTGACAG GAAAAGCTAA
      msa363690.2{690_M732}  GTTAGAGAAG GAAGTGTTTC GTCCTCAACT CTTTTGACAG GAAAAGCTAA
      msa363690.2{690_M781}  GTTAGAGAAG GAAGTGTTTC GTCCTCAACT CTTTTGACAG GAAAAGCTAA
       msa363690.2{690_090}  GTTAGAGAAG GAAGTGTTTC GTCCTCAACT CTTTTGACAG GAAAAGCTAA
    msa363690.2{690_CJB110}  GTTAGAGAAG GAAGTGTTTC GTCCTCAACT CTTTTGACAG GAAAAGCTAA
    msa363690.2{690_1169NT}  GTTAGAGAAG GAAGTGTTTC GTCCTCAACT CTTTTGACAG GAAAAGCTAA
    msa363690.2{690_18RS21}  GTTAGAGAAG GAAGTGTTTC GTCCTCAACT CTTTTGACAG GAAAAGCTAA
      msa363690.2{690_2603}  GTTAGAGAAG GAAGTGTTTC GTCCTCAACT CTTTTGACAG GAAAAGCTAA
      msa363690.2{690_A909}  GTTAGAGAAG GAAGTGTTTC GTCCTCAACT CTTTTGACAG GAAAAGCTAA
 msa363690.2{690_JM9130013}  GTTAGAGAAG GAAGTGTTTC GTCCTCAACT CTTTTGACAG GAAAAGCTAA
      msa363690.2{690_H36B}  GTTAGAGAAG GAAGTGTTTC GTCCTCAACT CTTTTGACAG GAAAAGCTAA
                  Consensus  ********** ********** ********** ********** **********

                             201                                               250
      msa363690.2{690_COH1}  GGCTAATCAA GAACAGTATG TGTATTTTGA TGCTAATAAa GGTAATCGAG
      msa363690.2{690_M732}  GGCTAATCAA GAACAGTATG TGTATTTTGA TGCTAATAAa GGTAATCGAG
      msa363690.2{690_M781}  GGCTAATCAA GAACAGTATG TGTATTTTGA TGCTAATAAa GGTAATCGAG
       msa363690.2{690_090}  GGCTAATCAA GAACAGTATG TGTATTTTGA TGCTAATAAa GGTAATCGAG
    msa363690.2{690_CJB110}  GGCTAATCAA GAACAGTATG TGTATTTTGA TGCTAATAAa GGTAATCGAG
    msa363690.2{690_1169NT}  GGCTAATCAA GAACAGTATG TGTATTTTGA TGCTAATAAa GGTAATCGAG
    msa363690.2{690_18RS21}  GGCTAATCAA GAACAGTATG TGTATTTTGA TGCTAATAAa GGTAATCGAG
      msa363690.2{690_2603}  GGCTAATCAA GAACAGTATG TGTATTTTGA TGCTAATAAa GGTAATCGAG
      msa363690.2{690_A909}  GGCTAATCAA GAACAGTATG TGTATTTTGA TGCTAATAAa GGTAATCGAG
 msa363690.2{690_JM9130013}  GGCTAATCAA GAACAGTATG TGTATTTTGA TGCTAATAAa GGTAATCGAG
      msa363690.2{690_H36B}  GGCTAATCAA GAACAGTATG TGTATTTTGA TGCTAATAAg GGTAATCGAG
                  Consensus  ********** ********** ********** *********_ **********

                             251                                               300
      msa363690.2{690_COH1}  CAACTGTtAC AGTTAAAGTG GGTGATAAAA TCACAGCTGG TCAGCAGTTA
      msa363690.2{690_M732}  CAACTGTtAC AGTTAAAGTG GGTGATAAAA TCACAGCTGG TCAGCAGTTA
      msa363690.2{690_M781}  CAACTGTtAC AGTTAAAGTG GGTGATAAAA TCACAGCTGG TCAGCAGTTA
       msa363690.2{690_090}  CAACTGTcAC AGTTAAAGTG GGTGATAAAA TCACAGCTGG TCAGCAGTTA
    msa363690.2{690_CJB110}  CAACTGTcAC AGTTAAAGTG GGTGATAAAA TCACAGCTGG TCAGCAGTTA
    msa363690.2{690_1169NT}  CAACTGTcAC AGTTAAAGTG GGTGATAAAA TCACAGCTGG TCAGCAGTTA
    msa363690.2{690_18RS21}  CAACTGTcAC AGTTAAAGTG GGTGATAAAA TCACAGCTGG TCAGCAGTTA
      msa363690.2{690_2603}  CAACTGTcAC AGTTAAAGTG GGTGATAAAA TCACAGCTGG TCAGCAGTTA
      msa363690.2{690_A909}  CAACTGTtAC AGTTAAAGTG GGTGATAAAA TCACAGCTGG TCAGCAGTTA
 msa363690.2{690_JM9130013}  CAACTGTtAC AGTTAAAGTG GGTGATAAAA TCACAGCTGG TCAGCAGTTA
      msa363690.2{690_H36B}  CAACTGTtAC AGTTAAAGTG GGTGATAAAA TCACAGCTGG TCAGCAGTTA
                  Consensus  *******_** ********** ********** ********** **********

                             301                                               350
      msa363690.2{690_COH1}  GTTCAATATG ATACAACAAC TGCACAAGCA GCCTACGACA CTGCTAATCG
      msa363690.2{690_M732}  GTTCAATATG ATACAACAAC TGCACAAGCA GCCTACGACA CTGCTAATCG
      msa363690.2{690_M781}  GTTCAATATG ATACAACAAC TGCACAAGCA GCCTACGACA CTGCTAATCG
       msa363690.2{690_090}  GTTCAATATG ATACAACAAC TGCACAAGCA GCCTACGACA CTGCTAATCG
    msa363690.2{690_CJB110}  GTTCAATATG ATACAACAAC TGCACAAGCA GCCTACGACA CTGCTAATCG
    msa363690.2{690_1169NT}  GTTCAATATG ATACAACAAC TGCACAAGCA GCCTACGACA CTGCTAATCG
    msa363690.2{690_18RS21}  GTTCAATATG ATACAACAAC TGCACAAGCA GCCTACGACA CTGCTAATCG
      msa363690.2{690_2603}  GTTCAATATG ATACAACAAC TGCACAAGCA GCCTACGACA CTGCTAATCG
      msa363690.2{690_A909}  GTTCAATATG ATACAACAAC TGCACAAGCA GCCTACGACA CTGCTAATCG
 msa363690.2{690_JM9130013}  GTTCAATATG ATACAACAAC TGCACAAGCA GCCTACGACA CTGCTAATCG
      msa363690.2{690_H36B}  GTTCAATATG ATACAACAAC TGCACAAGCA GCCTACGACA CTGCTAATCG
                  Consensus  ********** ********** ********** ********** **********

                             351                                               400
      msa363690.2{690_COH1}  TCAATTAAAT AAAGTAGCGC GTCAGATTAA TAATCTAAAG ACAACAGGgA
      msa363690.2{690_M732}  TCAATTAAAT AAAGTAGCGC GTCAGATTAA TAATCTAAAG ACAACAGGgA
      msa363690.2{690_M781}  TCAATTAAAT AAAGTAGCGC GTCAGATTAA TAATCTAAAG ACAACAGGgA
       msa363690.2{690_090}  TCAATTAAAT AAAGTAGCGC GTCAGATTAA TAATCTAAAG ACAACAGGaA
    msa363690.2{690_CJB110}  TCAATTAAAT AAAGTAGCGC GTCAGATTAA TAATCTAAAG ACAACAGGaA
    msa363690.2{690_1169NT}  TCAATTAAAT AAAGTAGCGC GTCAGATTAA TAATCTAAAG ACAACAGGaA
    msa363690.2{690_18RS21}  TCAATTAAAT AAAGTAGCGC GTCAGATTAA TAATCTAAAG ACAACAGGaA
      msa363690.2{690_2603}  TCAATTAAAT AAAGTAGCGC GTCAGATTAA TAATCTAAAG ACAACAGGaA
      msa363690.2{690_A909}  TCAATTAAAT AAAGTAGCGC GTCAGATTAA TAATCTAAAG ACAACAGGaA
 msa363690.2{690_JM9130013}  TCAATTAAAT AAAGTAGCGC GTCAGATTAA TAATCTAAAG ACAACAGGaA
      msa363690.2{690_H36B}  TCAATTAAAT AAAGTAGCGC GTCAGATTAA TAATCTAAAG ACAACAGGaA
                  Consensus  ********** ********** ********** ********** ********_*

                             401                                               450
      msa363690.2{690_COH1}  GTtTTCCAGC TATGGAATcA AGTGATCAAT CTTCaTCATC ATCACAAGGA
      msa363690.2{690_M732}  GTtTTCCAGC TATGGAATcA AGTGATCAAT CTTCaTCATC ATCACAAGGA
      msa363690.2{690_M781}  GTtTTCCAGC TATGGAATcA AGTGATCAAT CTTCaTCATC ATCACAAGGA
       msa363690.2{690_090}  GTcTTCCAGC TATGGAATtA AGTGATCAAT CTTCtTCATC ATCACAAGGA
    msa363690.2{690_CJB110}  GTcTTCCAGC TATGGAATtA AGTGATCAAT CTTCtTCATC ATCACAAGGA
    msa363690.2{690_1169NT}  GTcTTCCAGC TATGGAATcA AGTGATCAAT CTTCtTCATC ATCACAAGGA
    msa363690.2{690_18RS21}  GTcTTCCAGC TATGGAATcA AGTGATCAAT CTTCtTCATC ATCACAAGGA
```

Table 85: Comparative Sequences relating to SAG1361

```
      msa363690.2{690_2603}  GTcTTCCAGC TATGGAATcA AGTGATCAAT CTTCtTCATC ATCACAAGGA
      msa363690.2{690_A909}  GTcTTCCAGC TATGGAATcA AGTGATCAAT CTTCaTCATC ATCACAAGGA
 msa363690.2{690_JM9130013}  GTcTTCCAGC TATGGAATcA AGTGATCAAT CTTCaTCATC ATCACAAGGA
      msa363690.2{690_H36B}, GTcTTCCAGC TATGGAATcA AGTGATCAAT CTTCaTCATC ATCACAAGGA
                  Consensus  **-******* ********-* ********** ****-***** **********

                             451                                            500
      msa363690.2{690_COH1}  CAAGGGaCTC AATCGACTAG TGGTGCGACG AATCGTCTAC AGCAAAATTA
      msa363690.2{690_M732}  CAAGGGaCTC AATCGACTAG TGGTGCGACG AATCGTCTAC AGCAAAATTA
      msa363690.2{690_M781}  CAAGGGaCTC AATCGACTAG TGGTGCGACG AATCGTCTAC AGCAAAATTA
       msa363690.2{690_090}  CAAGGGaCTC AATCGACTAG TGGTGCGACG AATCGTCTAC AGCAAAATTA
    msa363690.2{690_CJB110}  CAAGGGaCTC AATCGACTAG TGGTGCGACG AATCGTCTAC AGCAAAATTA
    msa363690.2{690_1169NT}  CAAGGGaCTC AATCGACTAG TGGTGCGACG AATCGTCTAC AGCAAAATTA
    msa363690.2{690_18RS21}  CAAGGGaCTC AATCGACTAG TGGTGCGACG AATCGTCTAC AGCAAAATTA
      msa363690.2{690_2603}  CAAGGGaCTC AATCGACTAG TGGTGCGACG AATCGTCTAC AGCAAAATTA
      msa363690.2{690_A909}  CAAGGGgCTC AATCGACTAG TGGTGCGACG AATCGTCTAC AGCAAAATTA
 msa363690.2{690_JM9130013}  CAAGGGgCTC AATCGACTAG TGGTGCGACG AATCGTCTAC AGCAAAATTA
      msa363690.2{690_H36B}  CAAGGGaCTC AATCGACTAG TGGTGCGACG AATCGTCTAC AGCAAAATTA
                  Consensus  ******-*** ********** ********** ********** **********

                             501                                            550
      msa363690.2{690_COH1}  TCAAAGTCAA GCTAATGCTT CATACAACCA ACAACTTCAA GATTTGAATG
      msa363690.2{690_M732}  TCAAAGTCAA GCTAATGCTT CATACAACCA ACAACTTCAA GATTTGAATG
      msa363690.2{690_M781}  TCAAAGTCAA GCTAATGCTT CATACAACCA ACAACTTCAA GATTTGAATG
       msa363690.2{690_090}  TCAAAGTCAA GCTAATGCTT CATACAACCA ACAACTTCAA GATTTGAATG
    msa363690.2{690_CJB110}  TCAAAGTCAA GCTAATGCTT CATACAACCA ACAACTTCAA GATTTGAATG
    msa363690.2{690_1169NT}  TCAAAGTCAA GCTAATGCTT CATACAACCA ACAACTTCAA GATTTGAATG
    msa363690.2{690_18RS21}  TCAAAGTCAA GCTAATGCTT CATACAACCA ACAACTTCAA GATTTGAATG
      msa363690.2{690_2603}  TCAAAGTCAA GCTAATGCTT CATACAACCA ACAACTTCAA GATTTGAATG
      msa363690.2{690_A909}  TCAAAGTCAA GCTAATGCTT CATACAACCA ACAACTTCAA GATTTGAATG
 msa363690.2{690_JM9130013}  TCAAAGTCAA GCTAATGCTT CATACAACCA ACAACTTCAA GATTTGAATG
      msa363690.2{690_H36B}  TCAAAGTCAA GCTAATGCTT CATACAACCA ACAACTTCAA GATTTGAATG
                  Consensus  ********** ********** ********** ********** **********

                             551                                            600
      msa363690.2{690_COH1}  ATGCTTATGC AGATGCACAG GCAGAAGTAA ATAAAGCACA AAAAGCATTG
      msa363690.2{690_M732}  ATGCTTATGC AGATGCACAG GCAGAAGTAA ATAAAGCACA AAAAGCATTG
      msa363690.2{690_M781}  ATGCTTATGC AGATGCACAG GCAGAAGTAA ATAAAGCACA AAAAGCATTG
       msa363690.2{690_090}  ATGCTTATGC AGATGCACAG GCAGAAGTAA ATAAAGCACA AAAAGCATTG
    msa363690.2{690_CJB110}  ATGCTTATGC AGATGCACAG GCAGAAGTAA ATAAAGCACA AAAAGCATTG
    msa363690.2{690_1169NT}  ATGCTTATGC AGATGCACAG GCAGAAGTAA ATAAAGCACA AAAAGCATTG
    msa363690.2{690_18RS21}  ATGCTTATGC AGATGCACAG GCAGAAGTAA ATAAAGCACA AAAAGCATTG
      msa363690.2{690_2603}  ATGCTTATGC AGATGCACAG GCAGAAGTAA ATAAAGCACA AAAAGCATTG
      msa363690.2{690_A909}  ATGCTTATGC AGATGCACAG GCAGAAGTAA ATAAAGCACA AAAAGCATTG
 msa363690.2{690_JM9130013}  ATGCTTATGC AGATGCACAG GCAGAAGTAA ATAAAGCACA AAAAGCATTG
      msa363690.2{690_H36B}  ATGCTTATGC AGATGCACAG GCAGAAGTAA ATAAAGCACA AAAAGCATTG
                  Consensus  ********** ********** ********** ********** **********

                             601                                            650
      msa363690.2{690_COH1}  AATGATACTG TTATTACAAG TGACGTATCA GGGACAGTTG TTGAAGTTAA
      msa363690.2{690_M732}  AATGATACTG TTATTACAAG TGACGTATCA GGGACAGTTG TTGAAGTTAA
      msa363690.2{690_M781}  AATGATACTG TTATTACAAG TGACGTATCA GGGACAGTTG TTGAAGTTAA
       msa363690.2{690_090}  AATGATACTG TTATTACAAG TGACGTATCA GGGACAGTTG TTGAAGTTAA
    msa363690.2{690_CJB110}  AATGATACTG TTATTACAAG TGACGTATCA GGGACAGTTG TTGAAGTTAA
    msa363690.2{690_1169NT}  AATGATACTG TTATTACAAG TGACGTATCA GGGACAGTTG TTGAAGTTAA
    msa363690.2{690_18RS21}  AATGATACTG TTATTACAAG TGACGTATCA GGGACAGTTG TTGAAGTTAA
      msa363690.2{690_2603}  AATGATACTG TTATTACAAG TGACGTATCA GGGACAGTTG TTGAAGTTAA
      msa363690.2{690_A909}  AATGATACTG TTATTACAAG TGACGTATCA GGGACAGTTG TTGAAGTTAA
 msa363690.2{690_JM9130013}  AATGATACTG TTATTACAAG TGACGTATCA GGGACAGTTG TTGAAGTTAA
      msa363690.2{690_H36B}  AATGATACTG TTATTACAAG TGACGTATCA GGGACAGTTG TTGAAGTTAA
                  Consensus  ********** ********** ********** ********** **********

                             651                                            700
      msa363690.2{690_COH1}  TAGTGATATT GATCCAGCTT CAAAAACTAG TCAAGTACTT GTCCATGTAG
      msa363690.2{690_M732}  TAGTGATATT GATCCAGCTT CAAAAACTAG TCAAGTACTT GTCCATGTAG
      msa363690.2{690_M781}  TAGTGATATT GATCCAGCTT CAAAAACTAG TCAAGTACTT GTCCATGTAG
       msa363690.2{690_090}  TAGTGATATT GATCCAGCTT CAAAAACTAG TCAAGTACTT GTCCATGTAG
    msa363690.2{690_CJB110}  TAGTGATATT GATCCAGCTT CAAAAACTAG TCAAGTACTT GTCCATGTAG
    msa363690.2{690_1169NT}  TAGTGATATT GATCCAGCTT CAAAAACTAG TCAAGTACTT GTCCATGTAG
    msa363690.2{690_18RS21}  TAGTGATATT GATCCAGCTT CAAAAACTAG TCAAGTACTT GTCCATGTAG
      msa363690.2{690_2603}  TAGTGATATT GATCCAGCTT CAAAAACTAG TCAAGTACTT GTCCATGTAG
      msa363690.2{690_A909}  TAGTGATATT GATCCAGCTT CAAAAACTAG TCAAGTACTT GTCCATGTAG
 msa363690.2{690_JM9130013}  TAGTGATATT GATCCAGCTT CAAAAACTAG TCAAGTACTT GTCCATGTAG
      msa363690.2{690_H36B}  TAGTGATATT GATCCAGCTT CAAAAACTAG TCAAGTACTT GTCCATGTAG
                  Consensus  ********** ********** ********** ********** **********

                             701                                            750
      msa363690.2{690_COH1}  CAACTGAaGG TAAACTCCAA GTACAAGGAA CGATGAGTGA GTATGATTTG
      msa363690.2{690_M732}  CAACTGAaGG TAAACTCCAA GTACAAGGAA CGATGAGTGA GTATGATTTG
      msa363690.2{690_M781}  CAACTGAaGG TAAACTCCAA GTACAAGGAA CGATGAGTGA GTATGATTTG
       msa363690.2{690_090}  CAACTGAaGG TAAACTCCAA GTACAAGGAA CGATGAGTGA GTATGATTTG
    msa363690.2{690_CJB110}  CAACTGAaGG TAAACTCCAA GTACAAGGAA CGATGAGTGA GTATGATTTG
    msa363690.2{690_1169NT}  CAACTGAaGG TAAACTCCAA GTACAAGGAA CGATGAGTGA GTATGATTTG
```

Table 85: Comparative Sequences relating to SAG1361

```
   msa363690.2{690_18RS21}  CAACTGAaGG TAAACTCCAA GTACAAGGAA CGATGAGTGA GTATGATTTG
     msa363690.2{690_2603}  CAACTGAaGG TAAACTCCAA GTACAAGGAA CGATGAGTGA GTATGATTTG
     msa363690.2{690_A909}  CAACTGAgGG TAAACTCCAA GTACAAGGAA CGATGAGTGA GTATGATTTG
msa363690.2{690_JM9130013}  CAACTGAgGG TAAACTCCAA GTACAAGGAA CGATGAGTGA GTATGATTTG
     msa363690.2{690_H36B}  CAACTGAaGG TAAACTCCAA GTACAAGGAA CGATGAGTGA GTATGATTTG
                 Consensus  *******-** ********** ********** ********** **********

                            751                                                800
     msa363690.2{690_COH1}  GCTAATGTtA AAAAAGAtCA GgCTGTTAAA ATAAAATCTA AGGTCTATCC
     msa363690.2{690_M732}  GCTAATGTtA AAAAAGAtCA GgCTGTTAAA ATAAAATCTA AGGTCTATCC
     msa363690.2{690_M781}  GCTAATGTtA AAAAAGAtCA GgCTGTTAAA ATAAAATCTA AGGTCTATCC
      msa363690.2{690_090}  GCTAATGTtA AAAAAGAcCA GgCTGTTAAA ATAAAATCTA AGGTCTATCC
   msa363690.2{690_CJB110}  GCTAATGTtA AAAAAGAcCA GgCTGTTAAA ATAAAATCTA AGGTCTATCC
   msa363690.2{690_1169NT}  GCTAATGTtA AAAAAGAcCA GgCTGTTAAA ATAAAATCTA AGGTCTATCC
   msa363690.2{690_18RS21}  GCTAATGTtA AAAAAGAcCA GgCTGTTAAA ATAAAATCTA AGGTCTATCC
     msa363690.2{690_2603}  GCTAATGTtA AAAAAGAcCA GgCTGTTAAA ATAAAATCTA AGGTCTATCC
     msa363690.2{690_A909}  GCTAATGTtA AAAAAGAcCA GtCTGTTAAA ATAAAATCTA AGGTCTATCC
msa363690.2{690_JM9130013}  GCTAATGTtA AAAAAGAcCA GtCTGTTAAA ATAAAATCTA AGGTCTATCC
     msa363690.2{690_H36B}  GCTAATGTaA AAAAAGAcCA GgCTGTTAAA ATAAAATCTA AGGTCTATCC
                 Consensus  ********-* *******-** *-******** ********** **********

                            801                                                850
     msa363690.2{690_COH1}  TGACAAGGAA TGGGAAGGTA AAATTTCATA TATCTCAAAT TATCCAGAAG
     msa363690.2{690_M732}  TGACAAGGAA TGGGAAGGTA AAATTTCATA TATCTCAAAT TATCCAGAAG
     msa363690.2{690_M781}  TGACAAGGAA TGGGAAGGTA AAATTTCATA TATCTCAAAT TATCCAGAAG
      msa363690.2{690_090}  TGACAAGGAA TGGGAAGGTA AAATTTCATA TATCTCAAAT TATCCAGAAG
   msa363690.2{690_CJB110}  TGACAAGGAA TGGGAAGGTA AAATTTCATA TATCTCAAAT TATCCAGAAG
   msa363690.2{690_1169NT}  TGACAAGGAA TGGGAAGGTA AAATTTCATA TATCTCAAAT TATCCAGAAG
   msa363690.2{690_18RS21}  TGACAAGGAA TGGGAAGGTA AAATTTCATA TATCTCAAAT TATCCAGAAG
     msa363690.2{690_2603}  TGACAAGGAA TGGGAAGGTA AAATTTCATA TATCTCAAAT TATCCAGAAG
     msa363690.2{690_A909}  TGACAAGGAA TGGGAAGGTA AAATTTCATA TATCTCAAAT TATCCAGAAG
msa363690.2{690_JM9130013}  TGACAAGGAA TGGGAAGGTA AAATTTCATA TATCTCAAAT TATCCAGAAG
     msa363690.2{690_H36B}  TGACAAGGAA TGGGAAGGTA AAATTTCATA TATCTCAAAT TATCCAGAAG
                 Consensus  ********** ********** ********** ********** **********

                            851                                                900
     msa363690.2{690_COH1}  CAGAAGCAAA CAACAATGAC TCTAATAACG GCTCTAGTGC TGTAAATTAT
     msa363690.2{690_M732}  CAGAAGCAAA CAACAATGAC TCTAATAACG GCTCTAGTGC TGTAAATTAT
     msa363690.2{690_M781}  CAGAAGCAAA CAACAATGAC TCTAATAACG GCTCTAGTGC TGTAAATTAT
      msa363690.2{690_090}  CAGAAGCAAA CAACAATGAC TCTAATAACG GCTCTAGTGC TGTAAATTAT
   msa363690.2{690_CJB110}  CAGAAGCAAA CAACAATGAC TCTAATAACG GCTCTAGTGC TGTAAATTAT
   msa363690.2{690_1169NT}  CAGAAGCAAA CAACAATGAC TCTAATAACG GCTCTAGTGC TGTAAATTAT
   msa363690.2{690_18RS21}  CAGAAGCAAA CAACAATGAC TCTAATAACG GCTCTAGTGC TGTAAATTAT
     msa363690.2{690_2603}  CAGAAGCAAA CAACAATGAC TCTAATAACG GCTCTAGTGC TGTAAATTAT
     msa363690.2{690_A909}  CAGAAGCAAA CAACAATGAC TCTAATAACG GCTCTAGTGC TGTAAATTAT
msa363690.2{690_JM9130013}  CAGAAGCAAA CAACAATGAC TCTAATAACG GCTCTAGTGC TGTAAATTAT
     msa363690.2{690_H36B}  CAGAAGCAAA CAACAATGAC TCTAATAACG GCTCTAGTGC TGTAAATTAT
                 Consensus  ********** ********** ********** ********** **********

                            901                                                950
     msa363690.2{690_COH1}  AAATATAAAG TAGATATTAC TAGCCCTCTC GATGCATTAA AACAAGGTTT
     msa363690.2{690_M732}  AAATATAAAG TAGATATTAC TAGCCCTCTC GATGCATTAA AACAAGGTTT
     msa363690.2{690_M781}  AAATATAAAG TAGATATTAC TAGCCCTCTC GATGCATTAA AACAAGGTTT
      msa363690.2{690_090}  AAATATAAAG TAGATATTAC TAGCCCTCTC GATGCATTAA AACAAGGTTT
   msa363690.2{690_CJB110}  AAATATAAAG TAGATATTAC TAGCCCTCTC GATGCATTAA AACAAGGTTT
   msa363690.2{690_1169NT}  AAATATAAAG TAGATATTAC TAGCCCTCTC GATGCATTAA AACAAGGTTT
   msa363690.2{690_18RS21}  AAATATAAAG TAGATATTAC TAGCCCTCTC GATGCATTAA AACAAGGTTT
     msa363690.2{690_2603}  AAATATAAAG TAGATATTAC TAGCCCTCTC GATGCATTAA AACAAGGTTT
     msa363690.2{690_A909}  AAATATAAAG TAGATATTAC TAGCCCTCTC GATGCATTAA AACAAGGTTT
msa363690.2{690_JM9130013}  AAATATAAAG TAGATATTAC TAGCCCTCTC GATGCATTAA AACAAGGTTT
     msa363690.2{690_H36B}  AAATATAAAG TAGATATTAC TAGCCCTCTC GATGCATTAA AACAAGGTTT
                 Consensus  ********** ********** ********** ********** **********

                            951                                               1000
     msa363690.2{690_COH1}  TACcGTATCA GTTGAAGTAG TTAATGGAGA TAAGCACCTT ATTGTcCCTA
     msa363690.2{690_M732}  TACcGTATCA GTTGAAGTAG TTAATGGAGA TAAGCACCTT ATTGTcCCTA
     msa363690.2{690_M781}  TACcGTATCA GTTGAAGTAG TTAATGGAGA TAAGCACCTT ATTGTcCCTA
      msa363690.2{690_090}  TACcGTATCA GTTGAAGTAG TTAATGGAGA TAAGCACCTT ATTGTcCCTA
   msa363690.2{690_CJB110}  TACcGTATCA GTTGAAGTAG TTAATGGAGA TAAGCACCTT ATTGTcCCTA
   msa363690.2{690_1169NT}  TACcGTATCA GTTGAAGTAG TTAATGGAGA TAAGCACCTT ATTGTcCCTA
   msa363690.2{690_18RS21}  TACcGTATCA GTTGAAGTAG TTAATGGAGA TAAGCACCTT ATTGTcCCTA
     msa363690.2{690_2603}  TACcGTATCA GTTGAAGTAG TTAATGGAGA TAAGCACCTT ATTGTcCCTA
     msa363690.2{690_A909}  TACtGTATCA GTTGAAGTAG TTAATGGAGA TAAGCACCTT ATTGTtCCTA
msa363690.2{690_JM9130013}  TACtGTATCA GTTGAAGTAG TTAATGGAGA TAAGCACCTT ATTGTtCCTA
     msa363690.2{690_H36B}  TACtGTATCA GTTGAAGTAG TTAATGGAGA TAAGCACCTT ATTGTtCCTA
                 Consensus  ***-****** ********** ********** ********** *****-****

                            1001                                              1050
     msa363690.2{690_COH1}  CAAGTTCTGT GAtAAACAAA GATAATAAAC ACTTTGTTTG GGTATACAAT
     msa363690.2{690_M732}  CAAGTTCTGT GAtAAACAAA GATAATAAAC ACTTTGTTTG GGTATACAAT
     msa363690.2{690_M781}  CAAGTTCTGT GAtAAACAAA GATAATAAAC ACTTTGTTTG GGTATACAAT
      msa363690.2{690_090}  CAAGTTCTGT GAtAAACAAA GATAATAAAC ACTTTGTTTG GGTATACAAT
   msa363690.2{690_CJB110}  CAAGTTCTGT GAtAAACAAA GATAATAAAC ACTTTGTTTG GGTATACAAT
```

Table 85: Comparative Sequences relating to SAG1361

```
  msa363690.2{690_1169NT}  CAAGTTCTGT GAtAAACAAA GATAATAAAC ACTTTGTTTG GGTATACAAT
  msa363690.2{690_18RS21}  CAAGTTCTGT GAtAAACAAA GATAATAAAC ACTTTGTTTG GGTATACAAT
    msa363690.2{690_2603}  CAAGTTCTGT GAtAAACAAA GATAATAAAC ACTTTGTTTG GGTATACAAT
    msa363690.2{690_A909}  CAAGTTCTGT GAcAAACAAA GATAATAAAC ACTTTGTTTG GGTATACAAT
msa363690.2{690_JM9130013}  CAAGTTCTGT GAcAAACAAA GATAATAAAC ACTTTGTTTG GGTATACAAT
    msa363690.2{690_H36B}  CAAGTTCTGT GAcAAACAAA GATAATAAAC ACTTTGTTTG GGTATACAAT
                Consensus  ********** **-******* ********** ********** **********

                           1051                                               1100
    msa363690.2{690_COH1}  GATTCTAATC GTAAAATTTC CAAAGTTGAA GTCAAAATTG GTAAAGCTGA
    msa363690.2{690_M732}  GATTCTAATC GTAAAATTTC CAAAGTTGAA GTCAAAATTG GTAAAGCTGA
    msa363690.2{690_M781}  GATTCTAATC GTAAAATTTC CAAAGTTGAA GTCAAAATTG GTAAAGCTGA
     msa363690.2{690_090}  GATTCTAATC GTAAAATTTC CAAAGTTGAA GTCAAAATTG GTAAAGCTGA
  msa363690.2{690_CJB110}  GATTCTAATC GTAAAATTTC CAAAGTTGAA GTCAAAATTG GTAAAGCTGA
  msa363690.2{690_1169NT}  GATTCTAATC GTAAAATTTC CAAAGTTGAA GTCAAAATTG GTAAAGCTGA
  msa363690.2{690_18RS21}  GATTCTAATC GTAAAATTTC CAAAGTTGAA GTCAAAATTG GTAAAGCTGA
    msa363690.2{690_2603}  GATTCTAATC GTAAAATTTC CAAAGTTGAA GTCAAAATTG GTAAAGCTGA
    msa363690.2{690_A909}  GATTCTAATC GTAAAATTTC CAAAGTTGAA GTCAAAATTG GTAAAGCTGA
msa363690.2{690_JM9130013}  GATTCTAATC GTAAAATTTC CAAAGTTGAA GTCAAAATTG GTAAAGCTGA
    msa363690.2{690_H36B}  GATTCTAATC GTAAAATTTC CAAAGTTGAA GTCAAAATTG GTAAAGCTGA
                Consensus  ********** ********** ********** ********** **********

                           1101                                               1150
    msa363690.2{690_COH1}  TGCTAAGACA CAAGAAATTT TATCAGGTTT GAAAGCAGGA CAAATCGTgG
    msa363690.2{690_M732}  TGCTAAGACA CAAGAAATTT TATCAGGTTT GAAAGCAGGA CAAATCGTgG
    msa363690.2{690_M781}  TGCTAAGACA CAAGAAATTT TATCAGGTTT GAAAGCAGGA CAAATCGTgG
     msa363690.2{690_090}  TGCTAAGACA CAAGAAATTT TATCAGGTTT GAAAGCAGGA CAAATCGTgG
  msa363690.2{690_CJB110}  TGCTAAGACA CAAGAAATTT TATCAGGTTT GAAAGCAGGA CAAATCGTgG
  msa363690.2{690_1169NT}  TGCTAAGACA CAAGAAATTT TATCAGGTTT GAAAGCAGGA CAAATCGTgG
  msa363690.2{690_18RS21}  TGCTAAGACA CAAGAAATTT TATCAGGTTT GAAAGCAGGA CAAATCGTgG
    msa363690.2{690_2603}  TGCTAAGACA CAAGAAATTT TATCAGGTTT GAAAGCAGGA CAAATCGTgG
    msa363690.2{690_A909}  TGCTAAGACA CAAGAAATTT TATCAGGTTT GAAAGCAGGA CAAATCGTgG
msa363690.2{690_JM9130013}  TGCTAAGACA CAAGAAATTT TATCAGGTTT GAAAGCAGGA CAAATCGTgG
    msa363690.2{690_H36B}  TGCTAAGACA CAAGAAATTT TATCAGGTTT GAAAGCAGGA CAAATCGTaG
                Consensus  ********** ********** ********** ********** ********-*

                           1151                                               1200
    msa363690.2{690_COH1}  TTACTAATCC AAGcAAAaCt TTCAAGGATG GGCAAAAAAT TGATAATATT
    msa363690.2{690_M732}  TTACTAATCC AAGcAAAaCt TTCAAGGATG GGCAAAAAAT TGATAATATT
    msa363690.2{690_M781}  TTACTAATCC AAGcAAAaCt TTCAAGGATG GGCAAAAAAT TGATAATATT
     msa363690.2{690_090}  TTACTAATCC AAGtAAAaCc TTCAAGGATG GGCAAAAAAT TGATAATATT
  msa363690.2{690_CJB110}  TTACTAATCC AAGtAAAaCc TTCAAGGATG GGCAAAAAAT TGATAATATT
  msa363690.2{690_1169NT}  TTACTAATCC AAGtAAAaCc TTCAAGGATG GGCAAAAAAT TGATAATATT
  msa363690.2{690_18RS21}  TTACTAATCC AAGtAAAaCc TTCAAGGATG GGCAAAAAAT TGATAATATT
    msa363690.2{690_2603}  TTACTAATCC AAGtAAAaCc TTCAAGGATG GGCAAAAAAT TGATAATATT
    msa363690.2{690_A909}  TTACTAATCC AAGcAAAaCt TTCAAGGATG GGCAAAAAAT TGATAATATT
msa363690.2{690_JM9130013}  TTACTAATCC AAGcAAAaCt TTCAAGGATG GGCAAAAAAT TGATAATATT
    msa363690.2{690_H36B}  TTACTAATCC AAGtAAAgCt TTCAAGGATG GGCAAAAAAT TGATAATATT
                Consensus  ********** ***-***-*- ********** ********** **********

                           1201                                    1242
    msa363690.2{690_COH1}  GAATCAATcG ATCTTAAgTC TAATAAGAAA TCAGAGgtga a~
    msa363690.2{690_M732}  GAATCAATcG ATCTTAAgTC TAATAAGAAA TCAGAGgtga a~
    msa363690.2{690_M781}  GAATCAATcG ATCTTAAgTC TAATAAGAAA TCAGAGgtga a~
     msa363690.2{690_090}  GAATCAATcG ATCTTAAcTC TAATAAGAAA TCAGAGg~~~ ~~
  msa363690.2{690_CJB110}  GAATCAATcG ATCTTAAcTC TAATAAGAAA TCAGAGgtga ~~
  msa363690.2{690_1169NT}  GAATCAATcG ATCTTAAcTC TAATAAGAAA TCAGAGgtga a~
  msa363690.2{690_18RS21}  GAATCAATcG ATCTTAAcTC TAATAAGAAA TCAGAG~~~~ ~~
    msa363690.2{690_2603}  GAATCAATcG ATCTTAAcTC TAATAAGAAA TCAGAGgtga aA
    msa363690.2{690_A909}  GAATCAATaG ATCTTAAgTC TAATAAGAAA TCAGAGgtga aA
msa363690.2{690_JM9130013}  GAATCAATaG ATCTTAAgTC TAATAAGAAA TCAGAGgtga aA
    msa363690.2{690_H36B}  GAATCAATcG ATCTTAAgTC TAATAAGAAA TCAGAGgtg~ ~~
                Consensus  ********-* *******-** ********** ******---- -*
```

SEQ ID NO. 8511
STRAIN 2603 frame: 1
MSKRQNLGISKKGAIISGLSVALIVVIGGFLWVQSQPNKSAVKTNYKVFNVREGSVSSST
LLTGKAKANQEQYVYFDANKGNRATVTVKVGDKITAGQQLVQYDTTTAQAAYDTANRQLN
KVARQINNLKTTGSLPAMESSDQSSSSSQGQGTQSTSGATNRLQQNYQSQANASYNQQLQ
DLNDAYADAQAEVNKAQKALNDTVITSDVSGTVVEVNSDIDPASKTSQVLVHVATEGKLQ
VQGTMSEYDLANVKKDQAVKIKSKVYPDKEWEGKISYISNYPEAEANNNDSNNGSSAVNY
KYKVDITSPLDALKQGFTVSVEVVNGDKHLIVPTSSVINKDNKHFVWVYNDSNRKISKVE
VKIGKADAKTQEILSGLKAGQIVVTNPSKTFKDGQKIDNIESIDLNSNKKSEVK

SEQ ID NO. 8512
STRAIN 090 frame: 1
FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
VGDKITAGQQLVQYDTTTAQAAYDTANRQLNKVARQINNLKTTGSLPAMELSDQSSSSSQ
GQGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVYPDK
EWEGKISYISNYPEAEANNNDSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEVVNGDKH
LIVPTSSVINKDNKHFVWVYNDSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
TFKDGQKIDNIESIDLNSNKKSE

Table 85: Comparative Sequences relating to SAG1361

SEQ ID NO. 8513
STRAIN A909 frame: 1
FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
VGDKITAGQQLVQYDTTTAQAAYDTANRQLNKVARQINNLKTTGSLPAMESSDQSSSSSQ
GQGAQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSEYDLANVKKDQSVKIKSKVYPDK
EWEGKISYISNYPEAEANNNDSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEVVNGDKH
LIVPTSSVTNKDNKHFVWVYNDSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
TFKDGQKIDNIESIDLKSNKKSEVK

SEQ ID NO. 8514
STRAIN H36B frame: 1
FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
VGDKITAGQQLVQYDTTTAQAAYDTANRQLNKVARQINNLKTTGSLPAMESSDQSSSSSQ
GQGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVYPDK
EWEGKISYISNYPEAEANNNDSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEVVNGDKH
LIVPTSSVTNKDNKHFVWVYNDSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
AFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8515
STRAIN 18RS21 frame: 1
FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
VGDKITAGQQLVQYDTTTAQAAYDTANRQLNKVARQINNLKTTGSLPAMESSDQSSSSSQ
GQGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVYPDK
EWEGKISYISNYPEAEANNNDSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEVVNGDKH
LIVPTSSVINKDNKHFVWVYNDSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
TFKDGQKIDNIESIDLNSNKKSE

SEQ ID NO. 8516
STRAIN M732 frame: 1
FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
VGDKITAGQQLVQYDTTTAQAAYDTANRQLNKVARQINNLKTTGSFPAMESSDQSSSSSQ
GQGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVYPDK
EWEGKISYISNYPEAEANNNDSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEVVNGDKH
LIVPTSSVINKDNKHFVWVYNDSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8517
STRAIN COH1 frame: 1
FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
VGDKITAGQQLVQYDTTTAQAAYDTANRQLNKVARQINNLKTTGSFPAMESSDQSSSSSQ
GQGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVYPDK
EWEGKISYISNYPEAEANNNDSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEVVNGDKH
LIVPTSSVINKDNKHFVWVYNDSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8518
STRAIN M781 frame: 1
FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
VGDKITAGQQLVQYDTTTAQAAYDTANRQLNKVARQINNLKTTGSFPAMESSDQSSSSSQ
GQGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVYPDK
EWEGKISYISNYPEAEANNNDSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEVVNGDKH
LIVPTSSVINKDNKHFVWVYNDSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8519
STRAIN M781 frame: 1
FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
VGDKITAGQQLVQYDTTTAQAAYDTANRQLNKVARQINNLKTTGSFPAMESSDQSSSSSQ
GQGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVYPDK
EWEGKISYISNYPEAEANNNDSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEVVNGDKH
LIVPTSSVINKDNKHFVWVYNDSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8520
STRAIN CJB110 frame: 1
FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
VGDKITAGQQLVQYDTTTAQAAYDTANRQLNKVARQINNLKTTGSLPAMELSDQSSSSSQ
GQGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVYPDK
EWEGKISYISNYPEAEANNNDSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEVVNGDKH
LIVPTSSVINKDNKHFVWVYNDSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
TFKDGQKIDNIESIDLNSNKKSEV

SEQ ID NO. 8521

Table 85: Comparative Sequences relating to SAG1361

STRAIN 1169NT frame: 1

```
FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
VGDKITAGQQLVQYDTTTAQAAYDTANRQLNKVARQINNLKTTGSLPAMESSDQSSSSSQ
GQGTQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVYPDK
EWEGKISYISNYPEAEANNNDSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEVVNGDKH
LIVPTSSVINKDNKHFVWVYNDSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
TFKDGQKIDNIESIDLNSNKKSEV
```

SEQ ID NO. 8522

STRAIN JM9130013 frame: 1

```
FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGKAKANQEQYVYFDANKGNRATVTVK
VGDKITAGQQLVQYDTTTAQAAYDTANRQLNKVARQINNLKTTGSLPAMESSDQSSSSSQ
GQGAQSTSGATNRLQQNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
SGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSEYDLANVKKDQSVKIKSKVYPDK
EWEGKISYISNYPEAEANNNDSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEVVNGDKH
LIVPTSSVTNKDNKHFVWVYNDSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
TFKDGQKIDNIESIDLKSNKKSEVK
```

```
PRETTY of: /biotmp/msa375805.2{*}   April 1, 2003 02:58  ..

                                 1                                                  50
     msa375805.2{690_COH1}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~F LWVQSQPNKS AVKTNYKVFN
     msa375805.2{690_M732}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~F LWVQSQPNKS AVKTNYKVFN
     msa375805.2{690_M781}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~F LWVQSQPNKS AVKTNYKVFN
      msa375805.2{690_090}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~F LWVQSQPNKS AVKTNYKVFN
    msa375805.2{690_CJB110}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~F LWVQSQPNKS AVKTNYKVFN
    msa375805.2{690_1169NT}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~F LWVQSQPNKS AVKTNYKVFN
    msa375805.2{690_18RS21}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~F LWVQSQPNKS AVKTNYKVFN
     msa375805.2{690_2603}   mskrqnlgis kkgaiisgls valivviggF LWVQSQPNKS AVKTNYKVFN
     msa375805.2{690_A909}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~F LWVQSQPNKS AVKTNYKVFN
 msa375805.2{690_JM9130013}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~F LWVQSQPNKS AVKTNYKVFN
     msa375805.2{690_H36B}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~F LWVQSQPNKS AVKTNYKVFN
                Consensus   ********** ********** ********** ********** **********

                          51                                                 100
     msa375805.2{690_COH1}   VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV GDKITAGQQL
     msa375805.2{690_M732}   VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV GDKITAGQQL
     msa375805.2{690_M781}   VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV GDKITAGQQL
      msa375805.2{690_090}   VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV GDKITAGQQL
    msa375805.2{690_CJB110}   VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV GDKITAGQQL
    msa375805.2{690_1169NT}   VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV GDKITAGQQL
    msa375805.2{690_18RS21}   VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV GDKITAGQQL
     msa375805.2{690_2603}   VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV GDKITAGQQL
     msa375805.2{690_A909}   VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV GDKITAGQQL
 msa375805.2{690_JM9130013}   VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV GDKITAGQQL
     msa375805.2{690_H36B}   VREGSVSSST LLTGKAKANQ EQYVYFDANK GNRATVTVKV GDKITAGQQL
                Consensus   ********** ********** ********** ********** **********

                          101                                                150
     msa375805.2{690_COH1}   VQYDTTTAQA AYDTANRQLN KVARQINNLK TTGSfPAMEs SDQSSSSSQG
     msa375805.2{690_M732}   VQYDTTTAQA AYDTANRQLN KVARQINNLK TTGSfPAMEs SDQSSSSSQG
     msa375805.2{690_M781}   VQYDTTTAQA AYDTANRQLN KVARQINNLK TTGSfPAMEs SDQSSSSSQG
      msa375805.2{690_090}   VQYDTTTAQA AYDTANRQLN KVARQINNLK TTGSlPAMEl SDQSSSSSQG
    msa375805.2{690_CJB110}   VQYDTTTAQA AYDTANRQLN KVARQINNLK TTGSlPAMEl SDQSSSSSQG
    msa375805.2{690_1169NT}   VQYDTTTAQA AYDTANRQLN KVARQINNLK TTGSlPAMEs SDQSSSSSQG
    msa375805.2{690_18RS21}   VQYDTTTAQA AYDTANRQLN KVARQINNLK TTGSlPAMEs SDQSSSSSQG
     msa375805.2{690_2603}   VQYDTTTAQA AYDTANRQLN KVARQINNLK TTGSlPAMEs SDQSSSSSQG
     msa375805.2{690_A909}   VQYDTTTAQA AYDTANRQLN KVARQINNLK TTGSlPAMEs SDQSSSSSQG
 msa375805.2{690_JM9130013}   VQYDTTTAQA AYDTANRQLN KVARQINNLK TTGSlPAMEs SDQSSSSSQG
     msa375805.2{690_H36B}   VQYDTTTAQA AYDTANRQLN KVARQINNLK TTGSlPAMEs SDQSSSSSQG
                Consensus   ********** ********** ********** ****_****_ **********

                          151                                                200
     msa375805.2{690_COH1}   QGtQSTSGAT NRLQQNYQSQ ANASYNQQLQ DLNDAYADAQ AEVNKAQKAL
     msa375805.2{690_M732}   QGtQSTSGAT NRLQQNYQSQ ANASYNQQLQ DLNDAYADAQ AEVNKAQKAL
     msa375805.2{690_M781}   QGtQSTSGAT NRLQQNYQSQ ANASYNQQLQ DLNDAYADAQ AEVNKAQKAL
      msa375805.2{690_090}   QGtQSTSGAT NRLQQNYQSQ ANASYNQQLQ DLNDAYADAQ AEVNKAQKAL
    msa375805.2{690_CJB110}   QGtQSTSGAT NRLQQNYQSQ ANASYNQQLQ DLNDAYADAQ AEVNKAQKAL
    msa375805.2{690_1169NT}   QGtQSTSGAT NRLQQNYQSQ ANASYNQQLQ DLNDAYADAQ AEVNKAQKAL
    msa375805.2{690_18RS21}   QGtQSTSGAT NRLQQNYQSQ ANASYNQQLQ DLNDAYADAQ AEVNKAQKAL
     msa375805.2{690_2603}   QGtQSTSGAT NRLQQNYQSQ ANASYNQQLQ DLNDAYADAQ AEVNKAQKAL
     msa375805.2{690_A909}   QGaQSTSGAT NRLQQNYQSQ ANASYNQQLQ DLNDAYADAQ AEVNKAQKAL
 msa375805.2{690_JM9130013}   QGaQSTSGAT NRLQQNYQSQ ANASYNQQLQ DLNDAYADAQ AEVNKAQKAL
     msa375805.2{690_H36B}   QGtQSTSGAT NRLQQNYQSQ ANASYNQQLQ DLNDAYADAQ AEVNKAQKAL
                Consensus   **_******* ********** ********** ********** **********

                          201                                                250
     msa375805.2{690_COH1}   NDTVITSDVS GTVVEVNSDI DPASKTSQVL VHVATEGKLQ VQGTMSEYDL
     msa375805.2{690_M732}   NDTVITSDVS GTVVEVNSDI DPASKTSQVL VHVATEGKLQ VQGTMSEYDL
     msa375805.2{690_M781}   NDTVITSDVS GTVVEVNSDI DPASKTSQVL VHVATEGKLQ VQGTMSEYDL
      msa375805.2{690_090}   NDTVITSDVS GTVVEVNSDI DPASKTSQVL VHVATEGKLQ VQGTMSEYDL
```

Table 85: Comparative Sequences relating to SAG1361

```
    msa375805.2{690_CJB110}  NDTVITSDVS GTVVEVNSDI DPASKTSQVL VHVATEGKLQ VQGTMSEYDL
    msa375805.2{690_1169NT}  NDTVITSDVS GTVVEVNSDI DPASKTSQVL VHVATEGKLQ VQGTMSEYDL
    msa375805.2{690_18RS21}  NDTVITSDVS GTVVEVNSDI DPASKTSQVL VHVATEGKLQ VQGTMSEYDL
      msa375805.2{690_2603}  NDTVITSDVS GTVVEVNSDI DPASKTSQVL VHVATEGKLQ VQGTMSEYDL
      msa375805.2{690_A909}  NDTVITSDVS GTVVEVNSDI DPASKTSQVL VHVATEGKLQ VQGTMSEYDL
  msa375805.2{690_JM9130013}  NDTVITSDVS GTVVEVNSDI DPASKTSQVL VHVATEGKLQ VQGTMSEYDL
      msa375805.2{690_H36B}  NDTVITSDVS GTVVEVNSDI DPASKTSQVL VHVATEGKLQ VQGTMSEYDL
                 Consensus  ********** ********** ********** ********** **********

                            251                                                300
      msa375805.2{690_COH1}  ANVKKDQaVK IKSKVYPDKE WEGKISYISN YPEAEANNND SNNGSSAVNY
      msa375805.2{690_M732}  ANVKKDQaVK IKSKVYPDKE WEGKISYISN YPEAEANNND SNNGSSAVNY
      msa375805.2{690_M781}  ANVKKDQaVK IKSKVYPDKE WEGKISYISN YPEAEANNND SNNGSSAVNY
       msa375805.2{690_090}  ANVKKDQaVK IKSKVYPDKE WEGKISYISN YPEAEANNND SNNGSSAVNY
    msa375805.2{690_CJB110}  ANVKKDQaVK IKSKVYPDKE WEGKISYISN YPEAEANNND SNNGSSAVNY
    msa375805.2{690_1169NT}  ANVKKDQaVK IKSKVYPDKE WEGKISYISN YPEAEANNND SNNGSSAVNY
    msa375805.2{690_18RS21}  ANVKKDQaVK IKSKVYPDKE WEGKISYISN YPEAEANNND SNNGSSAVNY
      msa375805.2{690_2603}  ANVKKDQaVK IKSKVYPDKE WEGKISYISN YPEAEANNND SNNGSSAVNY
      msa375805.2{690_A909}  ANVKKDQsVK IKSKVYPDKE WEGKISYISN YPEAEANNND SNNGSSAVNY
  msa375805.2{690_JM9130013}  ANVKKDQsVK IKSKVYPDKE WEGKISYISN YPEAEANNND SNNGSSAVNY
      msa375805.2{690_H36B}  ANVKKDQaVK IKSKVYPDKE WEGKISYISN YPEAEANNND SNNGSSAVNY
                 Consensus  *******-** ********** ********** ********** **********

                            301                                                350
      msa375805.2{690_COH1}  KYKVDITSPL DALKQGFTVS VEVVNGDKHL IVPTSSViNK DNKHFVWVYN
      msa375805.2{690_M732}  KYKVDITSPL DALKQGFTVS VEVVNGDKHL IVPTSSViNK DNKHFVWVYN
      msa375805.2{690_M781}  KYKVDITSPL DALKQGFTVS VEVVNGDKHL IVPTSSViNK DNKHFVWVYN
       msa375805.2{690_090}  KYKVDITSPL DALKQGFTVS VEVVNGDKHL IVPTSSViNK DNKHFVWVYN
    msa375805.2{690_CJB110}  KYKVDITSPL DALKQGFTVS VEVVNGDKHL IVPTSSViNK DNKHFVWVYN
    msa375805.2{690_1169NT}  KYKVDITSPL DALKQGFTVS VEVVNGDKHL IVPTSSViNK DNKHFVWVYN
    msa375805.2{690_18RS21}  KYKVDITSPL DALKQGFTVS VEVVNGDKHL IVPTSSViNK DNKHFVWVYN
      msa375805.2{690_2603}  KYKVDITSPL DALKQGFTVS VEVVNGDKHL IVPTSSViNK DNKHFVWVYN
      msa375805.2{690_A909}  KYKVDITSPL DALKQGFTVS VEVVNGDKHL IVPTSSVtNK DNKHFVWVYN
  msa375805.2{690_JM9130013}  KYKVDITSPL DALKQGFTVS VEVVNGDKHL IVPTSSVtNK DNKHFVWVYN
      msa375805.2{690_H36B}  KYKVDITSPL DALKQGFTVS VEVVNGDKHL IVPTSSVtNK DNKHFVWVYN
                 Consensus  ********** ********** ********** *******-** **********

                            351                                                400
      msa375805.2{690_COH1}  DSNRKISKVE VKIGKADAKT QEILSGLKAG QIVVTNPSKt FKDGQKIDNI
      msa375805.2{690_M732}  DSNRKISKVE VKIGKADAKT QEILSGLKAG QIVVTNPSKt FKDGQKIDNI
      msa375805.2{690_M781}  DSNRKISKVE VKIGKADAKT QEILSGLKAG QIVVTNPSKt FKDGQKIDNI
       msa375805.2{690_090}  DSNRKISKVE VKIGKADAKT QEILSGLKAG QIVVTNPSKt FKDGQKIDNI
    msa375805.2{690_CJB110}  DSNRKISKVE VKIGKADAKT QEILSGLKAG QIVVTNPSKt FKDGQKIDNI
    msa375805.2{690_1169NT}  DSNRKISKVE VKIGKADAKT QEILSGLKAG QIVVTNPSKt FKDGQKIDNI
    msa375805.2{690_18RS21}  DSNRKISKVE VKIGKADAKT QEILSGLKAG QIVVTNPSKt FKDGQKIDNI
      msa375805.2{690_2603}  DSNRKISKVE VKIGKADAKT QEILSGLKAG QIVVTNPSKt FKDGQKIDNI
      msa375805.2{690_A909}  DSNRKISKVE VKIGKADAKT QEILSGLKAG QIVVTNPSKt FKDGQKIDNI
  msa375805.2{690_JM9130013}  DSNRKISKVE VKIGKADAKT QEILSGLKAG QIVVTNPSKt FKDGQKIDNI
      msa375805.2{690_H36B}  DSNRKISKVE VKIGKADAKT QEILSGLKAG QIVVTNPSKa FKDGQKIDNI
                 Consensus  ********** ********** ********** *********- **********

                            401          414
      msa375805.2{690_COH1}  ESIDLkSNKK SEv~
      msa375805.2{690_M732}  ESIDLkSNKK SEv~
      msa375805.2{690_M781}  ESIDLkSNKK SEv~
       msa375805.2{690_090}  ESIDLnSNKK SE~~
    msa375805.2{690_CJB110}  ESIDLnSNKK SEv~
    msa375805.2{690_1169NT}  ESIDLnSNKK SEv~
    msa375805.2{690_18RS21}  ESIDLnSNKK SE~~
      msa375805.2{690_2603}  ESIDLnSNKK SEvK
      msa375805.2{690_A909}  ESIDLkSNKK SEvK
  msa375805.2{690_JM9130013}  ESIDLkSNKK SEvK
      msa375805.2{690_H36B}  ESIDLkSNKK SEv~
                 Consensus  *****-**** **-*
```

Table 86: Comparative Sequences relating to SAG1393

SEQ ID NO. 8601
STRAIN 2603
atgaaaaaaattggaattattgtcctcacactactgaccttctttttggtatcttgcgga
caacaaactaaacaagaaagcactaaaacaactatttctaaaatgcctaaaattgaaggc
ttcacctattatggaaaaattcctgaaaatccgaaaaaagtaattaattttacatattct
tacactgggtatttattaaaactaggtgttaatgtttcaagttacagtttagacttagaa
aaagatagccccgtttttggtaaacaactgaaagaagctaaaaaattaactgctgatgat
acagaagctattgccgcacaaaaacctgatttaatcatggttttcgatcaagatccaaac
atcaatactctgaaaaaaattgcaccaactttagttattaaatatggtgcacaaaattat
ttagatatgatgccagccttggggaaagtattcggtaaagaaaaagaagctaatcagtgg
gttagccaatggaaaactaaaactctcgctgtcaaaaaagatttacaccatatcttaaag
cctaacactacttttactattatggatttttatgataaaaatatctatttatatggtaat
aattttggacgcggtggagaactaatctatgattcactaggttatgctgccccagaaaaa
gtcaaaaaagatgtctttaaaaaagggtggtttaccgtttcgcaagaagcaatcggtgat
tacgttggagattatgcccttgttaatataaacaaaacgactaaaaaagcagcttcatca
cttaaagaaagtgatgtctggaagaatttaccagctgtcaaaaaagggcacatcatagaa
agtaactacgacgtgttttatttctctgaccctctatctttagaagctcaattaaaatca
tttacaaaggctatcaaagaaaatacaaat

SEQ ID NO. 8602
STRAIN 090
GAAGGCTTCACCTATTATGGAAAAATTCCTGAAAATCCGAAAAAAGTAAT
TAATTTTACATATTCTTACACTGGGTATTTATTAAAACTAGGTGTTAATG
TTTCAAGTTACAGTTTAGACTTAGAAAAAGATAGCCCCGTTTTTGGTAAg
CAACTGAAAGAAGCTAAAAAATTAACTGCTGATGATACAGAAGCTATTGC
CGCACAAAAACCTGATTTAATCATGGTTTTCGATCAAGATCCAAACATCA
ATACTCTGAAAAAAATTGCACCAACTTTAGTTATTAAAtATGGTGCACAA
AATTATTTAGATATGATGCCAGCCTTGGGGAAAGTATTCGGTAAAGAAAA
AGAAGCTAATCAGTGGGTTAGCCAATGGAAAACTAAAACTCTCGCTGCCA
AAAAAGATTTACACCATATCTTAAAGCCTAACACTACTTTTACTATTATG
GATTTTTATGATAAAAATATCTATTTATATGGTAATAATTTTGGACGCGG
tGGAGAACTAATCTATGATTCACTAGGTTATGCTGCCCCAgAAAAAGTCA
AAAAAgATGTcTTTAAAAAAGGGTGGTTTACCGTTTCgCAAGAAGCAATC
GGtGATTACGTTGGAGATTATGCCCTTGTTAATATAAACAAAACGACTAA
AAAAGCAGCTTCatcACTTAAAGAAAGTGATGTCTGGAAGAATTTACCAG
CTGTCaAAAAAGGGCACATCATAGAAAGTAacTACGACGTGTTTTATTTC
TCTGACCCTCTATCTTTAGAAGCTCAATTAAAATCATTTACAAA

SEQ ID NO. 8603
STRAIN A909
GAAGGCTTCACCTATTATGGAAAAATTCCTG
AAAATCCGAAAAAAGTAATTAATTTTACATATTCTTACACTGGATATTTA
TTAAAACTAGGAGTTAATGTTTCAAGTTACAGTTTAGACTTAGAAAAAGA
TAgCCCCGTTTTTGGTAAaCAACTGAAAGGAGCTAAAAAATTAACTGCTG
ATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAaTCATGGTTTTT
GATCAAGATCCAAACATCAATACTCTGAAAAAAATTGCACCAACTTTAGT
TATTAAATATGGTGCACAAAATTATTTAgATaTGATGCCAGCTTTGGGGA
AAGTATTCGGTAAAGAAAAAGAAGCTAATCAGTGGGTTAGCCAaTGGAAA
ACTAAAACTCTCGCTGCCAAAAAAGATTTACACCATATCTTAAAACCTAA
CACTACTTTTACCATTATGGATTTTTATGATAAAAATATCTATTTATATG
GTAATAATTTTGGACGCGGTGGAGAACTAATCTATGATTCACTAGGTTAT
GCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAAAGGGTGGTTTAC
CGTTTCGCAAGAAGCAATCGGTgATTACGTTGGAGATTATGCCCTTGTTA
ATATAAACAAAACGACTAAAAAAGCAGCTTCATCACTTAAAGAAAGTGAT
GTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACATCATAGAAAGTAA
CTACGACGTGTTTTATTTCTCTGACCCTcTATCTTTAGAAGCTCAATTAA
AATCATTTACAAA

SEQ ID NO. 8604
STRAIN H36B
GAAGGCTTCACCTATTATGGAAAA
ATTCCTGAAAATCCGAAAAAAGTAATTAATTTTACATATTCTTACACTGG
ATATTTATTAAAACTAGGAGTTAATGTTTCAAGTTACAGTTTAGACTTAG
AAAAAGATAgCCCCGTTTTTGGTAAgCAACTGAAAGGAGCTAAAAAATTA
ACTGCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAaTCAT
GGTTTTTGATCAAgATCCAAACATCAATACTCTGAAAAAAATTGCACCAA
CTTTAGTTATTAAATATGGTGCACAAAATTATTTAgATaTgATGCCAGCT
TTGGGGAaAGTATTCGGTAAAGAAAAAGAAGCTAATCAGTGGGTTAGCCA
ATGGAAAACTAAAACTCTCGCTGCCAAAAAAGATTTACACCATATCTTAA
GGCCTaACAcTACTTTTACTATTATAGAtTTTTATGATAAAAATATCTAT
TTATATGGTAATAATTTTGGACGCGGtGGAgAACTAATCTATGATtCACT
AGGTTATGCTGCCCCAgAAAAAGTCAAAAAAgATGTCTTTAAAAAAGGGT
GGTTTACCGTTTCgCAAGAAGCAATCGGTgATTACGTTGGAGATTATGCC
CTTGTTAATATAAACAAAACGACTAAAAAAGCAGCTTCaTCACTTAAAGA
AAGTGATGTTTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACATCATAG
AAAGTAACTACGACGTGTTTTATTTCTCTGACCCTCTATCTTTAGAAGCT
CAATTAAAATCATTTACAAA

Table 86: Comparative Sequences relating to SAG1393

SEQ ID NO. 8605
STRAIN 18RS21
GAAGGCTTCACCTATTATGGA
AAAATTCCTGAAAATCCGAAAAAAGTAATTAATTTTACATATTCTTACAC
TGGGTATTTATTAAAACTAGGTGTTAATGTTTCAAGTTACAGTTTAGACT
TAGAAAAAGATAGCCCCGTTTTTGGTAAACAACTGAAAGAAGCTAAAAAA
TTAACTGCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAAT
CATGGTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGCAC
CAACTTTAGTTATTAAATATGGTGCACAAAATTATTTAgATaTGATGCCA
GCCTTGGGGAAAGTATTCGGTAAAGAAAAAgAAGCTAATCAGTGGGTTAG
CCAATGGAAAACTAAAACTCTCGCTGTCAAAAAAGATTTACACCATATCT
TAAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAATATC
TATTTATATGGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGATTC
ACTAGGTTATGCTGCCCCAgAAAAAGTCAAAAAAgATGTCTTTAAAAAAG
GGTGGTTTACCGTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTAT
GCCCTTGTTAATATAAACAAAACgACTAAAAAAGCAGCTTCATCACTTAA
AGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACATCA
TAGAAAGTAACTACGACGTGTTTTATTTCTCTGACCCTCTATCTTTAGAA
GCTCAATTAAAATCATTTACAAA

SEQ ID NO. 8606
STRAIN M732
GAAGGCTTCACCTATTATGG
AAAAATTCCTGAAAATCCGAAAAAAGTAATTAATTTTACATATTCTTACA
CTGGGTATTTATTAAAACTAGGTGTTAATGTTTCAAGTTACAGTTTAGAC
TTAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAA
ATTAACTGCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAA
TCATGGTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGCA
CCAACTTTAGTTATTAAATATGGTGCACAAAATTATTTAgATATGATGCC
AGCCTTGGGGAAAGTATTCGGTAAAGAAAAAGAAGCTAATCAGtGGGTTA
GCCAATGGAAAACTAAAACTCTCGCTGCCAAAAAAGATTTACACCATATC
TTAAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAATAT
CTATTTATATGGTAATAATTTTGGACgCGGtGGAgAACTAATCTATGATT
CACTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAAA
GGGTGGTTTACCGTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTA
TGCCCTTGTTAATATAAACAAAACGACTAAAAAAGCAGCTTCATCACTTA
AAGAAAGTGATGTCTGGAAGAAtTTACCAGCTGTCAAAAAAGGGCACATC
ATAGAAAGTAACTACGACGTGTTTTATTTCTCTGACCCTCTATCTTTAGA
AGCTCAATTAAAATCATTTACAAA

SEQ ID NO. 8607
STRAIN COH1
GAAGGCTTCACCTATTATG
GAAAAATTCCTGAAAATCCGAAAAAAGTAATTAATTTTACATATTCTTAC
ACTGGGTATTTATTAAAACTAGGTGTTAATGTTTCAAGTTACAGTTTAgA
CTTAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAA
AATTAACTGCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTA
ATCATGGTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGC
ACCAACTTTAGTTATTAAATATGGTGCACAAAATTATTTAgATATGATGC
CAGCCTTGGGGAAAGTaTTcGGTAAAGAAAAAGAAGCTAATCAGTGGGTT
AGCCAATGGAAAACTAAAACTCTCGCTGCCAAAAAAGATTTACACCATAT
CTTAAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAATA
TCTATTTATATGGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGAT
TCACTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAA
AGGGTGGTTTACCGTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATT
ATGCCCTTGTTAATATAAACAAAACGACTAAAAAAGCAGCTTCATCACTT
AAAGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACAT
CATAGAAAGTAACTACGACGTGTTTTATTTCTCTGACCCTCTATCTTTAG
AAGCTCAATTAAAATCATTTACAAA

SEQ ID NO. 8608
STRAIN M781
GAAGGCTTCACCTATTATGG
AAAAATTCCTGAAAATCCGAAAAAAGTAATTAATTTTACATATTCTTACA
CTGGGTATTTATTAAAACTAGGTGTTAATGTTTCAAGTTACAGTTTAGAC
TTAgAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAA<
ATTAACTGCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAA
TCATGGTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGCA
CCAACTTTAGTTATTAAATATGGTGCACAAAATTATTTAgATATGATGCC
AGCCTTGGGGAAAGTATTCGGtAAAGAAAAAGAAGCTAATCAGTGGGTTA
GCCAATGGAAAACTAAAACTCTCGCTGCCAAAAAAGATTTACACCATATC
TTAAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAATAT
CTATTTATATGGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGATT
CACTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAAA
GGGTGGTTTACCGTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTA
TGCCCTTGTTAATATAAACAAAACGACTAAAAAAGCAGCTTCATCACTTA

Table 86: Comparative Sequences relating to SAG1393

AAGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACATC
ATAGAAAGTAACTACGACGTGTTTTATTTCTCTGACCCTCTATCTTTAGA
AGCTCAATTAAAATCATTTACAAA

SEQ ID NO. 8609
STRAIN CJB110
GAAGGCTTCACCTATTATGGA
AAAATTCCTGAAAATCCGAAAAAAGTAATTAATTTTACATATTCTTACAC
TGGGTATTTATTAAAACTAGGTGTTAATGTTTCAAGTTACAGTTTAGACT
TAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAAA
TTAACTGCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAAT
CATGGTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGCAC
CAACTTTAGTTATTAAATATGGTGCACAAAATTATTTAgATATGATGCCA
GCCTTGGGGAAAGTATTCGGTAAAGAAAAAGAAGCTAATCAGTGGGTTAG
CCAATGGAAAACTAAAACTCTCGCTGCCAAAAAAGATTTACACCATATCT
TAAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAATATC
TATTTATATGGTAATAATTTTGGACGCGGtGGAGAACTAATCTATGATTC
ACTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAAAG
GGTGGTTTACCGTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTAT
GCCCTTGTTAATATAAACAAAACGACTAAAAAAGCAGCTTCATCACTTAA
AGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACATCA
TAGAAAGTAACTACGACGTGTTTTATTTCTCTGACCCTCTATCTTTAGAA
GCTCAATTAAAATCATTTACAAA

SEQ ID NO. 8610
STRAIN 1169NT
GAAGGCTTCACCTATTATGGAAAAATT
CCTGAAAATCCGAAAAAAGTAATTAATTTTACATATTCTTACACTGGGTA
TTTATTAAAACTAGGTGTTAATGTTTCAAGTTACAGTTTAGACTTAGAAA
AAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAAATTAACT
GCTGATGATACAGAAGCTATTGCCgcACAAaaACCTGATTTAATCATGGT
TTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGCACCAACTT
TAGTTATTAAATATGGTGCACAAAATTATTTAgATATGATGCCAGCCTTG
GGGAAAGTATTCGGTAAAGAAAAAGaaGCTAATCAGTGGGTTAGCCAATG
GAAAACTAAAACTCTCGCTGCCAAAAAAGATTTACACCATATCTTAAAGC
CTAACACTACTTTTACTATTATGGATTTTTATGATAAAAATATCTATTTA
TATGGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGATTCACTAGG
TTATGCTGCCCCAgAAAAAGTCAAAAAAGATGTCTTTAAAAAAGGGTGGT
TTACCGTTTCgCAAGAAGCAATCGGTGATTACGTTGGAGATTATGCCCTT
GTTAATATAAACAAAACGACTAAAAAAGCAGCTTCATCACTTAAAGAAAG
TGATGTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACATCATAGAAA
GTAACTACGACGTGTTTTATTTCTCTGACCCTCTATCTTTAGAAGCTCAA
TTAAAATCATTTACAAA

SEQ ID NO. 8611
STRAIN JM9130013
GAAGGCTTCACCTATTATG
GAAAAATTCCTGAAAATCCGAAAAAAGTAATTAATTTTACATATTCTTAC
ACTGGATATTTATTAAAACTAGGAGTTAATGTTTCAAGTTACAGTTTAGA
CTTAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGGAGCTAAAA
AATTAACTGCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTA
ATCATGGTTTTTGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGC
ACCAACTTTAGTTATTAAATATGGTGCACAAAATTATTTAgATATGATGC
CAGCTTTGGGGAAAGTATTCGGTAAAGAAAAAGAAGCTAATCAGTGGGTT
AGCCAATGGAAAACTAAAACTCTCGCTGCCAAAAAAGATTTACACCATAT
CTTAAAACCTAACACTACTTTTACCATTATGGATTTTTATGATAAAAATA
TCTATTTATATGGTAATAATTTTGGACGCGGtGGAGAACTAATCTATGAT
TCACTAGGTTATGCTGCCCCAgAAAAAGTCAAAAAAGATGTCTTTAAAAA
AGGGTGGTTTACCGTTTCgCAAGAAGCAATCGGTGATTACGTTGGAGATT
ATGCCCTTGTTAATATAAACAAAACGACTAAAAAAGCAGCTTCATCACTT
AAAGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACAT
CATAGAAAGTAACTACGACGTGTTTTATTTCTCTGACCCTCTATCTTTAG
AAGCTCAATTAAAATCATTTACAAA

```
PRETTY of: /biotmp/msa521731.2{*}   April 28, 2003 08:07  ..

                            1                                                50
      msa521731.2{691_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa521731.2{691_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa521731.2{691_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa521731.2{691_COH1}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa521731.2{691_M732}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa521731.2{691_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa521731.2{691_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa521731.2{691_2603}  atgaaaaaaa ttggaattat tgtcctcaca ctactgacct tctttttggt
```

Table 86: Comparative Sequences relating to SAG1393

```
     msa521731.2{691_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa521731.2{691_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa521731.2{691_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                 Consensus  ********** ********** ********** ********** **********

                            51                                                100
      msa521731.2{691_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa521731.2{691_1169NT}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa521731.2{691_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa521731.2{691_COH1}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa521731.2{691_M732}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa521731.2{691_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa521731.2{691_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa521731.2{691_2603}  atcttgcgga caacaaacta aacaagaaag cactaaaaca actatttcta
     msa521731.2{691_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa521731.2{691_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa521731.2{691_H36B}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                 Consensus  ********** ********** ********** ********** **********

                            101                                               150
      msa521731.2{691_090}  ~~~~~~~~~~ ~~~~GAAGGC TTCACCTATT ATGGAAAAAT TCCTGAAAAT
   msa521731.2{691_1169NT}  ~~~~~~~~~~ ~~~~GAAGGC TTCACCTATT ATGGAAAAAT TCCTGAAAAT
   msa521731.2{691_CJB110}  ~~~~~~~~~~ ~~~~GAAGGC TTCACCTATT ATGGAAAAAT TCCTGAAAAT
     msa521731.2{691_COH1}  ~~~~~~~~~~ ~~~~GAAGGC TTCACCTATT ATGGAAAAAT TCCTGAAAAT
     msa521731.2{691_M732}  ~~~~~~~~~~ ~~~~GAAGGC TTCACCTATT ATGGAAAAAT TCCTGAAAAT
     msa521731.2{691_M781}  ~~~~~~~~~~ ~~~~GAAGGC TTCACCTATT ATGGAAAAAT TCCTGAAAAT
   msa521731.2{691_18RS21}  ~~~~~~~~~~ ~~~~GAAGGC TTCACCTATT ATGGAAAAAT TCCTGAAAAT
     msa521731.2{691_2603}  aaatgcctaa aattGAAGGC TTCACCTATT ATGGAAAAAT TCCTGAAAAT
     msa521731.2{691_A909}  ~~~~~~~~~~ ~~~~GAAGGC TTCACCTATT ATGGAAAAAT TCCTGAAAAT
msa521731.2{691_JM9130013}  ~~~~~~~~~~ ~~~~GAAGGC TTCACCTATT ATGGAAAAAT TCCTGAAAAT
     msa521731.2{691_H36B}  ~~~~~~~~~~ ~~~~GAAGGC TTCACCTATT ATGGAAAAAT TCCTGAAAAT
                 Consensus  ********** ********** ********** ********** **********

                            151                                               200
      msa521731.2{691_090}  CCGAAAAAAG TAATTAATTT TACATATTCT TACACTGGgT ATTTATTAAA
   msa521731.2{691_1169NT}  CCGAAAAAAG TAATTAATTT TACATATTCT TACACTGGgT ATTTATTAAA
   msa521731.2{691_CJB110}  CCGAAAAAAG TAATTAATTT TACATATTCT TACACTGGgT ATTTATTAAA
     msa521731.2{691_COH1}  CCGAAAAAAG TAATTAATTT TACATATTCT TACACTGGgT ATTTATTAAA
     msa521731.2{691_M732}  CCGAAAAAAG TAATTAATTT TACATATTCT TACACTGGgT ATTTATTAAA
     msa521731.2{691_M781}  CCGAAAAAAG TAATTAATTT TACATATTCT TACACTGGgT ATTTATTAAA
   msa521731.2{691_18RS21}  CCGAAAAAAG TAATTAATTT TACATATTCT TACACTGGgT ATTTATTAAA
     msa521731.2{691_2603}  CCGAAAAAAG TAATTAATTT TACATATTCT TACACTGGgT ATTTATTAAA
     msa521731.2{691_A909}  CCGAAAAAAG TAATTAATTT TACATATTCT TACACTGGaT ATTTATTAAA
msa521731.2{691_JM9130013}  CCGAAAAAAG TAATTAATTT TACATATTCT TACACTGGaT ATTTATTAAA
     msa521731.2{691_H36B}  CCGAAAAAAG TAATTAATTT TACATATTCT TACACTGGaT ATTTATTAAA
                 Consensus  ********** ********** ********** ********_* **********

                            201                                               250
      msa521731.2{691_090}  ACTAGGtGTT AATGTTTCAA GTTACAGTTT AGACTTAGAA AAAGATAGCC
   msa521731.2{691_1169NT}  ACTAGGtGTT AATGTTTCAA GTTACAGTTT AGACTTAGAA AAAGATAGCC
   msa521731.2{691_CJB110}  ACTAGGtGTT AATGTTTCAA GTTACAGTTT AGACTTAGAA AAAGATAGCC
     msa521731.2{691_COH1}  ACTAGGtGTT AATGTTTCAA GTTACAGTTT AGACTTAGAA AAAGATAGCC
     msa521731.2{691_M732}  ACTAGGtGTT AATGTTTCAA GTTACAGTTT AGACTTAGAA AAAGATAGCC
     msa521731.2{691_M781}  ACTAGGtGTT AATGTTTCAA GTTACAGTTT AGACTTAGAA AAAGATAGCC
   msa521731.2{691_18RS21}  ACTAGGtGTT AATGTTTCAA GTTACAGTTT AGACTTAGAA AAAGATAGCC
     msa521731.2{691_2603}  ACTAGGtGTT AATGTTTCAA GTTACAGTTT AGACTTAGAA AAAGATAGCC
     msa521731.2{691_A909}  ACTAGGaGTT AATGTTTCAA GTTACAGTTT AGACTTAGAA AAAGATAGCC
msa521731.2{691_JM9130013}  ACTAGGaGTT AATGTTTCAA GTTACAGTTT AGACTTAGAA AAAGATAGCC
     msa521731.2{691_H36B}  ACTAGGaGTT AATGTTTCAA GTTACAGTTT AGACTTAGAA AAAGATAGCC
                 Consensus  ******_*** ********** ********** ********** **********

                            251                                               300
      msa521731.2{691_090}  CCGTTTTTGG TAAgCAACTG AAAGaAGCTA AAAAATTAAC TGCTGATGAT
   msa521731.2{691_1169NT}  CCGTTTTTGG TAAgCAACTG AAAGaAGCTA AAAAATTAAC TGCTGATGAT
   msa521731.2{691_CJB110}  CCGTTTTTGG TAAgCAACTG AAAGaAGCTA AAAAATTAAC TGCTGATGAT
     msa521731.2{691_COH1}  CCGTTTTTGG TAAgCAACTG AAAGaAGCTA AAAAATTAAC TGCTGATGAT
     msa521731.2{691_M732}  CCGTTTTTGG TAAgCAACTG AAAGaAGCTA AAAAATTAAC TGCTGATGAT
     msa521731.2{691_M781}  CCGTTTTTGG TAAgCAACTG AAAGaAGCTA AAAAATTAAC TGCTGATGAT
   msa521731.2{691_18RS21}  CCGTTTTTGG TAAaCAACTG AAAGaAGCTA AAAAATTAAC TGCTGATGAT
     msa521731.2{691_2603}  CCGTTTTTGG TAAaCAACTG AAAGaAGCTA AAAAATTAAC TGCTGATGAT
     msa521731.2{691_A909}  CCGTTTTTGG TAAaCAACTG AAAGgAGCTA AAAAATTAAC TGCTGATGAT
msa521731.2{691_JM9130013}  CCGTTTTTGG TAAgCAACTG AAAGgAGCTA AAAAATTAAC TGCTGATGAT
     msa521731.2{691_H36B}  CCGTTTTTGG TAAgCAACTG AAAGgAGCTA AAAAATTAAC TGCTGATGAT
                 Consensus  ********** ***_****** ****_***** ********** **********

                            301                                               350
      msa521731.2{691_090}  ACAGAAGCTA TTGCCGCACA AAAACCTGAT TTAATCATGG TTTTcGATCA
   msa521731.2{691_1169NT}  ACAGAAGCTA TTGCCGCACA AAAACCTGAT TTAATCATGG TTTTcGATCA
```

Table 86: Comparative Sequences relating to SAG1393

```
    msa521731.2{691_CJB110}  ACAGAAGCTA TTGCCGCACA AAAACCTGAT TTAATCATGG TTTTcGATCA
      msa521731.2{691_COH1}  ACAGAAGCTA TTGCCGCACA AAAACCTGAT TTAATCATGG TTTTcGATCA
      msa521731.2{691_M732}  ACAGAAGCTA TTGCCGCACA AAAACCTGAT TTAATCATGG TTTTcGATCA
      msa521731.2{691_M781}  ACAGAAGCTA TTGCCGCACA AAAACCTGAT TTAATCATGG TTTTcGATCA
    msa521731.2{691_18RS21}  ACAGAAGCTA TTGCCGCACA AAAACCTGAT TTAATCATGG TTTTcGATCA
      msa521731.2{691_2603}  ACAGAAGCTA TTGCCGCACA AAAACCTGAT TTAATCATGG TTTTcGATCA
      msa521731.2{691_A909}  ACAGAAGCTA TTGCCGCACA AAAACCTGAT TTAATCATGG TTTTtGATCA
 msa521731.2{691_JM9130013}  ACAGAAGCTA TTGCCGCACA AAAACCTGAT TTAATCATGG TTTTtGATCA
      msa521731.2{691_H36B}  ACAGAAGCTA TTGCCGCACA AAAACCTGAT TTAATCATGG TTTTtGATCA
                  Consensus  ********** ********** ********** ********** ****-*****

                             351                                                400
       msa521731.2{691_090}  AGATCCAAAC ATCAATACTC TGAAAAAAAT TGCACCAACT TTAGTTATTA
    msa521731.2{691_1169NT}  AGATCCAAAC ATCAATACTC TGAAAAAAAT TGCACCAACT TTAGTTATTA
    msa521731.2{691_CJB110}  AGATCCAAAC ATCAATACTC TGAAAAAAAT TGCACCAACT TTAGTTATTA
      msa521731.2{691_COH1}  AGATCCAAAC ATCAATACTC TGAAAAAAAT TGCACCAACT TTAGTTATTA
      msa521731.2{691_M732}  AGATCCAAAC ATCAATACTC TGAAAAAAAT TGCACCAACT TTAGTTATTA
      msa521731.2{691_M781}  AGATCCAAAC ATCAATACTC TGAAAAAAAT TGCACCAACT TTAGTTATTA
    msa521731.2{691_18RS21}  AGATCCAAAC ATCAATACTC TGAAAAAAAT TGCACCAACT TTAGTTATTA
      msa521731.2{691_2603}  AGATCCAAAC ATCAATACTC TGAAAAAAAT TGCACCAACT TTAGTTATTA
      msa521731.2{691_A909}  AGATCCAAAC ATCAATACTC TGAAAAAAAT TGCACCAACT TTAGTTATTA
 msa521731.2{691_JM9130013}  AGATCCAAAC ATCAATACTC TGAAAAAAAT TGCACCAACT TTAGTTATTA
      msa521731.2{691_H36B}  AGATCCAAAC ATCAATACTC TGAAAAAAAT TGCACCAACT TTAGTTATTA
                  Consensus  ********** ********** ********** ********** **********

                             401                                                450
       msa521731.2{691_090}  AATATGGTGC ACAAAATTAT TTAGATATGA TGCCAGCcTT GGGGAAAGTA
    msa521731.2{691_1169NT}  AATATGGTGC ACAAAATTAT TTAGATATGA TGCCAGCcTT GGGGAAAGTA
    msa521731.2{691_CJB110}  AATATGGTGC ACAAAATTAT TTAGATATGA TGCCAGCcTT GGGGAAAGTA
      msa521731.2{691_COH1}  AATATGGTGC ACAAAATTAT TTAGATATGA TGCCAGCcTT GGGGAAAGTA
      msa521731.2{691_M732}  AATATGGTGC ACAAAATTAT TTAGATATGA TGCCAGCcTT GGGGAAAGTA
      msa521731.2{691_M781}  AATATGGTGC ACAAAATTAT TTAGATATGA TGCCAGCcTT GGGGAAAGTA
    msa521731.2{691_18RS21}  AATATGGTGC ACAAAATTAT TTAGATATGA TGCCAGCcTT GGGGAAAGTA
      msa521731.2{691_2603}  AATATGGTGC ACAAAATTAT TTAGATATGA TGCCAGCcTT GGGGAAAGTA
      msa521731.2{691_A909}  AATATGGTGC ACAAAATTAT TTAGATATGA TGCCAGCtTT GGGGAAAGTA
 msa521731.2{691_JM9130013}  AATATGGTGC ACAAAATTAT TTAGATATGA TGCCAGCtTT GGGGAAAGTA
      msa521731.2{691_H36B}  AATATGGTGC ACAAAATTAT TTAGATATGA TGCCAGCtTT GGGGAAAGTA
                  Consensus  ********** ********** ********** *******-** **********

                             451                                                500
       msa521731.2{691_090}  TTCGGTAAAG AAAAAGAAGC TAATCAGTGG GTTAGCCAAT GGAAAACTAA
    msa521731.2{691_1169NT}  TTCGGTAAAG AAAAAGAAGC TAATCAGTGG GTTAGCCAAT GGAAAACTAA
    msa521731.2{691_CJB110}  TTCGGTAAAG AAAAAGAAGC TAATCAGTGG GTTAGCCAAT GGAAAACTAA
      msa521731.2{691_COH1}  TTCGGTAAAG AAAAAGAAGC TAATCAGTGG GTTAGCCAAT GGAAAACTAA
      msa521731.2{691_M732}  TTCGGTAAAG AAAAAGAAGC TAATCAGTGG GTTAGCCAAT GGAAAACTAA
      msa521731.2{691_M781}  TTCGGTAAAG AAAAAGAAGC TAATCAGTGG GTTAGCCAAT GGAAAACTAA
    msa521731.2{691_18RS21}  TTCGGTAAAG AAAAAGAAGC TAATCAGTGG GTTAGCCAAT GGAAAACTAA
      msa521731.2{691_2603}  TTCGGTAAAG AAAAAGAAGC TAATCAGTGG GTTAGCCAAT GGAAAACTAA
      msa521731.2{691_A909}  TTCGGTAAAG AAAAAGAAGC TAATCAGTGG GTTAGCCAAT GGAAAACTAA
 msa521731.2{691_JM9130013}  TTCGGTAAAG AAAAAGAAGC TAATCAGTGG GTTAGCCAAT GGAAAACTAA
      msa521731.2{691_H36B}  TTCGGTAAAG AAAAAGAAGC TAATCAGTGG GTTAGCCAAT GGAAAACTAA
                  Consensus  ********** ********** ********** ********** **********

                             501                                                550
       msa521731.2{691_090}  AACTCTCGCT GcCAAAAAAG ATTTACACCA TATCTTAAag CCTAACACTA
    msa521731.2{691_1169NT}  AACTCTCGCT GcCAAAAAAG ATTTACACCA TATCTTAAag CCTAACACTA
    msa521731.2{691_CJB110}  AACTCTCGCT GcCAAAAAAG ATTTACACCA TATCTTAAag CCTAACACTA
      msa521731.2{691_COH1}  AACTCTCGCT GcCAAAAAAG ATTTACACCA TATCTTAAag CCTAACACTA
      msa521731.2{691_M732}  AACTCTCGCT GcCAAAAAAG ATTTACACCA TATCTTAAag CCTAACACTA
      msa521731.2{691_M781}  AACTCTCGCT GcCAAAAAAG ATTTACACCA TATCTTAAag CCTAACACTA
    msa521731.2{691_18RS21}  AACTCTCGCT GtCAAAAAAG ATTTACACCA TATCTTAAag CCTAACACTA
      msa521731.2{691_2603}  AACTCTCGCT GtCAAAAAAG ATTTACACCA TATCTTAAag CCTAACACTA
      msa521731.2{691_A909}  AACTCTCGCT GcCAAAAAAG ATTTACACCA TATCTTAAaa CCTAACACTA
 msa521731.2{691_JM9130013}  AACTCTCGCT GcCAAAAAAG ATTTACACCA TATCTTAAaa CCTAACACTA
      msa521731.2{691_H36B}  AACTCTCGCT GcCAAAAAAG ATTTACACCA TATCTTAAgg CCTAACACTA
                  Consensus  ********** *-******** ********** ********-- **********

                             551                                                600
       msa521731.2{691_090}  CTTTTACtAT TATgGATTTT TATGATAAAA ATATCTATTT ATATGGTAAT
    msa521731.2{691_1169NT}  CTTTTACtAT TATgGATTTT TATGATAAAA ATATCTATTT ATATGGTAAT
    msa521731.2{691_CJB110}  CTTTTACtAT TATgGATTTT TATGATAAAA ATATCTATTT ATATGGTAAT
      msa521731.2{691_COH1}  CTTTTACtAT TATgGATTTT TATGATAAAA ATATCTATTT ATATGGTAAT
      msa521731.2{691_M732}  CTTTTACtAT TATgGATTTT TATGATAAAA ATATCTATTT ATATGGTAAT
      msa521731.2{691_M781}  CTTTTACtAT TATgGATTTT TATGATAAAA ATATCTATTT ATATGGTAAT
    msa521731.2{691_18RS21}  CTTTTACtAT TATgGATTTT TATGATAAAA ATATCTATTT ATATGGTAAT
      msa521731.2{691_2603}  CTTTTACtAT TATgGATTTT TATGATAAAA ATATCTATTT ATATGGTAAT
      msa521731.2{691_A909}  CTTTTACcAT TATgGATTTT TATGATAAAA ATATCTATTT ATATGGTAAT
 msa521731.2{691_JM9130013}  CTTTTACcAT TATgGATTTT TATGATAAAA ATATCTATTT ATATGGTAAT
```

Table 86: Comparative Sequences relating to SAG1393

```
    msa521731.2{691_H36B}   CTTTTACtAT TATaGATTTT TATGATAAAA ATATCTATTT ATATGGTAAT
                Consensus   *******-** ***-****** ********** ********** **********

                            601                                                650
     msa521731.2{691_090}   AATTTTGGAC GCGGTGGAGA ACTAATCTAT GATTCACTAG GTTATGCTGC
  msa521731.2{691_1169NT}   AATTTTGGAC GCGGTGGAGA ACTAATCTAT GATTCACTAG GTTATGCTGC
  msa521731.2{691_CJB110}   AATTTTGGAC GCGGTGGAGA ACTAATCTAT GATTCACTAG GTTATGCTGC
    msa521731.2{691_COH1}   AATTTTGGAC GCGGTGGAGA ACTAATCTAT GATTCACTAG GTTATGCTGC
    msa521731.2{691_M732}   AATTTTGGAC GCGGTGGAGA ACTAATCTAT GATTCACTAG GTTATGCTGC
    msa521731.2{691_M781}   AATTTTGGAC GCGGTGGAGA ACTAATCTAT GATTCACTAG GTTATGCTGC
  msa521731.2{691_18RS21}   AATTTTGGAC GCGGTGGAGA ACTAATCTAT GATTCACTAG GTTATGCTGC
    msa521731.2{691_2603}   AATTTTGGAC GCGGTGGAGA ACTAATCTAT GATTCACTAG GTTATGCTGC
    msa521731.2{691_A909}   AATTTTGGAC GCGGTGGAGA ACTAATCTAT GATTCACTAG GTTATGCTGC
msa521731.2{691_JM9130013}   AATTTTGGAC GCGGTGGAGA ACTAATCTAT GATTCACTAG GTTATGCTGC
    msa521731.2{691_H36B}   AATTTTGGAC GCGGTGGAGA ACTAATCTAT GATTCACTAG GTTATGCTGC
                Consensus   ********** ********** ********** ********** **********

                            651                                                700
     msa521731.2{691_090}   CCCAGAAAAA GTCAAAAAAG ATGTCTTTAA AAAAGGGTGG TTTACCGTTT
  msa521731.2{691_1169NT}   CCCAGAAAAA GTCAAAAAAG ATGTCTTTAA AAAAGGGTGG TTTACCGTTT
  msa521731.2{691_CJB110}   CCCAGAAAAA GTCAAAAAAG ATGTCTTTAA AAAAGGGTGG TTTACCGTTT
    msa521731.2{691_COH1}   CCCAGAAAAA GTCAAAAAAG ATGTCTTTAA AAAAGGGTGG TTTACCGTTT
    msa521731.2{691_M732}   CCCAGAAAAA GTCAAAAAAG ATGTCTTTAA AAAAGGGTGG TTTACCGTTT
    msa521731.2{691_M781}   CCCAGAAAAA GTCAAAAAAG ATGTCTTTAA AAAAGGGTGG TTTACCGTTT
  msa521731.2{691_18RS21}   CCCAGAAAAA GTCAAAAAAG ATGTCTTTAA AAAAGGGTGG TTTACCGTTT
    msa521731.2{691_2603}   CCCAGAAAAA GTCAAAAAAG ATGTCTTTAA AAAAGGGTGG TTTACCGTTT
    msa521731.2{691_A909}   CCCAGAAAAA GTCAAAAAAG ATGTCTTTAA AAAAGGGTGG TTTACCGTTT
msa521731.2{691_JM9130013}   CCCAGAAAAA GTCAAAAAAG ATGTCTTTAA AAAAGGGTGG TTTACCGTTT
    msa521731.2{691_H36B}   CCCAGAAAAA GTCAAAAAAG ATGTCTTTAA AAAAGGGTGG TTTACCGTTT
                Consensus   ********** ********** ********** ********** **********

                            701                                                750
     msa521731.2{691_090}   CGCAAGAAGC AATCGGTGAT TACGTTGGAG ATTATGCCCT TGTTAATATA
  msa521731.2{691_1169NT}   CGCAAGAAGC AATCGGTGAT TACGTTGGAG ATTATGCCCT TGTTAATATA
  msa521731.2{691_CJB110}   CGCAAGAAGC AATCGGTGAT TACGTTGGAG ATTATGCCCT TGTTAATATA
    msa521731.2{691_COH1}   CGCAAGAAGC AATCGGTGAT TACGTTGGAG ATTATGCCCT TGTTAATATA
    msa521731.2{691_M732}   CGCAAGAAGC AATCGGTGAT TACGTTGGAG ATTATGCCCT TGTTAATATA
    msa521731.2{691_M781}   CGCAAGAAGC AATCGGTGAT TACGTTGGAG ATTATGCCCT TGTTAATATA
  msa521731.2{691_18RS21}   CGCAAGAAGC AATCGGTGAT TACGTTGGAG ATTATGCCCT TGTTAATATA
    msa521731.2{691_2603}   CGCAAGAAGC AATCGGTGAT TACGTTGGAG ATTATGCCCT TGTTAATATA
    msa521731.2{691_A909}   CGCAAGAAGC AATCGGTGAT TACGTTGGAG ATTATGCCCT TGTTAATATA
msa521731.2{691_JM9130013}   CGCAAGAAGC AATCGGTGAT TACGTTGGAG ATTATGCCCT TGTTAATATA
    msa521731.2{691_H36B}   CGCAAGAAGC AATCGGTGAT TACGTTGGAG ATTATGCCCT TGTTAATATA
                Consensus   ********** ********** ********** ********** **********

                            751                                                800
     msa521731.2{691_090}   AACAAAACGA CTAAAAAAGC AGCTTCATCA CTTAAAGAAA GTGATGTcTG
  msa521731.2{691_1169NT}   AACAAAACGA CTAAAAAAGC AGCTTCATCA CTTAAAGAAA GTGATGTcTG
  msa521731.2{691_CJB110}   AACAAAACGA CTAAAAAAGC AGCTTCATCA CTTAAAGAAA GTGATGTcTG
    msa521731.2{691_COH1}   AACAAAACGA CTAAAAAAGC AGCTTCATCA CTTAAAGAAA GTGATGTcTG
    msa521731.2{691_M732}   AACAAAACGA CTAAAAAAGC AGCTTCATCA CTTAAAGAAA GTGATGTcTG
    msa521731.2{691_M781}   AACAAAACGA CTAAAAAAGC AGCTTCATCA CTTAAAGAAA GTGATGTcTG
  msa521731.2{691_18RS21}   AACAAAACGA CTAAAAAAGC AGCTTCATCA CTTAAAGAAA GTGATGTcTG
    msa521731.2{691_2603}   AACAAAACGA CTAAAAAAGC AGCTTCATCA CTTAAAGAAA GTGATGTcTG
    msa521731.2{691_A909}   AACAAAACGA CTAAAAAAGC AGCTTCATCA CTTAAAGAAA GTGATGTcTG
msa521731.2{691_JM9130013}   AACAAAACGA CTAAAAAAGC AGCTTCATCA CTTAAAGAAA GTGATGTcTG
    msa521731.2{691_H36B}   AACAAAACGA CTAAAAAAGC AGCTTCATCA CTTAAAGAAA GTGATGTtTG
                Consensus   ********** ********** ********** ********** *******-**

                            801                                                850
     msa521731.2{691_090}   GAAGAATTTA CCAGCTGTCA AAAAAGGGCA CATCATAGAA AGTAACTACG
  msa521731.2{691_1169NT}   GAAGAATTTA CCAGCTGTCA AAAAAGGGCA CATCATAGAA AGTAACTACG
  msa521731.2{691_CJB110}   GAAGAATTTA CCAGCTGTCA AAAAAGGGCA CATCATAGAA AGTAACTACG
    msa521731.2{691_COH1}   GAAGAATTTA CCAGCTGTCA AAAAAGGGCA CATCATAGAA AGTAACTACG
    msa521731.2{691_M732}   GAAGAATTTA CCAGCTGTCA AAAAAGGGCA CATCATAGAA AGTAACTACG
    msa521731.2{691_M781}   GAAGAATTTA CCAGCTGTCA AAAAAGGGCA CATCATAGAA AGTAACTACG
  msa521731.2{691_18RS21}   GAAGAATTTA CCAGCTGTCA AAAAAGGGCA CATCATAGAA AGTAACTACG
    msa521731.2{691_2603}   GAAGAATTTA CCAGCTGTCA AAAAAGGGCA CATCATAGAA AGTAACTACG
    msa521731.2{691_A909}   GAAGAATTTA CCAGCTGTCA AAAAAGGGCA CATCATAGAA AGTAACTACG
msa521731.2{691_JM9130013}   GAAGAATTTA CCAGCTGTCA AAAAAGGGCA CATCATAGAA AGTAACTACG
    msa521731.2{691_H36B}   GAAGAATTTA CCAGCTGTCA AAAAAGGGCA CATCATAGAA AGTAACTACG
                Consensus   ********** ********** ********** ********** **********

                            851                                                900
     msa521731.2{691_090}   ACGTGTTTTA TTTCTCTGAC CCTCTATCTT TAGAAGCTCA ATTAAAATCA
  msa521731.2{691_1169NT}   ACGTGTTTTA TTTCTCTGAC CCTCTATCTT TAGAAGCTCA ATTAAAATCA
  msa521731.2{691_CJB110}   ACGTGTTTTA TTTCTCTGAC CCTCTATCTT TAGAAGCTCA ATTAAAATCA
    msa521731.2{691_COH1}   ACGTGTTTTA TTTCTCTGAC CCTCTATCTT TAGAAGCTCA ATTAAAATCA
```

Table 86: Comparative Sequences relating to SAG1393

```
     msa521731.2{691_M732}  ACGTGTTTTA TTTCTCTGAC CCTCTATCTT TAGAAGCTCA ATTAAAATCA
     msa521731.2{691_M781}  ACGTGTTTTA TTTCTCTGAC CCTCTATCTT TAGAAGCTCA ATTAAAATCA
   msa521731.2{691_18RS21}  ACGTGTTTTA TTTCTCTGAC CCTCTATCTT TAGAAGCTCA ATTAAAATCA
     msa521731.2{691_2603}  ACGTGTTTTA TTTCTCTGAC CCTCTATCTT TAGAAGCTCA ATTAAAATCA
     msa521731.2{691_A909}  ACGTGTTTTA TTTCTCTGAC CCTCTATCTT TAGAAGCTCA ATTAAAATCA
msa521731.2{691_JM9130013}  ACGTGTTTTA TTTCTCTGAC CCTCTATCTT TAGAAGCTCA ATTAAAATCA
     msa521731.2{691_H36B}  ACGTGTTTTA TTTCTCTGAC CCTCTATCTT TAGAAGCTCA ATTAAAATCA
                 Consensus  ********** ********** ********** ********** **********

                            901                            930
      msa521731.2{691_090}  TTTACAAA~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa521731.2{691_1169NT}  TTTACAAA~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa521731.2{691_CJB110}  TTTACAAA~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa521731.2{691_COH1}  TTTACAAA~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa521731.2{691_M732}  TTTACAAA~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa521731.2{691_M781}  TTTACAAA~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa521731.2{691_18RS21}  TTTACAAA~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa521731.2{691_2603}  TTTACAAAgg ctatcaaaga aaatacaaat
     msa521731.2{691_A909}  TTTACAAA~~ ~~~~~~~~~~ ~~~~~~~~~~
msa521731.2{691_JM9130013}  TTTACAAA~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa521731.2{691_H36B}  TTTACAAA~~ ~~~~~~~~~~ ~~~~~~~~~~
                 Consensus  ********** ********** **********
```

SEQ ID NO. 8612

STRAIN 2603 frame: 1

```
MKKIGIIVLTLLTFFLVSCGQQTKQESTKTTISKMPKIEGFTYYGKIPENPKKVINFTYS
YTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLTADDTEAIAAQKPDLIMVFDQDPN
INTLKKIAPTLVIKYGAQNYLDMMPALGKVFGKEKEANQWVSQWKTKTLAVKKDLHHILK
PNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAPEKVKKDVFKKGWFTVSQEAIGD
YVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHIIESNYDVFYFSDPLSLEAQLKS
FTKAIKENTN
```

SEQ ID NO. 8613

STRAIN 090 frame: 1

```
EGFTYYGKIPENPKKVINFTYSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLTA
DDTEAIAAQKPDLIMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMPALGKVFGKEKEAN
QWVSQWKTKTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFYFSDPLSLEAQLKSFT
```

SEQ ID NO. 8614

STRAIN A909 frame: 1

```
EGFTYYGKIPENPKKVINFTYSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKGAKKLTA
DDTEAIAAQKPDLIMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMPALGKVFGKEKEAN
QWVSQWKTKTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFYFSDPLSLEAQLKSFT
```

SEQ ID NO. 8615

STRAIN H36B frame: 1

```
EGFTYYGKIPENPKKVINFTYSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKGAKKLTA
DDTEAIAAQKPDLIMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMPALGKVFGKEKEAN
QWVSQWKTKTLAAKKDLHHILRPNTTFTIIDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFYFSDPLSLEAQLKSFT
```

SEQ ID NO. 8616

STRAIN 18RS21 frame: 1

```
EGFTYYGKIPENPKKVINFTYSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLTA
DDTEAIAAQKPDLIMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMPALGKVFGKEKEAN
QWVSQWKTKTLAVKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFYFSDPLSLEAQLKSFT
```

SEQ ID NO. 8617

STRAIN M732 frame: 1

```
EGFTYYGKIPENPKKVINFTYSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLTA
DDTEAIAAQKPDLIMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMPALGKVFGKEKEAN
QWVSQWKTKTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFYFSDPLSLEAQLKSFT
```

SEQ ID NO. 8618

STRAIN COH1 frame: 1

```
EGFTYYGKIPENPKKVINFTYSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLTA
DDTEAIAAQKPDLIMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMPALGKVFGKEKEAN
```

Table 86: Comparative Sequences relating to SAG1393

QWVSQWKTKTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8619
STRAIN M781 frame: 1
EGFTYYGKIPENPKKVINFTYSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLTA
DDTEAIAAQKPDLIMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMPALGKVFGKEKEAN
QWVSQWKTKTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8620
STRAIN CJB110 frame: 1
EGFTYYGKIPENPKKVINFTYSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLTA
DDTEAIAAQKPDLIMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMPALGKVFGKEKEAN
QWVSQWKTKTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8621
STRAIN 1169NT frame: 1
EGFTYYGKIPENPKKVINFTYSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLTA
DDTEAIAAQKPDLIMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMPALGKVFGKEKEAN
QWVSQWKTKTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8622
STRAIN JM9130013 frame: 1
EGFTYYGKIPENPKKVINFTYSYTGYLLKLGVNVSSYSLDLEKDSPVFGKQLKGAKKLTA
DDTEAIAAQKPDLIMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMPALGKVFGKEKEAN
QWVSQWKTKTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFYFSDPLSLEAQLKSFT

```
 PRETTY of: /biotmp/msa522124.2{*}   April 28, 2003 08:17  ..

                             1                                                      50
     msa522124.2{691_090}    ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~EG FTYYGKIPEN
   msa522124.2{691_1169NT}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~EG FTYYGKIPEN
   msa522124.2{691_CJB110}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~EG FTYYGKIPEN
     msa522124.2{691_COH1}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~EG FTYYGKIPEN
     msa522124.2{691_M732}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~EG FTYYGKIPEN
     msa522124.2{691_M781}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~EG FTYYGKIPEN
   msa522124.2{691_18RS21}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~EG FTYYGKIPEN
     msa522124.2{691_2603}   mkkigiivlt lltfflvscg qqtkqestkt tiskmpkiEG FTYYGKIPEN
     msa522124.2{691_A909}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~EG FTYYGKIPEN
msa522124.2{691_JM9130013}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~EG FTYYGKIPEN
     msa522124.2{691_H36B}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~EG FTYYGKIPEN
                Consensus    ********** ********** ********** ********** **********

                             51                                                    100
     msa522124.2{691_090}    PKKVINFTYS YTGYLLKLGV NVSSYSLDLE KDSPVFGKQL KeAKKLTADD
   msa522124.2{691_1169NT}   PKKVINFTYS YTGYLLKLGV NVSSYSLDLE KDSPVFGKQL KeAKKLTADD
   msa522124.2{691_CJB110}   PKKVINFTYS YTGYLLKLGV NVSSYSLDLE KDSPVFGKQL KeAKKLTADD
     msa522124.2{691_COH1}   PKKVINFTYS YTGYLLKLGV NVSSYSLDLE KDSPVFGKQL KeAKKLTADD
     msa522124.2{691_M732}   PKKVINFTYS YTGYLLKLGV NVSSYSLDLE KDSPVFGKQL KeAKKLTADD
     msa522124.2{691_M781}   PKKVINFTYS YTGYLLKLGV NVSSYSLDLE KDSPVFGKQL KeAKKLTADD
   msa522124.2{691_18RS21}   PKKVINFTYS YTGYLLKLGV NVSSYSLDLE KDSPVFGKQL KeAKKLTADD
     msa522124.2{691_2603}   PKKVINFTYS YTGYLLKLGV NVSSYSLDLE KDSPVFGKQL KeAKKLTADD
     msa522124.2{691_A909}   PKKVINFTYS YTGYLLKLGV NVSSYSLDLE KDSPVFGKQL KgAKKLTADD
msa522124.2{691_JM9130013}   PKKVINFTYS YTGYLLKLGV NVSSYSLDLE KDSPVFGKQL KgAKKLTADD
     msa522124.2{691_H36B}   PKKVINFTYS YTGYLLKLGV NVSSYSLDLE KDSPVFGKQL KgAKKLTADD
                Consensus    ********** ********** ********** ********** *-********

                             101                                                   150
     msa522124.2{691_090}    TEAIAAQKPD LIMVFDQDPN INTLKKIAPT LVIKYGAQNY LDMMPALGKV
   msa522124.2{691_1169NT}   TEAIAAQKPD LIMVFDQDPN INTLKKIAPT LVIKYGAQNY LDMMPALGKV
   msa522124.2{691_CJB110}   TEAIAAQKPD LIMVFDQDPN INTLKKIAPT LVIKYGAQNY LDMMPALGKV
     msa522124.2{691_COH1}   TEAIAAQKPD LIMVFDQDPN INTLKKIAPT LVIKYGAQNY LDMMPALGKV
     msa522124.2{691_M732}   TEAIAAQKPD LIMVFDQDPN INTLKKIAPT LVIKYGAQNY LDMMPALGKV
     msa522124.2{691_M781}   TEAIAAQKPD LIMVFDQDPN INTLKKIAPT LVIKYGAQNY LDMMPALGKV
   msa522124.2{691_18RS21}   TEAIAAQKPD LIMVFDQDPN INTLKKIAPT LVIKYGAQNY LDMMPALGKV
     msa522124.2{691_2603}   TEAIAAQKPD LIMVFDQDPN INTLKKIAPT LVIKYGAQNY LDMMPALGKV
     msa522124.2{691_A909}   TEAIAAQKPD LIMVFDQDPN INTLKKIAPT LVIKYGAQNY LDMMPALGKV
msa522124.2{691_JM9130013}   TEAIAAQKPD LIMVFDQDPN INTLKKIAPT LVIKYGAQNY LDMMPALGKV
```

Table 86: Comparative Sequences relating to SAG1393

```
    msa522124.2{691_H36B}  TEAIAAQKPD LIMVFDQDPN INTLKKIAPT LVIKYGAQNY LDMMPALGKV
                Consensus  ********** ********** ********** ********** **********

                           151                                                200
     msa522124.2{691_090}  FGKEKEANQW VSQWKTKTLA aKKDLHHILk PNTTFTImDF YDKNIYLYGN
  msa522124.2{691_1169NT}  FGKEKEANQW VSQWKTKTLA aKKDLHHILk PNTTFTImDF YDKNIYLYGN
   msa522124.2{691_CJB110}  FGKEKEANQW VSQWKTKTLA aKKDLHHILk PNTTFTImDF YDKNIYLYGN
    msa522124.2{691_COH1}  FGKEKEANQW VSQWKTKTLA aKKDLHHILk PNTTFTImDF YDKNIYLYGN
    msa522124.2{691_M732}  FGKEKEANQW VSQWKTKTLA aKKDLHHILk PNTTFTImDF YDKNIYLYGN
    msa522124.2{691_M781}  FGKEKEANQW VSQWKTKTLA aKKDLHHILk PNTTFTImDF YDKNIYLYGN
  msa522124.2{691_18RS21}  FGKEKEANQW VSQWKTKTLA vKKDLHHILk PNTTFTImDF YDKNIYLYGN
    msa522124.2{691_2603}  FGKEKEANQW VSQWKTKTLA vKKDLHHILk PNTTFTImDF YDKNIYLYGN
    msa522124.2{691_A909}  FGKEKEANQW VSQWKTKTLA aKKDLHHILk PNTTFTImDF YDKNIYLYGN
msa522124.2{691_JM9130013}  FGKEKEANQW VSQWKTKTLA aKKDLHHILk PNTTFTImDF YDKNIYLYGN
    msa522124.2{691_H36B}  FGKEKEANQW VSQWKTKTLA aKKDLHHILr PNTTFTIiDF YDKNIYLYGN
                Consensus  ********** ********** -********- *******-** **********

                           201                                                250
     msa522124.2{691_090}  NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIGD YVGDYALVNI
  msa522124.2{691_1169NT}  NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIGD YVGDYALVNI
   msa522124.2{691_CJB110}  NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIGD YVGDYALVNI
    msa522124.2{691_COH1}  NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIGD YVGDYALVNI
    msa522124.2{691_M732}  NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIGD YVGDYALVNI
    msa522124.2{691_M781}  NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIGD YVGDYALVNI
  msa522124.2{691_18RS21}  NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIGD YVGDYALVNI
    msa522124.2{691_2603}  NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIGD YVGDYALVNI
    msa522124.2{691_A909}  NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIGD YVGDYALVNI
msa522124.2{691_JM9130013}  NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIGD YVGDYALVNI
    msa522124.2{691_H36B}  NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIGD YVGDYALVNI
                Consensus  ********** ********** ********** ********** **********

                           251                                                300
     msa522124.2{691_090}  NKTTKKAASS LKESDVWKNL PAVKKGHIIE SNYDVFYFSD PLSLEAQLKS
  msa522124.2{691_1169NT}  NKTTKKAASS LKESDVWKNL PAVKKGHIIE SNYDVFYFSD PLSLEAQLKS
   msa522124.2{691_CJB110}  NKTTKKAASS LKESDVWKNL PAVKKGHIIE SNYDVFYFSD PLSLEAQLKS
    msa522124.2{691_COH1}  NKTTKKAASS LKESDVWKNL PAVKKGHIIE SNYDVFYFSD PLSLEAQLKS
    msa522124.2{691_M732}  NKTTKKAASS LKESDVWKNL PAVKKGHIIE SNYDVFYFSD PLSLEAQLKS
    msa522124.2{691_M781}  NKTTKKAASS LKESDVWKNL PAVKKGHIIE SNYDVFYFSD PLSLEAQLKS
  msa522124.2{691_18RS21}  NKTTKKAASS LKESDVWKNL PAVKKGHIIE SNYDVFYFSD PLSLEAQLKS
    msa522124.2{691_2603}  NKTTKKAASS LKESDVWKNL PAVKKGHIIE SNYDVFYFSD PLSLEAQLKS
    msa522124.2{691_A909}  NKTTKKAASS LKESDVWKNL PAVKKGHIIE SNYDVFYFSD PLSLEAQLKS
msa522124.2{691_JM9130013}  NKTTKKAASS LKESDVWKNL PAVKKGHIIE SNYDVFYFSD PLSLEAQLKS
    msa522124.2{691_H36B}  NKTTKKAASS LKESDVWKNL PAVKKGHIIE SNYDVFYFSD PLSLEAQLKS
                Consensus  ********** ********** ********** ********** **********

                           301    310
     msa522124.2{691_090}  FT~~~~~~~~
  msa522124.2{691_1169NT}  FT~~~~~~~~
   msa522124.2{691_CJB110}  FT~~~~~~~~
    msa522124.2{691_COH1}  FT~~~~~~~~
    msa522124.2{691_M732}  FT~~~~~~~~
    msa522124.2{691_M781}  FT~~~~~~~~
  msa522124.2{691_18RS21}  FT~~~~~~~~
    msa522124.2{691_2603}  FTkaikentn
    msa522124.2{691_A909}  FT~~~~~~~~
msa522124.2{691_JM9130013}  FT~~~~~~~~
    msa522124.2{691_H36B}  FT~~~~~~~~
                Consensus  **********
```

Table 87: Comparative Sequences relating to SAG0645

SEQ ID NO. 8701
STRAIN 2603
ATGAAATTATCGAAGAAGTTATTGTTTTCGGCTGCTGTT
TTAACAATGGTGGCGGGGTCAACTGTTGAACCAGTAGCTCAGTTTGCGACTGGAATGAGT
ATTGTAAGAGCTGCAGAAGTGTCACAAGAACGCCCAGCGAAAACAACAGTAAATATCTAT
AAATTACAAGCTGATAGTTATAAATCGGAAATTACTTCTAATGGTGGTATCGAGAATAAA
GACGGCGAAGTAATATCTAACTATGCTAAACTTGGTGACAATGTAAAAGGTTTGCAAGGT
GTACAGTTTAAACGTTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTG
ACAACAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTCAGTCTA
CCTCAAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGATTCAAAAAGTAATGTG
AGATACTTGTATGTAGAAGATTTAAAGAATTCACCTTCAAACATTACCAAAGCTTATGCT
GTACCGTTTGTGTTGGAATTACCAGTTGCTAACTCTACAGGTACAGGTTTCCTTTCTGAA
ATTAATATTTACCCTAAAAACGTTGTAACTGATGAACCAAAAACAGATAAAGATGTTAAA
AAATTAGGTCAGGACGATGCAGGTTATACGATTGGTGAAGAATTCAAATGGTTCTTGAAA
TCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGAAATTACTGATAAATTTGCA
GATGGCTTGACTTATAAATCTGTTGGAAAAATCAAGATTGGTTCGAAAACACTGAATAGA
GATGAGCACTACACTATTGATGAACCAACAGTTGATAACCAAAATACATTAAAAATTACG
TTTAAACCAGAGAAATTTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCCTTGTTAAA
AATCAAGATGCTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTTTTGGAAATT
CCAGTTGCATCAACTATTAATGAAAAAGCAGTTTTAGGAAAAGCAATTGAAAATACTTTT
GAACTTCAATATGACCATACTCCTGATAAAGCTGACAATCCAAAACCATCTAATCCTCCA
AGAAAACCAGAAGTTCATACTGGTGGGAAACGATTTGTAAAGAAAGACTCAACAGAAACA
CAAACACTAGGTGGTGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAAATGG
ACAGATGCTCTTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGTTACT
GGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGAGATTAAAGGTTTGGCT
TATGCAGTTGATGCGAATGCAGAGGGTACAGCAGTAACTTACAAATTAAAAGAAACAAAA
GCACCAGAAGGTTATGTAATCCCTGATAAAGAAATCGAGTTTACAGTATCACAAACATCT
TATAATACAAAACCAACTGACATCACGGTTGATAGTGCTGATGCAACACCTGATACAATT
AAAAACAACAAACGTCCTTCAATCCCTAATACTGGTGGTATTGGTACGGCTATCTTTGTC
GCTATCGGTGCTGCGGTGATGGCTTTTGCTGTTAAGGGGATGAAGCGTCGTACAAAAGAT
AAC

SEQ ID NO. 8702
STRAIN 090
GCAGAAGTGTCACAAGAACGCCCAGCGAAAAC
AGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
CTTCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTAT
GCTAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAACG
TTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAA
CAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTC
AGTCTACCTCAAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGA
TTCAAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTCAC
CTTCAAACATTACCAAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCA
GTTGCTAACTCTACAGGTACAGGTTTCCTTTcTGAAATTAATATTTACCC
TAAAAACGTTGTAACTGATGAACCAAAAACAGATAAAGATGTTAAAAAAT
TAGGTCAGGACGATGCAGGTTATACGATTGGTGAAGAATTCAAATGGTTC
TTGAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGAAAT
TACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAAAAATCA
AGATTGGTTCGAAAACACTGAATAGAGATGAGCACTACACTATTGATGAA
CCAACAGTTGATAACCAAAATACATTAAAAATTACGTTTAAACCAGAGAA
ATTTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCCTTGTTAAAAATC
AAGATGCTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTTTTG
GAAATTCCAGTTGCATCAACTATTAATGAAAAAGCAGTTTTAGGAAAAGC
AATTGAAAATACTTTTGAACTTCAATATGACCATACTCCTGATAAAGCTG
ACAATCCAAAACCATCTAATCCTCCAAGAAAACCAGAAGTTCATACTGGT
GGGAAACGATTTGTAAAGAAAGACTCAACAGAAACACAAACACTAGGTGG
TGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAAATGGACAG
ATGCTCTTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCT
GTTACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGA
GATTAAAGGTTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAGCAG
TAACTTACAAATTAAAAGAAACAAAAGCACCAGAAGGTTATGTAATCCCT
GATAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAAACC
AACTGACATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTAAAA
ACAACAAACGTCCTTCA

SEQ ID NO. 8703
STRAIN A909
GCAGAAGTGTCACAAGAACGCCCAGCGAA
AACAACAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAA
TTACTTCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAAC
TATGCTAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAA
ACGTTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGA
CAACAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGT
GTCAGTCTACCTCAAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCT
GGATTCAAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATT
CACCTTCAAACATTACCAAAGCTTATGCTGTACCGTTTGTGTTGGAATTA
CCAGTTGCTAACTCTACAGGTACAGGTTTCCTTTCTGAAATTAATATTTA
CCCTAaaAACGTTGTAACTGATGAACCAAAAACAGATAAAGATGTTAAAA
AATTAGGTCAGGACGATGCAGGTTATACGATTGGTGAAGAATTCAAATGG
TTCTTGAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGA
AATTACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAAAAA
TCAAGATTGGTTCGAAAACACTGAATAGAGATGAGCACTACACTATTGAT
GAACCAACAGTTGATAACCAAAATACATTAAAAATTACGTTTAAACCAGA

Table 87: Comparative Sequences relating to SAG0645

GAAATTTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCCTTGTTAAAA
ATCAAGATGCTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTT
TTGGAAATTCCAGTTGCATCAACTATTAATGAAAAAGCAGTTTTAGGAAA
AGCAATTGAAAATACTTTTGAACTTCAATATGACCATACtCCTGATAAAG
CTGACAATCCAAAACCATCTAATCCTCCAAGAAAACCAGAAGTTCATACT
GGTGGGAAACGATTTGTAAAGAAAGACTCAACAGAAACACAAACACTAGG
TGGTGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAAATGGA
CAGATGCTCTTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAA
GCTGTTACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTT
TGAGATTAAAGGTTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAG
CAGTAACTTACAAATTAAAAGAAACAAAAGCACCAGAAGGTTATGTAATC
CCTGATAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAA
ACCAACTGACATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTA
AAAACAACAA

SEQ ID NO. 8704
STRAIN 18RS21
GCAGAAGTGTCACAAGAACGCCCAGCGAAAAC
AGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
CTTCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTAT
GCTAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAACG
TTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAA
CAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTC
AGTCTACCTCAAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGA
TTCAAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTCAC
CTTCAAACATTACCAAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCA
GTTGCTAACTCTACAGGTACAGGTTTCCTTTCTGAAATTAATATTTACCC
TAAAAACGTTGTAACTGATGAACCAAAAACAGATAAAGATGTTAAATAAT
TAGGTCAGGACGATGCAGGTTATACGATTGGTGAAGAATTCAAATGGTTC
TTGAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGAAAT
TACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAAAAATCA
AGATTGGTTCGAAAACACTGAATAGAGATGAGCACTACACTATTGATGAA
CCAACAGTTGATAACCAAAATACATTAAAAATTACGTTTAAACCAgAGAA
ATTTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCCTTGTTAAAAATC
AAGATGCTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTTTTG
GAAATTCCAGTTGCATCAACTATTAATGAAAAAGCAGTTTTAGGAAAAGC
AATTGAAAATACTTTTGAACTTCAATATGACCATACTCCTGAtAAAGCtG
ACAATCCAAAACCATCTAATCCTCCAAGAAAACCAGAAGTTCATACTGGT
GGGAAACGATTTGTAAAGAAAGACTCAACAGAAACACAAACACTAGGTGG
TGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAAATGGACAG
ATGCTCTTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCT
GTTACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGA
GATTAAAGGTTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAGCAG
TAACTTACAAATTAAAAGAAACAAAAGCACCAGAAGGTTATGTAATCCCT
GATAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAAACC
AACTGACATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTAAAA
ACAACAAACGTCCTTCA

SEQ ID NO. 8705
STRAIN M732
GCAGAAGTGTCACAAGAACGCCCAGCGAAAACAACAGT
AAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACTTCTA
ATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGCTAAA
CTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAACGTTATAA
AGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAACAGtTG
AAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTCAGTCTA
CCTCAAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGATTCAAA
AAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTCACCTTCAA
ACATTACCAAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCAGTTGCT
AACTCTACAGGTACAGGTTTCCTTTCTGaAATTAATATTTACCCTAAAAA
CGTTGTAACTGATGAACCAAAAACAGATAAAGATGTTAAAAAATTAGGTC
AGGACGATGCAGGTTATACGATTGGTGAAGAATTCAAATGGTTCTTGAAA
TCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGAAATTACTGA
TAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAAAAATCAAGATTG
GTTCGAAAACACTGAATAGAGATGAGCACTACACTATTGATGAACCAACA
GTTGATAACCAAAATACATTAAAAATTACGTTTAAACCAGAGAAATTTAA
AGAAATTGCTGAGCTACTTAAAGGAATGACCCTTGTTAAAAATCAAGATG
CTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTTTTGGAAATT
CCAGTTGCATCAACTATTAATGAAAAAGCAGTTTTAGGAAAAGCAATTGA
AAATACTTTTGAACTTCAATATGACCATACTCCTGATAAAGCTGACAATC
CAAAACCATCTAATCCTCCAAGAAAACCAGAAGTTCATACTGGTGGGAAA
CGATTTGTAAAGAAAGACTCAACAGAAACACAAACACTAGGTGGTGCTGA
GTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAAATGGACAGATGCTC
TTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGTTACT
GGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGAGATTAA
AGGTTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAGCAGTAACTT
ACAAATTAAAAGAAACAAAAGCACCAGAAGGTTATGTAATCCCTGATAAA
GAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAAACCAACTGA
CATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTAAAAACAACA
AACGTCCTTCA

SEQ ID NO. 8706
STRAIN COH1

Table 87: Comparative Sequences relating to SAG0645

GCAGAAGTGTCACAAGAACGCCCAGCGAAAAC
AGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
CTTnTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTAT
GCTAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAACG
TTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAA
CAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTC
AGTCTACCTCAAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGA
TTCAAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTCAC
CTTCAAACATTACCAAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCA
GTTGCTAACTCTACAGGTACAGGTTTCCTTTCTGAAATTAATATTTACCC
TAAAAACGTTGTAACTGATGAACCAAAAACAGATAAAGATGTTAAAAAAT
TAGGTCAGGACGATGCAGGTTATACGATTGGTGAAGAATTCAAATGGTTC
TTGAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGAAAT
TACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAAAAATCA
AGATTGGTTCGAAAACACTGAATAGAGATGAGCACTACACTATTGATGAA
CCAACAGTTGATAACCAAAATACATTAAAAATTACGTTTAAACCAGAGAA
ATTTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCCTTGTTAAAAATC
AAGATGCTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTTTTG
GAAATTCCAGTTGCATCAACTATTAATGAAAAAGCAGTTTTAGGAAAAGC
AATTGAAAATACTTTTGAACTTCAATATGACCATACTCCTGATAAAGCTG
ACAATCCAAAACCATCTAATCCTCCAAGAAAACCAGAAGTTCATACTGGT
GGGAAACGATTTGTAAAGAAAGACTCAACAGAAACACAAACACTAGGTGG
TGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAAATGGACAG
ATGCTCTTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCT
GTTACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGA
GATTAAAGGTTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAGCAG
TAACTTACAAATTAAAAGAAACAAAAGCACCAGAAGGTTATGTAATCCCT
GATAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAAACC
AACTGACATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTAAAA
ACAACAAACGTCCTTCA

SEQ ID NO. 8707
STRAIN M781
GCAGAAGTGTCACAAGAACGCCCAGCGAAAACAG
CAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACT
TCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGC
TAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAACGTT
ATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAACA
GTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTCAG
TCTACCTCAAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGATT
CAAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTCACCT
TCAAACATTACCAAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCAGT
TGCTAACTCTACAGGTACAGGTTTCCTTTCTGaAATTAATATTTACCCTA
AAAACGTTGTAACTGATGAACCAAAAACAGATAAAGATGTTAAAAAATTA
GGTCAGGACGATGCAGGTTATACGATTGGTGAAGAATTCAAATGGTTCTT
GAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGAAATTA
CTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAAAAATCAAG
ATTGGTTCGAAAACACTGAATAGAGATGAGCACTACACTATTGATGAACC
AACAGTTGATAACCAAAATACATTAAAAATTACGTTTAAACCAGAGAAAT
TTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCCTTGTTAAAAATCAA
GATGCTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTTTTGGA
AATTCCAGTTGCATCAACTATTAATGAAAAAGCAGTTTTAGGAAAAGCAA
TTGAAAATACTTTTGAACTTCAATATGACCATACTCCTGATAAAGCTGAC
AATCCAAAACCATCTAATCCTCCAAGAAAACCAGAAGTTCATACTGGTGG
GAAACGATTTGTAAAGAAAGACTCAACAGAAACACAAACACTAGGTGGTG
CTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAAATGGACAGAT
GCTCTTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGT
TACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGAGA
TTAAAGGTTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAGCAGTA
ACTTACAAATTAAAAGAAACAAAAGCACCAGAAGGTTATGTAATCCCTGA
TAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAAACCAA
CTGACATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTAAAAAC
AACAAACGT

SEQ ID NO. 8708
STRAIN CJB110
GCAGAAGTGTCACAAGAACGCCCAGCGAA
AACAGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATTGGAAA
TTACTTCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAAC
TATGCTAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAA
ACGTTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGA
CAACAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGT
GTCAGTCTACCTCAAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCT
GGATTCAAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATT
CACCTTCAAACATTACCAAAGCTTATGCTGTACCGTTTGTGTTGGAATTA
CCAGTTGCTAACTCTACAGGTACAGGTTTCCTTTCTGAAATTAATATTTA
CCCTAAAAACGTTGTAACTGATGAACCAAAAACAGATAAAGATGTTAAAA
AATTAGGTCAGGACGATGCAGGTTATACGATTGGTGAAGAATTCAAATGG
TTCTTGAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGA
AATTACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAAAAA
TCAAGATTGGTTCGAAAACACTGAATAGAGATGAGCACTACACTATTGAT
GAACCAACAGTTGATAACCAAAATACATTAAAAATTACGTTTAAACCAGA
GAAATTTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCCTTGTTAAAA

Table 87: Comparative Sequences relating to SAG0645

ATCAAGATGCTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTT
TTGGAAATTCCAGTTGCATCAACTATTAATGAAAAAGCAGTTTTAGGAAA
AGCAATTGAAAATACTTTTGAACTTCAATATGACCATACTCCTGATAAAG
CTGACAATcCAAAACCATCTAATCCTCCAAGAAAACCAGAAGTTCATACT
GGTGGGAAACGATTTGTAAAGAAAGACTCAACAGAAACACAAACACTAGG
TGGTGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAAATGGA
CAGATGCTCTTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAA
GCTGTTACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTT
TGAGATTAAAGGTTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAG
CAGTAACTTACAAATTAAAAGAAACAAAAGCACCAGAAGGTTATGTAATC
CCTGATAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATCCAAA
ACCAACTGACATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTA
AAAACAACAAACGTCCTTCA

SEQ ID NO. 8709
STRAIN JM9130013
GCAGAAGTGTCACAAGAACGCCCAGCGAAAACAGCAGTA
AATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACTTCTAA
TGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGCTAAAC
TTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAACGTTATAAA
GTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAACAGTTGA
AGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTCAGTCTAC
CTCAAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGATTCAAAA
AGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTCACCTTCAAA
CATTACCAAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCAGTTGCTA
ACTCTACAGGTACAGGTTTCCTTTCTGAAATTAATATTTACCCTAAAAAC
GTTGTAACTGATGAACCAAAAACAGATAAAGATGTTAAAAAATTAGGTCA
GGACGATGCAGGTTATACGATTGGTGAAGAATTCAAATGGTTCTTGAAAT
CTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGAAATTACTGAT
AAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAAAAATCAAGATTGG
TTCGAAAACACTGAATAGAGATGAGCACTACACTATTGATGAACCAACAG
TTGATAACCAAAATACATTAAAAATTACGTTTAAACCAGAGAAATTTAAA
GAAATTGCTGAGCTACTTAAAGGAATGACCCTTGTTAAAAATCAAGATGC
TCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTTTTGGAAATTC
CAGTTGCATCAACTATTAATGAAAAAGCAGTTTTAGGAAAAGCAATTGAA
AATACTTTTGAACTTCAATATGACCATACTCCTGATAAAGCTGACAATCC
AAAACCATCTAATcCTcCAAGAAAACCAGAAGTTCATACTGGTGGGAAAC
GATTTGTAAAGAAAGACTCAACAGAAACACAAACACTAGGTGGTGCTGAG
TTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAAATGGACAGATGCTCT
TATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGTTACTG
GGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGAGATTAAA
GGTTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAGCAGTAACTTA
CAAATTAAAAGAAACAAAAGCACCAGAAGGTTATGTAATCCCTGATAAAG
AAATCGAGTTTACAGTATCACAAACATCTTATAATACAAAACCAACTGAC
ATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTAAAAACAACAA
ACGTCCTTCA

```
PRETTY of: /biotmp/msa123961.2{*}   April 30, 2003 07:17  ..

                                  1                                                50
        msa123961.2{80_2603}   atgaaattat cgaagaagtt attgttttcg gctgctgttt taacaatggt
        msa123961.2{80_A909}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
        msa123961.2{80_M732}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
         msa123961.2{80_090}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
        msa123961.2{80_COH1}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
        msa123961.2{80_M781}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa123961.2{801_JM9130013}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa123961.2{80_18RS21}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa123961.2{80h_CJB110}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                   Consensus   ---------- ---------- ---------- ---------- ----------

                                  51                                              100
        msa123961.2{80_2603}   ggcggggtca actgttgaac cagtagctca gtttgcgact ggaatgagta
        msa123961.2{80_A909}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
        msa123961.2{80_M732}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
         msa123961.2{80_090}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
        msa123961.2{80_COH1}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
        msa123961.2{80_M781}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
  msa123961.2{801_JM9130013}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa123961.2{80_18RS21}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa123961.2{80h_CJB110}   ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                   Consensus   ---------- ---------- ---------- ---------- ----------

                                  101                                             150
        msa123961.2{80_2603}   ttgtaagagc tGCAGAAGTG TCACAAGAAC GCCCAGCGAA AACAaCAGTA
        msa123961.2{80_A909}   ~~~~~~~~~~ ~GCAGAAGTG TCACAAGAAC GCCCAGCGAA AACAaCAGTA
        msa123961.2{80_M732}   ~~~~~~~~~~ ~GCAGAAGTG TCACAAGAAC GCCCAGCGAA AACAaCAGTA
         msa123961.2{80_090}   ~~~~~~~~~~ ~GCAGAAGTG TCACAAGAAC GCCCAGCGAA AACAgCAGTA
        msa123961.2{80_COH1}   ~~~~~~~~~~ ~GCAGAAGTG TCACAAGAAC GCCCAGCGAA AACAgCAGTA
        msa123961.2{80_M781}   ~~~~~~~~~~ ~GCAGAAGTG TCACAAGAAC GCCCAGCGAA AACAgCAGTA
  msa123961.2{801_JM9130013}   ~~~~~~~~~~ ~GCAGAAGTG TCACAAGAAC GCCCAGCGAA AACAgCAGTA
      msa123961.2{80_18RS21}   ~~~~~~~~~~ ~GCAGAAGTG TCACAAGAAC GCCCAGCGAA AACAgCAGTA
```

Table 87: Comparative Sequences relating to SAG0645

```
     msa123961.2{80h_CJB110}  ---------- ~GCAGAAGTG TCACAAGAAC GCCCAGCGAA AACAgCAGTA
                   Consensus  ---------- -********* ********** ********** ****_*****

                              151                                               200
       msa123961.2{80_2603}  AATATCTATA AATTACAAGC TGATAGTTAT AAATcGGAAA TTACTTcTAA
       msa123961.2{80_A909}  AATATCTATA AATTACAAGC TGATAGTTAT AAATcGGAAA TTACTTcTAA
       msa123961.2{80_M732}  AATATCTATA AATTACAAGC TGATAGTTAT AAATcGGAAA TTACTTcTAA
        msa123961.2{80_090}  AATATCTATA AATTACAAGC TGATAGTTAT AAATcGGAAA TTACTTcTAA
       msa123961.2{80_COH1}  AATATCTATA AATTACAAGC TGATAGTTAT AAATcGGAAA TTACTTnTAA
       msa123961.2{80_M781}  AATATCTATA AATTACAAGC TGATAGTTAT AAATcGGAAA TTACTTcTAA
 msa123961.2{801_JM9130013}  AATATCTATA AATTACAAGC TGATAGTTAT AAATcGGAAA TTACTTcTAA
     msa123961.2{80_18RS21}  AATATCTATA AATTACAAGC TGATAGTTAT AAATcGGAAA TTACTTcTAA
    msa123961.2{80h_CJB110}  AATATCTATA AATTACAAGC TGATAGTTAT AAATtGGAAA TTACTTcTAA
                  Consensus  ********** ********** ********** ****_***** ******_***

                             201                                               250
       msa123961.2{80_2603}  TGGTGGTATC GAGAATAAAG ACGGCGAAGT AATATCTAAC TATGCTAAAC
       msa123961.2{80_A909}  TGGTGGTATC GAGAATAAAG ACGGCGAAGT AATATCTAAC TATGCTAAAC
       msa123961.2{80_M732}  TGGTGGTATC GAGAATAAAG ACGGCGAAGT AATATCTAAC TATGCTAAAC
        msa123961.2{80_090}  TGGTGGTATC GAGAATAAAG ACGGCGAAGT AATATCTAAC TATGCTAAAC
       msa123961.2{80_COH1}  TGGTGGTATC GAGAATAAAG ACGGCGAAGT AATATCTAAC TATGCTAAAC
       msa123961.2{80_M781}  TGGTGGTATC GAGAATAAAG ACGGCGAAGT AATATCTAAC TATGCTAAAC
 msa123961.2{801_JM9130013}  TGGTGGTATC GAGAATAAAG ACGGCGAAGT AATATCTAAC TATGCTAAAC
     msa123961.2{80_18RS21}  TGGTGGTATC GAGAATAAAG ACGGCGAAGT AATATCTAAC TATGCTAAAC
    msa123961.2{80h_CJB110}  TGGTGGTATC GAGAATAAAG ACGGCGAAGT AATATCTAAC TATGCTAAAC
                  Consensus  ********** ********** ********** ********** **********

                             251                                               300
       msa123961.2{80_2603}  TTGGTGACAA TGTAAAAGGT TTGCAAGGTG TACAGTTTAA ACGTTATAAA
       msa123961.2{80_A909}  TTGGTGACAA TGTAAAAGGT TTGCAAGGTG TACAGTTTAA ACGTTATAAA
       msa123961.2{80_M732}  TTGGTGACAA TGTAAAAGGT TTGCAAGGTG TACAGTTTAA ACGTTATAAA
        msa123961.2{80_090}  TTGGTGACAA TGTAAAAGGT TTGCAAGGTG TACAGTTTAA ACGTTATAAA
       msa123961.2{80_COH1}  TTGGTGACAA TGTAAAAGGT TTGCAAGGTG TACAGTTTAA ACGTTATAAA
       msa123961.2{80_M781}  TTGGTGACAA TGTAAAAGGT TTGCAAGGTG TACAGTTTAA ACGTTATAAA
 msa123961.2{801_JM9130013}  TTGGTGACAA TGTAAAAGGT TTGCAAGGTG TACAGTTTAA ACGTTATAAA
     msa123961.2{80_18RS21}  TTGGTGACAA TGTAAAAGGT TTGCAAGGTG TACAGTTTAA ACGTTATAAA
    msa123961.2{80h_CJB110}  TTGGTGACAA TGTAAAAGGT TTGCAAGGTG TACAGTTTAA ACGTTATAAA
                  Consensus  ********** ********** ********** ********** **********

                             301                                               350
       msa123961.2{80_2603}  GTCAAGACGG ATATTTCTGT TGATGAATTG AAAAAATTGA CAACAGTTGA
       msa123961.2{80_A909}  GTCAAGACGG ATATTTCTGT TGATGAATTG AAAAAATTGA CAACAGTTGA
       msa123961.2{80_M732}  GTCAAGACGG ATATTTCTGT TGATGAATTG AAAAAATTGA CAACAGTTGA
        msa123961.2{80_090}  GTCAAGACGG ATATTTCTGT TGATGAATTG AAAAAATTGA CAACAGTTGA
       msa123961.2{80_COH1}  GTCAAGACGG ATATTTCTGT TGATGAATTG AAAAAATTGA CAACAGTTGA
       msa123961.2{80_M781}  GTCAAGACGG ATATTTCTGT TGATGAATTG AAAAAATTGA CAACAGTTGA
 msa123961.2{801_JM9130013}  GTCAAGACGG ATATTTCTGT TGATGAATTG AAAAAATTGA CAACAGTTGA
     msa123961.2{80_18RS21}  GTCAAGACGG ATATTTCTGT TGATGAATTG AAAAAATTGA CAACAGTTGA
    msa123961.2{80h_CJB110}  GTCAAGACGG ATATTTCTGT TGATGAATTG AAAAAATTGA CAACAGTTGA
                  Consensus  ********** ********** ********** ********** **********

                             351                                               400
       msa123961.2{80_2603}  AGCAGCAGAT GCAAAAGTTG GAACGATTCT TGAAGAAGGT GTCAGTCTAC
       msa123961.2{80_A909}  AGCAGCAGAT GCAAAAGTTG GAACGATTCT TGAAGAAGGT GTCAGTCTAC
       msa123961.2{80_M732}  AGCAGCAGAT GCAAAAGTTG GAACGATTCT TGAAGAAGGT GTCAGTCTAC
        msa123961.2{80_090}  AGCAGCAGAT GCAAAAGTTG GAACGATTCT TGAAGAAGGT GTCAGTCTAC
       msa123961.2{80_COH1}  AGCAGCAGAT GCAAAAGTTG GAACGATTCT TGAAGAAGGT GTCAGTCTAC
       msa123961.2{80_M781}  AGCAGCAGAT GCAAAAGTTG GAACGATTCT TGAAGAAGGT GTCAGTCTAC
 msa123961.2{801_JM9130013}  AGCAGCAGAT GCAAAAGTTG GAACGATTCT TGAAGAAGGT GTCAGTCTAC
     msa123961.2{80_18RS21}  AGCAGCAGAT GCAAAAGTTG GAACGATTCT TGAAGAAGGT GTCAGTCTAC
    msa123961.2{80h_CJB110}  AGCAGCAGAT GCAAAAGTTG GAACGATTCT TGAAGAAGGT GTCAGTCTAC
                  Consensus  ********** ********** ********** ********** **********

                             401                                               450
       msa123961.2{80_2603}  CTCAAAAAAC TAATGCTCAA GGTTTGGTCG TCGATGCTCT GGATTCAAAA
       msa123961.2{80_A909}  CTCAAAAAAC TAATGCTCAA GGTTTGGTCG TCGATGCTCT GGATTCAAAA
       msa123961.2{80_M732}  CTCAAAAAAC TAATGCTCAA GGTTTGGTCG TCGATGCTCT GGATTCAAAA
        msa123961.2{80_090}  CTCAAAAAAC TAATGCTCAA GGTTTGGTCG TCGATGCTCT GGATTCAAAA
       msa123961.2{80_COH1}  CTCAAAAAAC TAATGCTCAA GGTTTGGTCG TCGATGCTCT GGATTCAAAA
       msa123961.2{80_M781}  CTCAAAAAAC TAATGCTCAA GGTTTGGTCG TCGATGCTCT GGATTCAAAA
 msa123961.2{801_JM9130013}  CTCAAAAAAC TAATGCTCAA GGTTTGGTCG TCGATGCTCT GGATTCAAAA
     msa123961.2{80_18RS21}  CTCAAAAAAC TAATGCTCAA GGTTTGGTCG TCGATGCTCT GGATTCAAAA
    msa123961.2{80h_CJB110}  CTCAAAAAAC TAATGCTCAA GGTTTGGTCG TCGATGCTCT GGATTCAAAA
                  Consensus  ********** ********** ********** ********** **********

                             451                                               500
       msa123961.2{80_2603}  AGTAATGTGA GATACTTGTA TGTAGAAGAT TTAAAGAATT CACCTTCAAA
       msa123961.2{80_A909}  AGTAATGTGA GATACTTGTA TGTAGAAGAT TTAAAGAATT CACCTTCAAA
       msa123961.2{80_M732}  AGTAATGTGA GATACTTGTA TGTAGAAGAT TTAAAGAATT CACCTTCAAA
        msa123961.2{80_090}  AGTAATGTGA GATACTTGTA TGTAGAAGAT TTAAAGAATT CACCTTCAAA
       msa123961.2{80_COH1}  AGTAATGTGA GATACTTGTA TGTAGAAGAT TTAAAGAATT CACCTTCAAA
       msa123961.2{80_M781}  AGTAATGTGA GATACTTGTA TGTAGAAGAT TTAAAGAATT CACCTTCAAA
 msa123961.2{801_JM9130013}  AGTAATGTGA GATACTTGTA TGTAGAAGAT TTAAAGAATT CACCTTCAAA
```

Table 87: Comparative Sequences relating to SAG0645

```
      msa123961.2{80_18RS21}  AGTAATGTGA GATACTTGTA TGTAGAAGAT TTAAAGAATT CACCTTCAAA
     msa123961.2{80h_CJB110}  AGTAATGTGA GATACTTGTA TGTAGAAGAT TTAAAGAATT CACCTTCAAA
                   Consensus  ********** ********** ********** ********** **********

                              501                                               550
        msa123961.2{80_2603}  CATTACCAAA GCTTATGCTG TACCGTTTGT GTTGGAATTA CCAGTTGCTA
        msa123961.2{80_A909}  CATTACCAAA GCTTATGCTG TACCGTTTGT GTTGGAATTA CCAGTTGCTA
        msa123961.2{80_M732}  CATTACCAAA GCTTATGCTG TACCGTTTGT GTTGGAATTA CCAGTTGCTA
         msa123961.2{80_090}  CATTACCAAA GCTTATGCTG TACCGTTTGT GTTGGAATTA CCAGTTGCTA
        msa123961.2{80_COH1}  CATTACCAAA GCTTATGCTG TACCGTTTGT GTTGGAATTA CCAGTTGCTA
        msa123961.2{80_M781}  CATTACCAAA GCTTATGCTG TACCGTTTGT GTTGGAATTA CCAGTTGCTA
 msa123961.2{80l_JM9130013}  CATTACCAAA GCTTATGCTG TACCGTTTGT GTTGGAATTA CCAGTTGCTA
      msa123961.2{80_18RS21}  CATTACCAAA GCTTATGCTG TACCGTTTGT GTTGGAATTA CCAGTTGCTA
     msa123961.2{80h_CJB110}  CATTACCAAA GCTTATGCTG TACCGTTTGT GTTGGAATTA CCAGTTGCTA
                   Consensus  ********** ********** ********** ********** **********

                              551                                               600
        msa123961.2{80_2603}  ACTCTACAGG TACAGGTTTC CTTTCTGAAA TTAATATTTA CCCTAAAAAC
        msa123961.2{80_A909}  ACTCTACAGG TACAGGTTTC CTTTCTGAAA TTAATATTTA CCCTAAAAAC
        msa123961.2{80_M732}  ACTCTACAGG TACAGGTTTC CTTTCTGAAA TTAATATTTA CCCTAAAAAC
         msa123961.2{80_090}  ACTCTACAGG TACAGGTTTC CTTTCTGAAA TTAATATTTA CCCTAAAAAC
        msa123961.2{80_COH1}  ACTCTACAGG TACAGGTTTC CTTTCTGAAA TTAATATTTA CCCTAAAAAC
        msa123961.2{80_M781}  ACTCTACAGG TACAGGTTTC CTTTCTGAAA TTAATATTTA CCCTAAAAAC
 msa123961.2{80l_JM9130013}  ACTCTACAGG TACAGGTTTC CTTTCTGAAA TTAATATTTA CCCTAAAAAC
      msa123961.2{80_18RS21}  ACTCTACAGG TACAGGTTTC CTTTCTGAAA TTAATATTTA CCCTAAAAAC
     msa123961.2{80h_CJB110}  ACTCTACAGG TACAGGTTTC CTTTCTGAAA TTAATATTTA CCCTAAAAAC
                   Consensus  ********** ********** ********** ********** **********

                              601                                               650
        msa123961.2{80_2603}  GTTGTAACTG ATGAACCAAA AACAGATAAA GATGTTAAAa AATTAGGTCA
        msa123961.2{80_A909}  GTTGTAACTG ATGAACCAAA AACAGATAAA GATGTTAAAa AATTAGGTCA
        msa123961.2{80_M732}  GTTGTAACTG ATGAACCAAA AACAGATAAA GATGTTAAAa AATTAGGTCA
         msa123961.2{80_090}  GTTGTAACTG ATGAACCAAA AACAGATAAA GATGTTAAAa AATTAGGTCA
        msa123961.2{80_COH1}  GTTGTAACTG ATGAACCAAA AACAGATAAA GATGTTAAAa AATTAGGTCA
        msa123961.2{80_M781}  GTTGTAACTG ATGAACCAAA AACAGATAAA GATGTTAAAa AATTAGGTCA
 msa123961.2{80l_JM9130013}  GTTGTAACTG ATGAACCAAA AACAGATAAA GATGTTAAAa AATTAGGTCA
      msa123961.2{80_18RS21}  GTTGTAACTG ATGAACCAAA AACAGATAAA GATGTTAAAt AATTAGGTCA
     msa123961.2{80h_CJB110}  GTTGTAACTG ATGAACCAAA AACAGATAAA GATGTTAAAa AATTAGGTCA
                   Consensus  ********** ********** ********** *********- **********

                              651                                               700
        msa123961.2{80_2603}  GGACGATGCA GGTTATACGA TTGGTGAAGA ATTCAAATGG TTCTTGAAAT
        msa123961.2{80_A909}  GGACGATGCA GGTTATACGA TTGGTGAAGA ATTCAAATGG TTCTTGAAAT
        msa123961.2{80_M732}  GGACGATGCA GGTTATACGA TTGGTGAAGA ATTCAAATGG TTCTTGAAAT
         msa123961.2{80_090}  GGACGATGCA GGTTATACGA TTGGTGAAGA ATTCAAATGG TTCTTGAAAT
        msa123961.2{80_COH1}  GGACGATGCA GGTTATACGA TTGGTGAAGA ATTCAAATGG TTCTTGAAAT
        msa123961.2{80_M781}  GGACGATGCA GGTTATACGA TTGGTGAAGA ATTCAAATGG TTCTTGAAAT
 msa123961.2{80l_JM9130013}  GGACGATGCA GGTTATACGA TTGGTGAAGA ATTCAAATGG TTCTTGAAAT
      msa123961.2{80_18RS21}  GGACGATGCA GGTTATACGA TTGGTGAAGA ATTCAAATGG TTCTTGAAAT
     msa123961.2{80h_CJB110}  GGACGATGCA GGTTATACGA TTGGTGAAGA ATTCAAATGG TTCTTGAAAT
                   Consensus  ********** ********** ********** ********** **********

                              701                                               750
        msa123961.2{80_2603}  CTACAATCCC TGCCAATTTA GGTGACTATG AAAAATTTGA AATTACTGAT
        msa123961.2{80_A909}  CTACAATCCC TGCCAATTTA GGTGACTATG AAAAATTTGA AATTACTGAT
        msa123961.2{80_M732}  CTACAATCCC TGCCAATTTA GGTGACTATG AAAAATTTGA AATTACTGAT
         msa123961.2{80_090}  CTACAATCCC TGCCAATTTA GGTGACTATG AAAAATTTGA AATTACTGAT
        msa123961.2{80_COH1}  CTACAATCCC TGCCAATTTA GGTGACTATG AAAAATTTGA AATTACTGAT
        msa123961.2{80_M781}  CTACAATCCC TGCCAATTTA GGTGACTATG AAAAATTTGA AATTACTGAT
 msa123961.2{80l_JM9130013}  CTACAATCCC TGCCAATTTA GGTGACTATG AAAAATTTGA AATTACTGAT
      msa123961.2{80_18RS21}  CTACAATCCC TGCCAATTTA GGTGACTATG AAAAATTTGA AATTACTGAT
     msa123961.2{80h_CJB110}  CTACAATCCC TGCCAATTTA GGTGACTATG AAAAATTTGA AATTACTGAT
                   Consensus  ********** ********** ********** ********** **********

                              751                                               800
        msa123961.2{80_2603}  AAATTTGCAG ATGGCTTGAC TTATAAATCT GTTGGAAAAA TCAAGATTGG
        msa123961.2{80_A909}  AAATTTGCAG ATGGCTTGAC TTATAAATCT GTTGGAAAAA TCAAGATTGG
        msa123961.2{80_M732}  AAATTTGCAG ATGGCTTGAC TTATAAATCT GTTGGAAAAA TCAAGATTGG
         msa123961.2{80_090}  AAATTTGCAG ATGGCTTGAC TTATAAATCT GTTGGAAAAA TCAAGATTGG
        msa123961.2{80_COH1}  AAATTTGCAG ATGGCTTGAC TTATAAATCT GTTGGAAAAA TCAAGATTGG
        msa123961.2{80_M781}  AAATTTGCAG ATGGCTTGAC TTATAAATCT GTTGGAAAAA TCAAGATTGG
 msa123961.2{80l_JM9130013}  AAATTTGCAG ATGGCTTGAC TTATAAATCT GTTGGAAAAA TCAAGATTGG
      msa123961.2{80_18RS21}  AAATTTGCAG ATGGCTTGAC TTATAAATCT GTTGGAAAAA TCAAGATTGG
     msa123961.2{80h_CJB110}  AAATTTGCAG ATGGCTTGAC TTATAAATCT GTTGGAAAAA TCAAGATTGG
                   Consensus  ********** ********** ********** ********** **********

                              801                                               850
        msa123961.2{80_2603}  TTCGAAAACA CTGAATAGAG ATGAGCACTA CACTATTGAT GAACCAACAG
        msa123961.2{80_A909}  TTCGAAAACA CTGAATAGAG ATGAGCACTA CACTATTGAT GAACCAACAG
        msa123961.2{80_M732}  TTCGAAAACA CTGAATAGAG ATGAGCACTA CACTATTGAT GAACCAACAG
         msa123961.2{80_090}  TTCGAAAACA CTGAATAGAG ATGAGCACTA CACTATTGAT GAACCAACAG
        msa123961.2{80_COH1}  TTCGAAAACA CTGAATAGAG ATGAGCACTA CACTATTGAT GAACCAACAG
        msa123961.2{80_M781}  TTCGAAAACA CTGAATAGAG ATGAGCACTA CACTATTGAT GAACCAACAG
```

Table 87: Comparative Sequences relating to SAG0645

```
msa123961.2{801_JM9130013}  TTCGAAAACA CTGAATAGAG ATGAGCACTA CACTATTGAT GAACCAACAG
   msa123961.2{80_18RS21}  TTCGAAAACA CTGAATAGAG ATGAGCACTA CACTATTGAT GAACCAACAG
  msa123961.2{80h_CJB110}  TTCGAAAACA CTGAATAGAG ATGAGCACTA CACTATTGAT GAACCAACAG
                Consensus  ********** ********** ********** ********** **********

                           851                                              900
     msa123961.2{80_2603}  TTGATAACCA AAATACATTA AAAATTACGT TTAAACCAGA GAAATTTAAA
     msa123961.2{80_A909}  TTGATAACCA AAATACATTA AAAATTACGT TTAAACCAGA GAAATTTAAA
     msa123961.2{80_M732}  TTGATAACCA AAATACATTA AAAATTACGT TTAAACCAGA GAAATTTAAA
      msa123961.2{80_090}  TTGATAACCA AAATACATTA AAAATTACGT TTAAACCAGA GAAATTTAAA
     msa123961.2{80_COH1}  TTGATAACCA AAATACATTA AAAATTACGT TTAAACCAGA GAAATTTAAA
     msa123961.2{80_M781}  TTGATAACCA AAATACATTA AAAATTACGT TTAAACCAGA GAAATTTAAA
msa123961.2{801_JM9130013}  TTGATAACCA AAATACATTA AAAATTACGT TTAAACCAGA GAAATTTAAA
   msa123961.2{80_18RS21}  TTGATAACCA AAATACATTA AAAATTACGT TTAAACCAGA GAAATTTAAA
  msa123961.2{80h_CJB110}  TTGATAACCA AAATACATTA AAAATTACGT TTAAACCAGA GAAATTTAAA
                Consensus  ********** ********** ********** ********** **********

                           901                                              950
     msa123961.2{80_2603}  GAAATTGCTG AGCTACTTAA AGGAATGACC CTTGTTAAAA ATCAAGATGC
     msa123961.2{80_A909}  GAAATTGCTG AGCTACTTAA AGGAATGACC CTTGTTAAAA ATCAAGATGC
     msa123961.2{80_M732}  GAAATTGCTG AGCTACTTAA AGGAATGACC CTTGTTAAAA ATCAAGATGC
      msa123961.2{80_090}  GAAATTGCTG AGCTACTTAA AGGAATGACC CTTGTTAAAA ATCAAGATGC
     msa123961.2{80_COH1}  GAAATTGCTG AGCTACTTAA AGGAATGACC CTTGTTAAAA ATCAAGATGC
     msa123961.2{80_M781}  GAAATTGCTG AGCTACTTAA AGGAATGACC CTTGTTAAAA ATCAAGATGC
msa123961.2{801_JM9130013}  GAAATTGCTG AGCTACTTAA AGGAATGACC CTTGTTAAAA ATCAAGATGC
   msa123961.2{80_18RS21}  GAAATTGCTG AGCTACTTAA AGGAATGACC CTTGTTAAAA ATCAAGATGC
  msa123961.2{80h_CJB110}  GAAATTGCTG AGCTACTTAA AGGAATGACC CTTGTTAAAA ATCAAGATGC
                Consensus  ********** ********** ********** ********** **********

                           951                                             1000
     msa123961.2{80_2603}  TCTTGATAAA GCTACTGCAA ATACAGATGA TGCGGCATTT TTGGAAATTC
     msa123961.2{80_A909}  TCTTGATAAA GCTACTGCAA ATACAGATGA TGCGGCATTT TTGGAAATTC
     msa123961.2{80_M732}  TCTTGATAAA GCTACTGCAA ATACAGATGA TGCGGCATTT TTGGAAATTC
      msa123961.2{80_090}  TCTTGATAAA GCTACTGCAA ATACAGATGA TGCGGCATTT TTGGAAATTC
     msa123961.2{80_COH1}  TCTTGATAAA GCTACTGCAA ATACAGATGA TGCGGCATTT TTGGAAATTC
     msa123961.2{80_M781}  TCTTGATAAA GCTACTGCAA ATACAGATGA TGCGGCATTT TTGGAAATTC
msa123961.2{801_JM9130013}  TCTTGATAAA GCTACTGCAA ATACAGATGA TGCGGCATTT TTGGAAATTC
   msa123961.2{80_18RS21}  TCTTGATAAA GCTACTGCAA ATACAGATGA TGCGGCATTT TTGGAAATTC
  msa123961.2{80h_CJB110}  TCTTGATAAA GCTACTGCAA ATACAGATGA TGCGGCATTT TTGGAAATTC
                Consensus  ********** ********** ********** ********** **********

                           1001                                            1050
     msa123961.2{80_2603}  CAGTTGCATC AACTATTAAT GAAAAAGCAG TTTTAGGAAA AGCAATTGAA
     msa123961.2{80_A909}  CAGTTGCATC AACTATTAAT GAAAAAGCAG TTTTAGGAAA AGCAATTGAA
     msa123961.2{80_M732}  CAGTTGCATC AACTATTAAT GAAAAAGCAG TTTTAGGAAA AGCAATTGAA
      msa123961.2{80_090}  CAGTTGCATC AACTATTAAT GAAAAAGCAG TTTTAGGAAA AGCAATTGAA
     msa123961.2{80_COH1}  CAGTTGCATC AACTATTAAT GAAAAAGCAG TTTTAGGAAA AGCAATTGAA
     msa123961.2{80_M781}  CAGTTGCATC AACTATTAAT GAAAAAGCAG TTTTAGGAAA AGCAATTGAA
msa123961.2{801_JM9130013}  CAGTTGCATC AACTATTAAT GAAAAAGCAG TTTTAGGAAA AGCAATTGAA
   msa123961.2{80_18RS21}  CAGTTGCATC AACTATTAAT GAAAAAGCAG TTTTAGGAAA AGCAATTGAA
  msa123961.2{80h_CJB110}  CAGTTGCATC AACTATTAAT GAAAAAGCAG TTTTAGGAAA AGCAATTGAA
                Consensus  ********** ********** ********** ********** **********

                           1051                                            1100
     msa123961.2{80_2603}  AATACTTTTG AACTTCAATA TGACCATACT CCTGATAAAG CTGACAATCC
     msa123961.2{80_A909}  AATACTTTTG AACTTCAATA TGACCATACT CCTGATAAAG CTGACAATCC
     msa123961.2{80_M732}  AATACTTTTG AACTTCAATA TGACCATACT CCTGATAAAG CTGACAATCC
      msa123961.2{80_090}  AATACTTTTG AACTTCAATA TGACCATACT CCTGATAAAG CTGACAATCC
     msa123961.2{80_COH1}  AATACTTTTG AACTTCAATA TGACCATACT CCTGATAAAG CTGACAATCC
     msa123961.2{80_M781}  AATACTTTTG AACTTCAATA TGACCATACT CCTGATAAAG CTGACAATCC
msa123961.2{801_JM9130013}  AATACTTTTG AACTTCAATA TGACCATACT CCTGATAAAG CTGACAATCC
   msa123961.2{80_18RS21}  AATACTTTTG AACTTCAATA TGACCATACT CCTGATAAAG CTGACAATCC
  msa123961.2{80h_CJB110}  AATACTTTTG AACTTCAATA TGACCATACT CCTGATAAAG CTGACAATCC
                Consensus  ********** ********** ********** ********** **********

                           1101                                            1150
     msa123961.2{80_2603}  AAAACCATCT AATCCTCCAA GAAAACCAGA AGTTCATACT GGTGGGAAAC
     msa123961.2{80_A909}  AAAACCATCT AATCCTCCAA GAAAACCAGA AGTTCATACT GGTGGGAAAC
     msa123961.2{80_M732}  AAAACCATCT AATCCTCCAA GAAAACCAGA AGTTCATACT GGTGGGAAAC
      msa123961.2{80_090}  AAAACCATCT AATCCTCCAA GAAAACCAGA AGTTCATACT GGTGGGAAAC
     msa123961.2{80_COH1}  AAAACCATCT AATCCTCCAA GAAAACCAGA AGTTCATACT GGTGGGAAAC
     msa123961.2{80_M781}  AAAACCATCT AATCCTCCAA GAAAACCAGA AGTTCATACT GGTGGGAAAC
msa123961.2{801_JM9130013}  AAAACCATCT AATCCTCCAA GAAAACCAGA AGTTCATACT GGTGGGAAAC
   msa123961.2{80_18RS21}  AAAACCATCT AATCCTCCAA GAAAACCAGA AGTTCATACT GGTGGGAAAC
  msa123961.2{80h_CJB110}  AAAACCATCT AATCCTCCAA GAAAACCAGA AGTTCATACT GGTGGGAAAC
                Consensus  ********** ********** ********** ********** **********

                           1151                                            1200
     msa123961.2{80_2603}  GATTTGTAAA GAAAGACTCA ACAGAAACAC AAACACTAGG TGGTGCTGAG
     msa123961.2{80_A909}  GATTTGTAAA GAAAGACTCA ACAGAAACAC AAACACTAGG TGGTGCTGAG
     msa123961.2{80_M732}  GATTTGTAAA GAAAGACTCA ACAGAAACAC AAACACTAGG TGGTGCTGAG
      msa123961.2{80_090}  GATTTGTAAA GAAAGACTCA ACAGAAACAC AAACACTAGG TGGTGCTGAG
     msa123961.2{80_COH1}  GATTTGTAAA GAAAGACTCA ACAGAAACAC AAACACTAGG TGGTGCTGAG
```

Table 87: Comparative Sequences relating to SAG0645

```
       msa123961.2{80_M781}   GATTTGTAAA GAAAGACTCA ACAGAAACAC AAACACTAGG TGGTGCTGAG
 msa123961.2{801_JM9130013}   GATTTGTAAA GAAAGACTCA ACAGAAACAC AAACACTAGG TGGTGCTGAG
      msa123961.2{80_18RS21}  GATTTGTAAA GAAAGACTCA ACAGAAACAC AAACACTAGG TGGTGCTGAG
    msa123961.2{80h_CJB110}   GATTTGTAAA GAAAGACTCA ACAGAAACAC AAACACTAGG TGGTGCTGAG
                  Consensus   ********** ********** ********** ********** **********

                              1201                                              1250
       msa123961.2{80_2603}   TTTGATTTGT TGGCTTCTGA TGGGACAGCA GTAAAATGGA CAGATGCTCT
       msa123961.2{80_A909}   TTTGATTTGT TGGCTTCTGA TGGGACAGCA GTAAAATGGA CAGATGCTCT
       msa123961.2{80_M732}   TTTGATTTGT TGGCTTCTGA TGGGACAGCA GTAAAATGGA CAGATGCTCT
        msa123961.2{80_090}   TTTGATTTGT TGGCTTCTGA TGGGACAGCA GTAAAATGGA CAGATGCTCT
       msa123961.2{80_COH1}   TTTGATTTGT TGGCTTCTGA TGGGACAGCA GTAAAATGGA CAGATGCTCT
       msa123961.2{80_M781}   TTTGATTTGT TGGCTTCTGA TGGGACAGCA GTAAAATGGA CAGATGCTCT
 msa123961.2{801_JM9130013}   TTTGATTTGT TGGCTTCTGA TGGGACAGCA GTAAAATGGA CAGATGCTCT
     msa123961.2{80_18RS21}   TTTGATTTGT TGGCTTCTGA TGGGACAGCA GTAAAATGGA CAGATGCTCT
    msa123961.2{80h_CJB110}   TTTGATTTGT TGGCTTCTGA TGGGACAGCA GTAAAATGGA CAGATGCTCT
                  Consensus   ********** ********** ********** ********** **********

                              1251                                              1300
       msa123961.2{80_2603}   TATTAAAGCG AATACTAATA AAAACTATAT TGCTGGAGAA GCTGTTACTG
       msa123961.2{80_A909}   TATTAAAGCG AATACTAATA AAAACTATAT TGCTGGAGAA GCTGTTACTG
       msa123961.2{80_M732}   TATTAAAGCG AATACTAATA AAAACTATAT TGCTGGAGAA GCTGTTACTG
        msa123961.2{80_090}   TATTAAAGCG AATACTAATA AAAACTATAT TGCTGGAGAA GCTGTTACTG
       msa123961.2{80_COH1}   TATTAAAGCG AATACTAATA AAAACTATAT TGCTGGAGAA GCTGTTACTG
       msa123961.2{80_M781}   TATTAAAGCG AATACTAATA AAAACTATAT TGCTGGAGAA GCTGTTACTG
 msa123961.2{801_JM9130013}   TATTAAAGCG AATACTAATA AAAACTATAT TGCTGGAGAA GCTGTTACTG
     msa123961.2{80_18RS21}   TATTAAAGCG AATACTAATA AAAACTATAT TGCTGGAGAA GCTGTTACTG
    msa123961.2{80h_CJB110}   TATTAAAGCG AATACTAATA AAAACTATAT TGCTGGAGAA GCTGTTACTG
                  Consensus   ********** ********** ********** ********** **********

                              1301                                              1350
       msa123961.2{80_2603}   GGCAACCAAT CAAATTGAAA TCACATACAG ACGGTACGTT TGAGATTAAA
       msa123961.2{80_A909}   GGCAACCAAT CAAATTGAAA TCACATACAG ACGGTACGTT TGAGATTAAA
       msa123961.2{80_M732}   GGCAACCAAT CAAATTGAAA TCACATACAG ACGGTACGTT TGAGATTAAA
        msa123961.2{80_090}   GGCAACCAAT CAAATTGAAA TCACATACAG ACGGTACGTT TGAGATTAAA
       msa123961.2{80_COH1}   GGCAACCAAT CAAATTGAAA TCACATACAG ACGGTACGTT TGAGATTAAA
       msa123961.2{80_M781}   GGCAACCAAT CAAATTGAAA TCACATACAG ACGGTACGTT TGAGATTAAA
 msa123961.2{801_JM9130013}   GGCAACCAAT CAAATTGAAA TCACATACAG ACGGTACGTT TGAGATTAAA
     msa123961.2{80_18RS21}   GGCAACCAAT CAAATTGAAA TCACATACAG ACGGTACGTT TGAGATTAAA
    msa123961.2{80h_CJB110}   GGCAACCAAT CAAATTGAAA TCACATACAG ACGGTACGTT TGAGATTAAA
                  Consensus   ********** ********** ********** ********** **********

                              1351                                              1400
       msa123961.2{80_2603}   GGTTTGGCTT ATGCAGTTGA TGCGAATGCA GAGGGTACAG CAGTAACTTA
       msa123961.2{80_A909}   GGTTTGGCTT ATGCAGTTGA TGCGAATGCA GAGGGTACAG CAGTAACTTA
       msa123961.2{80_M732}   GGTTTGGCTT ATGCAGTTGA TGCGAATGCA GAGGGTACAG CAGTAACTTA
        msa123961.2{80_090}   GGTTTGGCTT ATGCAGTTGA TGCGAATGCA GAGGGTACAG CAGTAACTTA
       msa123961.2{80_COH1}   GGTTTGGCTT ATGCAGTTGA TGCGAATGCA GAGGGTACAG CAGTAACTTA
       msa123961.2{80_M781}   GGTTTGGCTT ATGCAGTTGA TGCGAATGCA GAGGGTACAG CAGTAACTTA
 msa123961.2{801_JM9130013}   GGTTTGGCTT ATGCAGTTGA TGCGAATGCA GAGGGTACAG CAGTAACTTA
     msa123961.2{80_18RS21}   GGTTTGGCTT ATGCAGTTGA TGCGAATGCA GAGGGTACAG CAGTAACTTA
    msa123961.2{80h_CJB110}   GGTTTGGCTT ATGCAGTTGA TGCGAATGCA GAGGGTACAG CAGTAACTTA
                  Consensus   ********** ********** ********** ********** **********

                              1401                                              1450
       msa123961.2{80_2603}   CAAATTAAAA GAAACAAAAG CACCAGAAGG TTATGTAATC CCTGATAAAG
       msa123961.2{80_A909}   CAAATTAAAA GAAACAAAAG CACCAGAAGG TTATGTAATC CCTGATAAAG
       msa123961.2{80_M732}   CAAATTAAAA GAAACAAAAG CACCAGAAGG TTATGTAATC CCTGATAAAG
        msa123961.2{80_090}   CAAATTAAAA GAAACAAAAG CACCAGAAGG TTATGTAATC CCTGATAAAG
       msa123961.2{80_COH1}   CAAATTAAAA GAAACAAAAG CACCAGAAGG TTATGTAATC CCTGATAAAG
       msa123961.2{80_M781}   CAAATTAAAA GAAACAAAAG CACCAGAAGG TTATGTAATC CCTGATAAAG
 msa123961.2{801_JM9130013}   CAAATTAAAA GAAACAAAAG CACCAGAAGG TTATGTAATC CCTGATAAAG
     msa123961.2{80_18RS21}   CAAATTAAAA GAAACAAAAG CACCAGAAGG TTATGTAATC CCTGATAAAG
    msa123961.2{80h_CJB110}   CAAATTAAAA GAAACAAAAG CACCAGAAGG TTATGTAATC CCTGATAAAG
                  Consensus   ********** ********** ********** ********** **********

                              1451                                              1500
       msa123961.2{80_2603}   AAATCGAGTT TACAGTATCA CAAACATCTT ATAATaCAAA ACCAACTGAC
       msa123961.2{80_A909}   AAATCGAGTT TACAGTATCA CAAACATCTT ATAATaCAAA ACCAACTGAC
       msa123961.2{80_M732}   AAATCGAGTT TACAGTATCA CAAACATCTT ATAATaCAAA ACCAACTGAC
        msa123961.2{80_090}   AAATCGAGTT TACAGTATCA CAAACATCTT ATAATaCAAA ACCAACTGAC
       msa123961.2{80_COH1}   AAATCGAGTT TACAGTATCA CAAACATCTT ATAATaCAAA ACCAACTGAC
       msa123961.2{80_M781}   AAATCGAGTT TACAGTATCA CAAACATCTT ATAATaCAAA ACCAACTGAC
 msa123961.2{801_JM9130013}   AAATCGAGTT TACAGTATCA CAAACATCTT ATAATaCAAA ACCAACTGAC
     msa123961.2{80_18RS21}   AAATCGAGTT TACAGTATCA CAAACATCTT ATAATaCAAA ACCAACTGAC
    msa123961.2{80h_CJB110}   AAATCGAGTT TACAGTATCA CAAACATCTT ATAATcCAAA ACCAACTGAC
                  Consensus   ********** ********** ********** *****-**** **********

                              1501                                              1550
       msa123961.2{80_2603}   ATCACGGTTG ATAGTGCTGA TGCAACACCT GATACAATTA AAAACAACAA
       msa123961.2{80_A909}   ATCACGGTTG ATAGTGCTGA TGCAACACCT GATACAATTA AAAACAACAA
       msa123961.2{80_M732}   ATCACGGTTG ATAGTGCTGA TGCAACACCT GATACAATTA AAAACAACAA
        msa123961.2{80_090}   ATCACGGTTG ATAGTGCTGA TGCAACACCT GATACAATTA AAAACAACAA
```

Table 87: Comparative Sequences relating to SAG0645

```
          msa123961.2{80_COH1}  ATCACGGTTG ATAGTGCTGA TGCAACACCT GATACAATTA AAAACAACAA
          msa123961.2{80_M781}  ATCACGGTTG ATAGTGCTGA TGCAACACCT GATACAATTA AAAACAACAA
    msa123961.2{801_JM9130013}  ATCACGGTTG ATAGTGCTGA TGCAACACCT GATACAATTA AAAACAACAA
        msa123961.2{80_18RS21}  ATCACGGTTG ATAGTGCTGA TGCAACACCT GATACAATTA AAAACAACAA
       msa123961.2{80h_CJB110}  ATCACGGTTG ATAGTGCTGA TGCAACACCT GATACAATTA AAAACAACAA
                     Consensus  ********** ********** ********** ********** **********

                                1551                                              1600
          msa123961.2{80_2603}  acgtccttca atccctaata ctggtggtat tggtacggct atctttgtcg
          msa123961.2{80_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
          msa123961.2{80_M732}  acgtccttca ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
           msa123961.2{80_090}  acgtccttca ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
          msa123961.2{80_COH1}  acgtccttca ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
          msa123961.2{80_M781}  acgt~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa123961.2{801_JM9130013}  acgtccttca ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
        msa123961.2{80_18RS21}  acgtccttca ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
       msa123961.2{80h_CJB110}  acgtccttca ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                     Consensus  ---------- ---------- ---------- ---------- ----------

                                1601                                              1650
          msa123961.2{80_2603}  ctatcggtgc tgcggtgatg gcttttgctg ttaaggggat gaagcgtcgt
          msa123961.2{80_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
          msa123961.2{80_M732}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
           msa123961.2{80_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
          msa123961.2{80_COH1}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
          msa123961.2{80_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa123961.2{801_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
        msa123961.2{80_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
       msa123961.2{80h_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                     Consensus  ---------- ---------- ---------- ---------- ----------

                                1651     1662
          msa123961.2{80_2603}  acaaaagata ac
          msa123961.2{80_A909}  ~~~~~~~~~~ ~~
          msa123961.2{80_M732}  ~~~~~~~~~~ ~~
           msa123961.2{80_090}  ~~~~~~~~~~ ~~
          msa123961.2{80_COH1}  ~~~~~~~~~~ ~~
          msa123961.2{80_M781}  ~~~~~~~~~~ ~~
    msa123961.2{801_JM9130013}  ~~~~~~~~~~ ~~
        msa123961.2{80_18RS21}  ~~~~~~~~~~ ~~
       msa123961.2{80h_CJB110}  ~~~~~~~~~~ ~~
                     Consensus  ---------- --
```

SEQ ID NO. 8710

STRAIN 2603 frame: 1

```
MKLSKKLLFSAAVLTMVAGSTVEPVAQFATGMSIVRAAEVSQERPAKTTVNIYKLQADSY
KSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFKRYKVKTDISVDELKKLTTVEAAD
AKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLYVEDLKNSPSNITKAYAVPFVLEL
PVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQDDAGYTIGEEFKWFLKSTIPANL
GDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHYTIDEPTVDNQNTLKITFKPEKFK
EIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVASTINEKAVLGKAIENTFELQYDHT
PDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLGGAEFDLLASDGTAVKWTDALIKA
NTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVDANAEGTAVTYKLKETKAPEGYVI
PDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNKRPSIPNTGGIGTAIFVAIGAAVM
AFAVKGMKRRTKDN
```

SEQ ID NO. 8711

STRAIN 090 frame: 1

```
AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIGEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
RPS
```

SEQ ID NO. 8712

STRAIN 18RS21 frame: 1

```
AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVK.LGQ
DDAGYTIGEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
RPS
```

SEQ ID NO. 8713

STRAIN M732 frame: 1

```
AEVSQERPAKTTVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
```

Table 87: Comparative Sequences relating to SAG0645

RYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIGEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8714
STRAIN M781 frame: 1
AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIGEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
R

SEQ ID NO. 8715
STRAIN COH1 frame: 1
AEVSQERPAKTAVNIYKLQADSYKSEITXNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIGEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8716
STRAIN CJB110 frame: 1
AEVSQERPAKTAVNIYKLQADSYKLEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIGEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNPKPTDITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8717
STRAIN JM9130013 frame: 1
AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIGEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8718
STRAIN A909 frame: 1
AEVSQERPAKTTVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
VEDLKNSPSNITKAYAVPFVLELPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIGEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNN

```
PRETTY of: /biotmp/msa124060.2{*}   April 30, 2003 07:19  ..

                                   1                                                50
       msa124060.2{80_2603}  mklskkllfs aavltmvags tvepvaqfat gmsivraAEV SQERPAKTtV
       msa124060.2{80_M732}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~AEV SQERPAKTtV
       msa124060.2{80_A909}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~AEV SQERPAKTtV
        msa124060.2{80_090}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~AEV SQERPAKTaV
       msa124060.2{80_M781}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~AEV SQERPAKTaV
       msa124060.2{80_COH1}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~AEV SQERPAKTaV
msa124060.2{801_JM9130013}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~AEV SQERPAKTaV
     msa124060.2{80_18RS21}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~AEV SQERPAKTaV
    msa124060.2{80h_CJB110}  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~AEV SQERPAKTaV
                  Consensus  ---------- ---------- ---------- -------*** ********-*
```

Table 87: Comparative Sequences relating to SAG0645

```
                                 51                                                   100
     msa124060.2{80_2603}        NIYKLQADSY KsEITsNGGI ENKDGEVISN YAKLGDNVKG LQGVQFKRYK
     msa124060.2{80_M732}        NIYKLQADSY KsEITsNGGI ENKDGEVISN YAKLGDNVKG LQGVQFKRYK
     msa124060.2{80_A909}        NIYKLQADSY KsEITsNGGI ENKDGEVISN YAKLGDNVKG LQGVQFKRYK
      msa124060.2{80_090}        NIYKLQADSY KsEITsNGGI ENKDGEVISN YAKLGDNVKG LQGVQFKRYK
     msa124060.2{80_M781}        NIYKLQADSY KsEITsNGGI ENKDGEVISN YAKLGDNVKG LQGVQFKRYK
     msa124060.2{80_COH1}        NIYKLQADSY KsEITxNGGI ENKDGEVISN YAKLGDNVKG LQGVQFKRYK
msa124060.2{801_JM9130013}       NIYKLQADSY KsEITsNGGI ENKDGEVISN YAKLGDNVKG LQGVQFKRYK
   msa124060.2{80_18RS21}        NIYKLQADSY KsEITsNGGI ENKDGEVISN YAKLGDNVKG LQGVQFKRYK
  msa124060.2{80h_CJB110}        NIYKLQADSY KlEITsNGGI ENKDGEVISN YAKLGDNVKG LQGVQFKRYK
                Consensus        ********** *_***_**** ********** ********** **********

                                 101                                                  150
     msa124060.2{80_2603}        VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK
     msa124060.2{80_M732}        VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK
     msa124060.2{80_A909}        VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK
      msa124060.2{80_090}        VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK
     msa124060.2{80_M781}        VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK
     msa124060.2{80_COH1}        VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK
msa124060.2{801_JM9130013}       VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK
   msa124060.2{80_18RS21}        VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK
  msa124060.2{80h_CJB110}        VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK
                Consensus        ********** ********** ********** ********** **********

                                 151                                                  200
     msa124060.2{80_2603}        SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN
     msa124060.2{80_M732}        SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN
     msa124060.2{80_A909}        SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN
      msa124060.2{80_090}        SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN
     msa124060.2{80_M781}        SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN
     msa124060.2{80_COH1}        SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN
msa124060.2{801_JM9130013}       SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN
   msa124060.2{80_18RS21}        SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN
  msa124060.2{80h_CJB110}        SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN
                Consensus        ********** ********** ********** ********** **********

                                 201                                                  250
     msa124060.2{80_2603}        VVTDEPKTDK DVKkLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD
     msa124060.2{80_M732}        VVTDEPKTDK DVKkLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD
     msa124060.2{80_A909}        VVTDEPKTDK DVKkLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD
      msa124060.2{80_090}        VVTDEPKTDK DVKkLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD
     msa124060.2{80_M781}        VVTDEPKTDK DVKkLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD
     msa124060.2{80_COH1}        VVTDEPKTDK DVKkLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD
msa124060.2{801_JM9130013}       VVTDEPKTDK DVKkLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD
   msa124060.2{80_18RS21}        VVTDEPKTDK DVK.LGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD
  msa124060.2{80h_CJB110}        VVTDEPKTDK DVKkLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD
                Consensus        ********** ***_****** ********** ********** **********

                                 251                                                  300
     msa124060.2{80_2603}        KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK
     msa124060.2{80_M732}        KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK
     msa124060.2{80_A909}        KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK
      msa124060.2{80_090}        KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK
     msa124060.2{80_M781}        KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK
     msa124060.2{80_COH1}        KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK
msa124060.2{801_JM9130013}       KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK
   msa124060.2{80_18RS21}        KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK
  msa124060.2{80h_CJB110}        KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK
                Consensus        ********** ********** ********** ********** **********

                                 301                                                  350
     msa124060.2{80_2603}        EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE
     msa124060.2{80_M732}        EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE
     msa124060.2{80_A909}        EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE
      msa124060.2{80_090}        EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE
     msa124060.2{80_M781}        EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE
     msa124060.2{80_COH1}        EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE
msa124060.2{801_JM9130013}       EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE
   msa124060.2{80_18RS21}        EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE
  msa124060.2{80h_CJB110}        EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE
                Consensus        ********** ********** ********** ********** **********

                                 351                                                  400
     msa124060.2{80_2603}        NTFELQYDHT PDKADNPKPS NPPRKPEVHT GGKRFVKKDS TETQTLGGAE
     msa124060.2{80_M732}        NTFELQYDHT PDKADNPKPS NPPRKPEVHT GGKRFVKKDS TETQTLGGAE
     msa124060.2{80_A909}        NTFELQYDHT PDKADNPKPS NPPRKPEVHT GGKRFVKKDS TETQTLGGAE
      msa124060.2{80_090}        NTFELQYDHT PDKADNPKPS NPPRKPEVHT GGKRFVKKDS TETQTLGGAE
     msa124060.2{80_M781}        NTFELQYDHT PDKADNPKPS NPPRKPEVHT GGKRFVKKDS TETQTLGGAE
     msa124060.2{80_COH1}        NTFELQYDHT PDKADNPKPS NPPRKPEVHT GGKRFVKKDS TETQTLGGAE
msa124060.2{801_JM9130013}       NTFELQYDHT PDKADNPKPS NPPRKPEVHT GGKRFVKKDS TETQTLGGAE
   msa124060.2{80_18RS21}        NTFELQYDHT PDKADNPKPS NPPRKPEVHT GGKRFVKKDS TETQTLGGAE
  msa124060.2{80h_CJB110}        NTFELQYDHT PDKADNPKPS NPPRKPEVHT GGKRFVKKDS TETQTLGGAE
                Consensus        ********** ********** ********** ********** **********
```

Table 87: Comparative Sequences relating to SAG0645

```
                          401                                                450
     msa124060.2{80_2603}  FDLLASDGTA VKWTDALIKA NTNKNYIAGE AVTGQPIKLK SHTDGTFEIK
     msa124060.2{80_M732}  FDLLASDGTA VKWTDALIKA NTNKNYIAGE AVTGQPIKLK SHTDGTFEIK
     msa124060.2{80_A909}  FDLLASDGTA VKWTDALIKA NTNKNYIAGE AVTGQPIKLK SHTDGTFEIK
      msa124060.2{80_090}  FDLLASDGTA VKWTDALIKA NTNKNYIAGE AVTGQPIKLK SHTDGTFEIK
     msa124060.2{80_M781}  FDLLASDGTA VKWTDALIKA NTNKNYIAGE AVTGQPIKLK SHTDGTFEIK
     msa124060.2{80_COH1}  FDLLASDGTA VKWTDALIKA NTNKNYIAGE AVTGQPIKLK SHTDGTFEIK
msa124060.2{801_JM9130013}  FDLLASDGTA VKWTDALIKA NTNKNYIAGE AVTGQPIKLK SHTDGTFEIK
    msa124060.2{80_18RS21}  FDLLASDGTA VKWTDALIKA NTNKNYIAGE AVTGQPIKLK SHTDGTFEIK
   msa124060.2{80h_CJB110}  FDLLASDGTA VKWTDALIKA NTNKNYIAGE AVTGQPIKLK SHTDGTFEIK
                Consensus  ********** ********** ********** ********** **********

                          451                                                500
     msa124060.2{80_2603}  GLAYAVDANA EGTAVTYKLK ETKAPEGYVI PDKEIEFTVS QTSYNtKPTD
     msa124060.2{80_M732}  GLAYAVDANA EGTAVTYKLK ETKAPEGYVI PDKEIEFTVS QTSYNtKPTD
     msa124060.2{80_A909}  GLAYAVDANA EGTAVTYKLK ETKAPEGYVI PDKEIEFTVS QTSYNtKPTD
      msa124060.2{80_090}  GLAYAVDANA EGTAVTYKLK ETKAPEGYVI PDKEIEFTVS QTSYNtKPTD
     msa124060.2{80_M781}  GLAYAVDANA EGTAVTYKLK ETKAPEGYVI PDKEIEFTVS QTSYNtKPTD
     msa124060.2{80_COH1}  GLAYAVDANA EGTAVTYKLK ETKAPEGYVI PDKEIEFTVS QTSYNtKPTD
msa124060.2{801_JM9130013}  GLAYAVDANA EGTAVTYKLK ETKAPEGYVI PDKEIEFTVS QTSYNtKPTD
    msa124060.2{80_18RS21}  GLAYAVDANA EGTAVTYKLK ETKAPEGYVI PDKEIEFTVS QTSYNtKPTD
   msa124060.2{80h_CJB110}  GLAYAVDANA EGTAVTYKLK ETKAPEGYVI PDKEIEFTVS QTSYNpKPTD
                Consensus  ********** ********** ********** ********** *****-****

                          501                                                550
     msa124060.2{80_2603}  ITVDSADATP DTIKNNkrps ipntggigta ifvaigaavm afavkgmkrr
     msa124060.2{80_M732}  ITVDSADATP DTIKNNkrps ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa124060.2{80_A909}  ITVDSADATP DTIKNN~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
      msa124060.2{80_090}  ITVDSADATP DTIKNNkrps ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa124060.2{80_M781}  ITVDSADATP DTIKNNkr~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
     msa124060.2{80_COH1}  ITVDSADATP DTIKNNkrps ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
msa124060.2{801_JM9130013}  ITVDSADATP DTIKNNkrps ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
    msa124060.2{80_18RS21}  ITVDSADATP DTIKNNkrps ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
   msa124060.2{80h_CJB110}  ITVDSADATP DTIKNNkrps ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
                Consensus  ********** ******---- ---------- ---------- ----------

                          551
     msa124060.2{80_2603}  tkdn
     msa124060.2{80_M732}  ~~~~
     msa124060.2{80_A909}  ~~~~
      msa124060.2{80_090}  ~~~~
     msa124060.2{80_M781}  ~~~~
     msa124060.2{80_COH1}  ~~~~
msa124060.2{801_JM9130013}  ~~~~
    msa124060.2{80_18RS21}  ~~~~
   msa124060.2{80h_CJB110}  ~~~~
                Consensus  ----
```

Table 88: Comparative Sequences relating to SAG0477

SEQ ID NO. 8801
STRAIN 2603
ATGCCTAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAGTTGTCTTAACGGAATGGCAA
AAGCGTAACCTTGAATTTTTAAAAAAACGCAAAGAAGATGAAGAAGAACAAAAACGTATT
AACGAAAAATTACGCTTAGATAAAAGAAGTAAATTAAATATTTCTTCTCCTGAAGAACCT
CAAAATACTACTAAAATTAAGAAGCTTCATTTTCCAAAGATTTCAAGACCTAAGATTGAA
AAGAAACAGAAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAACTAATCGCATTAGAACT
GCACCTATATTTGTAGTAGCATTCCTAGTCATTTTAGTTTCCGTTTTCCTACTAACTCCT
TTTAGTAAGCAAAAAACAATAACAGTTAGTGGAAATCAGCATACACCTGATGATATTTTG
ATAGAGAAAACGAATATTCAAAAAAACGATTATTTCTTTTCTTTAATTTTTAAACATAAA
GCTATTGAACAACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
CAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAATAAGATTATTGCATATGCACAT
ACAAAGCAAGGATATCAACCTGTCTTGGAAACTGGAAAAAAGGCTGATCCTGTAAATAGT
TCAGAGCTACCAAAGCACTTCTTAACAATTAACCTTGATAAGGAAGATAGTATTAAGCTA
TTAATTAAAGATTTAAAGGCTTTAGACCCTGATTTAATAAGTGAGATTCAGGTGATAAGT
TTAGCTGATTCTAAAACGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGT
ATTAGAATACCATTATCTAAATTTAAAGAAAGACTTCCTTTTTACAAACAAATTAAGAAG
AACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTTTACACAACAACAAATACC
ATTGAATCAACCCCTGTTAAAGCAGAAGATACAAAAAATAAATCAACTGATAAAACACAA
ACACAAAATGGTCAGGTTGCGGAAAATAGTCAAGGACAAACAAATAACTCAAATACTAAT
CAACAAGGACAACAGATAGCAACAGAGCAGGCACCTAACCCTCAAAATGTTAAT

SEQ ID NO. 8802
STRAIN H36B
CCTAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAGTT
GTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTTAAAAAAACGCAA
AGAAGATGAAGAAGAACAAAAACGTATTAACGAAAAATTACGCTTAGATA
AAAGAAGTAAATTAAATATTTCTTCTCCTGAAGAACCTCAAAATACTACT
AAAATTAAGAAGCTTCATTTTCCAAAGATTTCAAGACCTAAGATTGAAAA
GAAACAGAAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAACTAATCGCA
TTAGAACTGCACCTATATTTGTAGTAGCATTCCTAGTCATTTTAGTTTCC
GTTTTCCTACTAACTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGG
AAATCAGCATACACCTGATGATATTTTGATAGAGAAAACGAATATTCAAA
AAAACGATTATTTCTTTTCTTTAATTTTTAAACATAAAGCTATTGAACAA
CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAATAAGATTATTGCAT
ATGCACATACAAAGCAAGGATATCAACCTGTCTTGGAAACTGGAAAAAAG
GCTGATCCTGTAAATAGTTCAGAGCTACCAAAGCACTTCTTAACAATTAA
CCTTGATAAGGAAGATAGTATTAAGCTATTAATTAAAGATTTAAAGGCTT
TAGACCCTGATTTAATAAGTGAGATTCAGGTGATAAGTTTAGCTGATTCT
AAAACGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGTAT
TAGAATACCATTATCTAAATTTAAAGAAAGACTTCCTTTTTACAAACAAA
TTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTT
TACACAACAACAAATACCATTGAATCAACCCCTGTTAAAGCAGAAGATAC
AAAAAATAAATCAACTGATAAAACACAAACACAAAATGGTCAGGTTGCGG
AAAATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAAGGACAA
CAGATAGCAACAGAGCAGGCACCTAACCCTCAAAATGTTAAT

SEQ ID NO. 8803
STRAIN 18RS21
CCTAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAGTT
GTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTTAAAAAAACGCAA
AGAAGATGAAGAAGAACAAAAACGTATTAACGAAAAATTACGCTTAGATA
AAAGAAGTAAATTAAATATTTCTTCTCCTGAAGAACCTCAAAATACTACT
AAAATTAAGAAGCTTCATTTTCCAAAGATTTCAAGACCTAAGATTGAAAA
GAAACAGAAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAACTAATCGCA
TTAGAACTGCACCTATATTTGTAGTAGCATTCCTAGTCATTTTAGTTTCC
GTTTTCCTACTAACTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGG
AAATCAGCATACACCTGATGATATTTTGATAGAGAAAACGAATATTCAAA
AAAACGATTATTTCTTTTCTTTAATTTTTAAACATAAAGCTATTGAACAA
CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAATAAGATTATTGCAT
ATGCACATACAAAGCAAGGATATCAACCTGTCTTGGAAACTGGAAAAAAG
GCTGATCCTGTAAATAGTTCAGAGCTACCAAAGCACTTCTTAACAATTAA
CCTTGATAAGGAAGATAGTATTAAGCTATTAATTAAAGATTTAAAGGCTT
TAGACCCTGATTTAATAAGTGAGATTCAGGTGATAAGTTTAGCTGATTCT
AAAACGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGTAT
TAGAATACCATTATCTAAATTTAAAGAAAGACTTCCTTTTTACAAACAAA
TTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTT
TACACAACAACAAATACCATTGAATCAACCCCTGTTAAAGCAGAAGATAC
AAAAAATAAATCAACTGATAAAACACAAACACAAAATGGTCAGGTTGCGG
AAAATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAAGGACAA
CAGATAGCAACAGAGCAGGCACCTAACCCTCAAAATGTTAAT

SEQ ID NO. 8804
STRAIN M732
CCTAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAG
TTGTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTTAAAAAAACGC
AAAGAAGATGAAGAAGAACAAAAACGTATTAACGAAAAATTACGCTTAGA
TAAAAGAAGTAAATTAAATATTTCTTCTCCTGAAGAACCTCAAAATACTA
CTAAAATTAAGAAGCTTCATTTTCCAAAGATTTCAAAACCTAAGATTGAA
AAGAAACAGAAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAACTAATCG
CATTAGAACTGCACCTATATTTGTAGTAGCATTCCTAGTCATTTTAGTTT

Table 88: Comparative Sequences relating to SAG0477

CCGTTTTCCTACTAACTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGT
GGAAATCAGCATACACCTGATGATATTTTGATAGAAAAAACGAATATTCA
AAAAAACGATTATTTCTTTTCTTTAATTTTTAAACATAAAGCTATTGAAC
AACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
CAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAATAAGATTATTGC
ATATGCACATACAAAGCAAGGATATCAGCCTGTCTTGGAAACTGGAAAAA
AGGCTGATCCTGTAAATAGTTCAGAGCTACCAAAGCACTTCTTAACAATT
AACCTTGATAAGGAAGATAGTATTAAGCTATTAATTAAAGATTTAAAGGC
TTTAGACCCTGATTTAATAAGTGAGATTCAGGTGATAAGTTTAGCTGATT
CTAAAACGACACCTGACCTCCTGCTGTTAGATATGCATGATGGAAATAGT
ATTAGAATACCATTATCTAAATTTAAAGAAAGACTTCCTTTTTACAAACA
AATTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAG
TTTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGAT
ACAAAAAATAAATCAACTGATAAAACACAAACACAAAATGGTCAGGTTGC
GGAAAATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAAGGAC
AACAGATAGCAACAGAGCAGGCACCCAACCCTCAAAATGTTAAT

SEQ ID NO. 8805
STRAIN COH1
CCTAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAGTT
GTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTTAAAAAAACGCAA
AGAAGATGAAGAAGAACAAAAACGTATTAACGAAAAATTACGCTTAGATA
AAAGAAGTAAATTAAATATTTCTTCTCCTGAAGAACCTCAAAATACTACT
AAAATTAAGAAGCTTCATTTTCCAAAGATTTCAAAACCTAAGATTGAAAA
GAAACAGAAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAACTAATCGCA
TTAGAACTGCACCTATATTTGTAGTAGCATTCCTAGTCATTTTAGTTTCC
GTTTTCCTACTAACTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGG
AAATCAGCATACACCTGATGATATTTTGATAGAAAAAACGAATATTCAAA
AAAACGATTATTTCTTTTCTTTAATTTTTAAACATAAAGCTATTGAACAA
CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAATAAGATTATTGCAT
ATGCACATACAAAGCAAGGATATCAGCCTGTCTTGGAAACTGGAAAAAAG
GCTGATCCTGTAAATAGTTCAGAGCTACCAAAGCACTTCTTAACAATTAA
CCTTGATAAGGAAGATAGTATTAAGCTATTAATTAAAGATTTAAAGGCTT
TAGACCCTGATTTAATAAGTGAGATTCAGGTGATAAGTTTAGCTGATTCT
AAAACGACACCTGACCTCCTGCTGTTAGATATGCATGATGGAAATAGTAT
TAGAATACCATTATCTAAATTTAAAGAAAGACTTCCTTTTTACAAACAAA
TTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTT
TACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGATAC
AAAAAATAAATCAACTGATAAAACACAAACACAAAATGGTCAGGTTGCGG
AAAATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAAGGACAA
CAGATAGCAACAGAGCAGGCACCCAACCCTCAAAATGTTAAT

SEQ ID NO. 8806
STRAIN M781
CCTAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAG
TTGTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTTAAAAAAACGC
AAAGAAGATGAAGAAGAACAAAAACGTATTAACGAAAAATTACGCTTAGA
TAAAAGAAGTAAATTAAATATTTCTTCTCCTGAAGAACCTCAAAATACTA
CTAAAATTAAGAAGCTTCATTTTCCAAAGATTTCAAAACCTAAGATTGAA
AAGAAACAGAAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAACTAATCG
CATTAGAACTGCACCTATATTTGTAGTAGCATTCCTAGTCATTTTAGTTT
CCGTTTTCCTACTAACTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGT
GGAAATCAGCATACACCTGATGATATTTTGATAGAAAAAACGAATATTCA
AAAAAACGATTATTTCTTTTCTTTAATTTTTAAACATAAAGCTATTGAAC
AACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
CAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAATAAGATTATTGC
ATATGCACATACAAAGCAAGGATATCAGCCTGTCTTGGAAACTGGAAAAA
AGGCTGATCCTGTAAATAGTTCAGAGCTACCAAAGCACTTCTTAACAATT
AACCTTGATAAGGAAGATAGTATTAAGCTATTAATTAAAGATTTAAAGGC
TTTAGACCCTGATTTAATAAGTGAGATTCAGGTGATAAGTTTAGCTGATT
CTAAAACGACACCTGACCTCCTGCTGTTAGATATGCATGATGGAAATAGT
ATTAGAATACCATTATCTAAATTTAAAGAAAGACTTCCTTTTTACAAACA
AATTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAG
TTTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGAT
ACAAAAAATAAATCAACTGATAAAACACAAACACAAAATGGTCAGGTTGC
GGAAAATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAAGGAC
AACAGATAGCAACAGAGCAGGCACCCAACCCTCAAAATGTTAAT

SEQ ID NO. 8807
STRAIN CJB110
CCTAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAG
TTGTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTTAAAAAAACGC
AAAGAAGATGAAGAAGAACAAAAACGTATTAACGAAAAATTACGCTTAGA
TAAAAGAAGTAAATTAAATATTTCTTCTCCTGAAGAACCTCAAAATACTA
CTAAAATTAAGAAGCTTCATTTTCCAAAGATTTCAAAACCTAAGATTGAA
AAGAAACAGAAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAACTAATCG
CATTAGAACTGCACCTATATTTGTAGTAGCATTCCTAGTCATTTTAGTTT
CCGTTTTCCTACTAACTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGT
GGAAATCAGCATACACCTGATGATATTTTGATAGAAAAAACGAATATTCA
AAAAAACGATTATTTCTTTTCTTTAATTTTTAAACATAAAGCTATTGAAC
AACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
CAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAATAAGATTATTGC

Table 88: Comparative Sequences relating to SAG0477

ATATGCACATACAAAGCAAGGATATCAGCCTGTCTTGGAAACTGGAAAAA
AGGCTGATCCTGTAAATAGTTCAGAGCTACCAAAGCACTTCTTAACAATT
AACCTTGATAAGGAAGATAGTATTAAGCTATTAATTAAAGATTTAAAGGC
TTTAGACCCTGATTTAATAAGTGAGATTCAGGTGATAAGTTTAGCTGATT
CTAAAACGACACCTGACCTCCTGCTGTTAGATATGCATGATGGAAATAGT
ATTAGAATACCATTATCTAAATTTAAAGAAAGACTTCCTTTTTACAAACA
AATTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAG
TTTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGAT
ACAAAAAATAAATCAACTGATAAAACACAAACACAAAATGGTCAGGTTGC
GGAAAATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAAGGAC
AACAGATAGCAACAGAGCAGGCACCCAACCCTCAAAATGTTAAT

SEQ ID NO. 8808
STRAIN 1169NT
CCTAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAGT
TGTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTTAAAAAAACGCA
AAGAAGATGAAGAAGAACAAAAACGTATTAACGAAAAATTACGCTTAGAT
AAAAGAAGTAAATTAAATATTTCTTCTCCTGAAGAACCTCAAAATACTAC
TAAAATTAAGAAGCTTCATTTTCCAAAGATTTCAAAACCTAAGATTGAAA
AGAAACAGAAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAACTAATCGC
ATTAGAACTGCACCTATATTTATAGTAGCATTCCTAGTCATTTTAGTTTC
CGTTTTCCTACTAACTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGTG
GAAATCAGCATACACCTGATGATATTTTGATAGAGAAAACGAATATTCAA
AAAAACGATTATTTCTTTTCTTTAATTTTTAAACATAAAGCTATTGAACA
ACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATC
AATTTCCCAACAAGTTTCATATTCAAGTTCAAGAAAATAAGATTATTGCA
TAtGCACATACAAAGCAAGGATATCAGCCTGTCTTGGAAACTGGAAAAAA
GGCTGATCCTGTAAATAGTTCAGAGCTACCAAAGCACTTCTTAACAATTA
ACCTTGATAAGGAAGATAGTATTAAGCTATTAATTAAAGATTTAAAGGCT
TTAGACCCTGATTTAATAAGTGAGATTCAGGTGATAAGTTTAGCTGATTC
TAAAACGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGTA
TTAGAATACCATTATCTAAATTTAAAGAAAGACTTCCTTTTTACAAACAA
ATTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGT
TTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGATA
CAAAAAATAAATCAACTGATAAAACACAAACCCAAAATGGTCAGGTTGCG
GAAAATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAAGGACA
ACAACAGATAGCAACGGAGCAGGCACCCAACCCTCAAAATGTTAAT

SEQ ID NO. 8809
STRAIN JM9130013
CCTAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAGTT
GTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTTAAAAAAACGCAA
AGAAGATGAAGAAGAACAAAAACGTATTAACGAAAAATTACGCTTAGATA
AAAGAAGTAAATTAAATATTTCTTCTCCTGAAGAACCTCAAAATACTACT
AAAATTAAGAAGCTTCATTTTCCAAAGATTTCAAGACCTAAGATTGAAAA
GAAACAGAAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAACTAATCGCA
TTAGAACTGCACCTATATTTGTAGTAGCATTCCTAGTCATTTTAGTTTCC
GTTTTCCTACTAACTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGG
AAATCAGCATACACCTGATGATATTTTGATAGAGAAAACGAATATTCAAA
AAAACGATTATTTCTTTTCTTTAATTTTTAAACATAAAGCTATTGAACAA
CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAATAAGATTATTGCAT
ATGCACATACAAAGCAAGGATATCAACCTGTCTTGGAAACTGGAAAAAAG
GCTGATCCTGTAAATAGTTCAGAGCTACCAAAGCACTTCTTAACAATTAA
CCTTGATAAGGAAGATAGTATTAAGCTATTAATTAAAGATTTAAAGGCTT
TAGACCCTGATTTAATAAGTGAGATTCAGGTGATAAGTTTAGCTGATTCT
AAAACGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGTAT
TAGAATACCATTATCTAAATTTAAAGAAAGACTTCCTTTTTACAAACAAA
TTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTT
TACACAACAACAAATACCATTGAATCAACCCCTGTTAAAGCAGAAGATAC
AAAAAATAAATCAACTGATAAAACACAAACACAAAATGGTCAGGTTGCGG
AAAATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAAGGACAA
CAGATAGCAACAGAGCAGGCACCTAACCCTCAAAATGTTAAT

SEQ ID NO. 8810
STRAIN A909
CCTAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAGTTGTC
TTAACGGAATGGCAAAAGCGTAACCTTGAATTTTTaaAAAAACGCAAAGA
AGATGAAGAAGAaCAAAAACGTATTAACGAAAAATTACGCTTAGATAAAA
GAAGTAAATTAAATATTTCTTCTCCTGAAGAACCTCAAAATACTACTAAA
ATTAAGAAGCTTCATTTTCCAAAGATTTCAAGACCTAAGATTGAAAAGAA
ACAGAAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAACTAATCGCATTA
GAACTGCACCTATATTTGTAGTAGCATTCCTAGTCATTTTAGTTTCCGTT
TTCCTACTAACTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGGAAA
TCAGCATACACCTGATGATATTTTGATAGAGAAAACGAATATTCAAAAAA
ACGATTATTTCTTTTCTTTAATTTTTAAACATAAAGCTATTGAACAACGT
TTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCAATT
TCCCAATAAGTTTCATATTCAAGTTCAAGAAAATAAGATTATTGCATATG
CACATACAAAGCAAGGATATCAACCTGTCTTGGAAACTGGAAAAAAGGCT
GATCCTGTAAATAGTTCAGAGCTACCAAAGCACTTCTTAACAATTAACCT
TGATAAGGAAGATAGTATTAAGCTATTAATTAAAGATTTAAAGGCTTTAG
ACCCTGATTTAATAAGTGAGATTCAGGTGATAAGTTTAGCTGATTCTAAA
ACGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGTATTAs

Table 88: Comparative Sequences relating to SAG0477

AATACCATTATCTAAATTTAAAGAAAGACTTCCTTTTTACAAACAAATTA
AGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTTTAC
ACAACAACAAATACCATTGAATCAACCCCTGTTAAAGCAGAAGATACAAA
AAATAAATCAACTGATAAAACACAAACACAAAATGGTCAGGTTGCGGAAA
ATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAAGGACAACAG
ATAGCAACAGAGCAGGCACCTAACCCTCAAAATGTTAAT

SEQ ID NO. 8811
STRAIN 090
TAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAGTTGTCTTAACGGAAT
GGCAAAAGCGTAACCTTGAATTTTTAAAAAAACGCAAAGAAGATGAAGAA
GAACAAAAACGTATTAACGAAAAATTACGCTTAGATAAAAGAAGTaaaTT
AAATATTTCTTCTCCTGAAGAACCTCAAAATACTACTAAAATTAAGAAGC
TTCATTTTCCAAAGATTTCAAAACCTAAGATTGAAAAGAAACAGAAAAAA
GAAAAAATAGTCAACAGCTTAGCCAAAACTAATCGCATTAGAACTGCACC
TATATTTGTAGTAGCATTCCTAGTCATTTTAGTTTCCGTTTTCCTACTAA
CTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGGAAATCAGCATACA
CCTGATGATATTTTGATAGAAAAAACGAATATTCAAAAAAACGATTATTT
CTTTTCTTTAATTTTTAAACATAAAGCTATTGAACAACGTTTAGCTGCAG
AAGATGTATGGGTAAAAACAGCTCAGATGACTTATCAATTTCCCAATAAG
TTTCATATTCAAGTTCAAGAAAATAAGATTATTGCATATGCACATACAAA
GCAAGGATATCAGCCTGTCTTGGAAACTGGAAAAAAGGCTGATCCTGTAA
ATAGTTCAGAGCTACCAAAGCACTTCTTAACAATTAACCTTGATAAGGAA
GATAGTATTAAGCTATTAATTAAAGATTTAAAGGCTTTAGACCCTGATTT
AATAAGTGAGATTCAGGTGATAAGTTTAGCTGATTCTAAAACGACACCTG
ACCTCCTGCTGTTAGATATGCATGATGGAAATAGTATTAGAATACCATTA
TCTAAATTTAAAGAAAGACTTCCTTTTTACAAACAAATTAAGAAGAACCT
TAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTTTACACAACAACAA
GTACTATTGAATCAACCCCTGTGAAAGCGGAAGATACAAAAAATAAATCA
ACTGATAAAACACAAACACAAAATGGTCAGGTTGCGGAAAATAGTCAAGG
ACAAACAAATAACTCAAATACTAATCAACAAGGACAACAGATAGCAACAG
AGCAGGCACCCAACCCTCAAAATGTTAAT

```
PRETTY of: /biotmp/msa24691.2{*}   August 5, 2002 05:14  ..

                               1                                                   50
  msa252409.2{85_090.con_}  ~~TAAGAAGA AATCAGATAC CCCAGAAAAA GAAGAAGTTG TCTTAACGGA
     msa252409.2{85_CJB110}  CCTAAGAAGA AATCAGATAC CCCAGAAAAA GAAGAAGTTG TCTTAACGGA
       msa252409.2{85_COH1}  CCTAAGAAGA AATCAGATAC CCCAGAAAAA GAAGAAGTTG TCTTAACGGA
       msa252409.2{85_M732}  CCTAAGAAGA AATCAGATAC CCCAGAAAAA GAAGAAGTTG TCTTAACGGA
       msa252409.2{85_M781}  CCTAAGAAGA AATCAGATAC CCCAGAAAAA GAAGAAGTTG TCTTAACGGA
     msa252409.2{85_18RS21}  CCTAAGAAGA AATCAGATAC CCCAGAAAAA GAAGAAGTTG TCTTAACGGA
       msa252409.2{85_2603}  CCTAAGAAGA AATCAGATAC CCCAGAAAAA GAAGAAGTTG TCTTAACGGA
       msa252409.2{85_A909}  CCTAAGAAGA AATCAGATAC CCCAGAAAAA GAAGAAGTTG TCTTAACGGA
       msa252409.2{85_H36B}  CCTAAGAAGA AATCAGATAC CCCAGAAAAA GAAGAAGTTG TCTTAACGGA
  msa252409.2{85_JM9130013}  CCTAAGAAGA AATCAGATAC CCCAGAAAAA GAAGAAGTTG TCTTAACGGA
    msa252409.2{85_1169NT}  CCTAAGAAGA AATCAGATAC CCCAGAAAAA GAAGAAGTTG TCTTAACGGA
                 Consensus  ********** ********** ********** ********** **********

                            51                                                   100
  msa252409.2{85_090.con_}  ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAAA GAAGATGAAG
     msa252409.2{85_CJB110}  ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAAA GAAGATGAAG
       msa252409.2{85_COH1}  ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAAA GAAGATGAAG
       msa252409.2{85_M732}  ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAAA GAAGATGAAG
       msa252409.2{85_M781}  ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAAA GAAGATGAAG
     msa252409.2{85_18RS21}  ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAAA GAAGATGAAG
       msa252409.2{85_2603}  ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAAA GAAGATGAAG
       msa252409.2{85_A909}  ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAAA GAAGATGAAG
       msa252409.2{85_H36B}  ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAAA GAAGATGAAG
  msa252409.2{85_JM9130013}  ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAAA GAAGATGAAG
    msa252409.2{85_1169NT}  ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAAA GAAGATGAAG
                 Consensus  ********** ********** ********** ********** **********

                            101                                                  150
  msa252409.2{85_090.con_}  AAGAACAAAA ACGTATTAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA
     msa252409.2{85_CJB110}  AAGAACAAAA ACGTATTAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA
       msa252409.2{85_COH1}  AAGAACAAAA ACGTATTAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA
       msa252409.2{85_M732}  AAGAACAAAA ACGTATTAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA
       msa252409.2{85_M781}  AAGAACAAAA ACGTATTAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA
     msa252409.2{85_18RS21}  AAGAACAAAA ACGTATTAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA
       msa252409.2{85_2603}  AAGAACAAAA ACGTATTAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA
       msa252409.2{85_A909}  AAGAACAAAA ACGTATTAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA
       msa252409.2{85_H36B}  AAGAACAAAA ACGTATTAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA
  msa252409.2{85_JM9130013}  AAGAACAAAA ACGTATTAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA
    msa252409.2{85_1169NT}  AAGAACAAAA ACGTATTAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA
                 Consensus  ********** ********** ********** ********** **********

                            151                                                  200
  msa252409.2{85_090.con_}  TTAAATATTT CTTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA
     msa252409.2{85_CJB110}  TTAAATATTT CTTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA
       msa252409.2{85_COH1}  TTAAATATTT CTTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA
       msa252409.2{85_M732}  TTAAATATTT CTTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA
```

Table 88: Comparative Sequences relating to SAG0477

```
          msa252409.2{85_M781}  TTAAATATTT CTTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA
        msa252409.2{85_18RS21}  TTAAATATTT CTTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA
          msa252409.2{85_2603}  TTAAATATTT CTTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA
          msa252409.2{85_A909}  TTAAATATTT CTTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA
          msa252409.2{85_H36B}  TTAAATATTT CTTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA
     msa252409.2{85_JM9130013}  TTAAATATTT CTTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA
        msa252409.2{85_1169NT}  TTAAATATTT CTTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA
                     Consensus  ********** ********** ********** ********** **********

                                201                                               250
      msa252409.2{85_090.con_}  GCTTCATTTT CCAAAGATTT CAAaACCTAA GATTGAAAAG AAACAGAAAA
        msa252409.2{85_CJB110}  GCTTCATTTT CCAAAGATTT CAAaACCTAA GATTGAAAAG AAACAGAAAA
          msa252409.2{85_COH1}  GCTTCATTTT CCAAAGATTT CAAaACCTAA GATTGAAAAG AAACAGAAAA
          msa252409.2{85_M732}  GCTTCATTTT CCAAAGATTT CAAaACCTAA GATTGAAAAG AAACAGAAAA
          msa252409.2{85_M781}  GCTTCATTTT CCAAAGATTT CAAaACCTAA GATTGAAAAG AAACAGAAAA
        msa252409.2{85_18RS21}  GCTTCATTTT CCAAAGATTT CAAgACCTAA GATTGAAAAG AAACAGAAAA
          msa252409.2{85_2603}  GCTTCATTTT CCAAAGATTT CAAgACCTAA GATTGAAAAG AAACAGAAAA
          msa252409.2{85_A909}  GCTTCATTTT CCAAAGATTT CAAgACCTAA GATTGAAAAG AAACAGAAAA
          msa252409.2{85_H36B}  GCTTCATTTT CCAAAGATTT CAAgACCTAA GATTGAAAAG AAACAGAAAA
     msa252409.2{85_JM9130013}  GCTTCATTTT CCAAAGATTT CAAgACCTAA GATTGAAAAG AAACAGAAAA
        msa252409.2{85_1169NT}  GCTTCATTTT CCAAAGATTT CAAaACCTAA GATTGAAAAG AAACAGAAAA
                     Consensus  ********** ********** ***-****** ********** **********

                                251                                               300
      msa252409.2{85_090.con_}  AAGAAAAAAT AGTCAACAGC TTAGCCAAAA CTAATCGCAT TAGAACTGCA
        msa252409.2{85_CJB110}  AAGAAAAAAT AGTCAACAGC TTAGCCAAAA CTAATCGCAT TAGAACTGCA
          msa252409.2{85_COH1}  AAGAAAAAAT AGTCAACAGC TTAGCCAAAA CTAATCGCAT TAGAACTGCA
          msa252409.2{85_M732}  AAGAAAAAAT AGTCAACAGC TTAGCCAAAA CTAATCGCAT TAGAACTGCA
          msa252409.2{85_M781}  AAGAAAAAAT AGTCAACAGC TTAGCCAAAA CTAATCGCAT TAGAACTGCA
        msa252409.2{85_18RS21}  AAGAAAAAAT AGTCAACAGC TTAGCCAAAA CTAATCGCAT TAGAACTGCA
          msa252409.2{85_2603}  AAGAAAAAAT AGTCAACAGC TTAGCCAAAA CTAATCGCAT TAGAACTGCA
          msa252409.2{85_A909}  AAGAAAAAAT AGTCAACAGC TTAGCCAAAA CTAATCGCAT TAGAACTGCA
          msa252409.2{85_H36B}  AAGAAAAAAT AGTCAACAGC TTAGCCAAAA CTAATCGCAT TAGAACTGCA
     msa252409.2{85_JM9130013}  AAGAAAAAAT AGTCAACAGC TTAGCCAAAA CTAATCGCAT TAGAACTGCA
        msa252409.2{85_1169NT}  AAGAAAAAAT AGTCAACAGC TTAGCCAAAA CTAATCGCAT TAGAACTGCA
                     Consensus  ********** ********** ********** ********** **********

                                301                                               350
      msa252409.2{85_090.con_}  CCTATATTTg TAGTAGCATT CCTAGTCATT TTAGTTTCCG TTTTCCTACT
        msa252409.2{85_CJB110}  CCTATATTTg TAGTAGCATT CCTAGTCATT TTAGTTTCCG TTTTCCTACT
          msa252409.2{85_COH1}  CCTATATTTg TAGTAGCATT CCTAGTCATT TTAGTTTCCG TTTTCCTACT
          msa252409.2{85_M732}  CCTATATTTg TAGTAGCATT CCTAGTCATT TTAGTTTCCG TTTTCCTACT
          msa252409.2{85_M781}  CCTATATTTg TAGTAGCATT CCTAGTCATT TTAGTTTCCG TTTTCCTACT
        msa252409.2{85_18RS21}  CCTATATTTg TAGTAGCATT CCTAGTCATT TTAGTTTCCG TTTTCCTACT
          msa252409.2{85_2603}  CCTATATTTg TAGTAGCATT CCTAGTCATT TTAGTTTCCG TTTTCCTACT
          msa252409.2{85_A909}  CCTATATTTg TAGTAGCATT CCTAGTCATT TTAGTTTCCG TTTTCCTACT
          msa252409.2{85_H36B}  CCTATATTTg TAGTAGCATT CCTAGTCATT TTAGTTTCCG TTTTCCTACT
     msa252409.2{85_JM9130013}  CCTATATTTg TAGTAGCATT CCTAGTCATT TTAGTTTCCG TTTTCCTACT
        msa252409.2{85_1169NT}  CCTATATTTa TAGTAGCATT CCTAGTCATT TTAGTTTCCG TTTTCCTACT
                     Consensus  *********- ********** ********** ********** **********

                                351                                               400
      msa252409.2{85_090.con_}  AACTCCTTTT AGTAAGCAAA AAACAATAAC AGTTAGTGGA AATCAGCATA
        msa252409.2{85_CJB110}  AACTCCTTTT AGTAAGCAAA AAACAATAAC AGTTAGTGGA AATCAGCATA
          msa252409.2{85_COH1}  AACTCCTTTT AGTAAGCAAA AAACAATAAC AGTTAGTGGA AATCAGCATA
          msa252409.2{85_M732}  AACTCCTTTT AGTAAGCAAA AAACAATAAC AGTTAGTGGA AATCAGCATA
          msa252409.2{85_M781}  AACTCCTTTT AGTAAGCAAA AAACAATAAC AGTTAGTGGA AATCAGCATA
        msa252409.2{85_18RS21}  AACTCCTTTT AGTAAGCAAA AAACAATAAC AGTTAGTGGA AATCAGCATA
          msa252409.2{85_2603}  AACTCCTTTT AGTAAGCAAA AAACAATAAC AGTTAGTGGA AATCAGCATA
          msa252409.2{85_A909}  AACTCCTTTT AGTAAGCAAA AAACAATAAC AGTTAGTGGA AATCAGCATA
          msa252409.2{85_H36B}  AACTCCTTTT AGTAAGCAAA AAACAATAAC AGTTAGTGGA AATCAGCATA
     msa252409.2{85_JM9130013}  AACTCCTTTT AGTAAGCAAA AAACAATAAC AGTTAGTGGA AATCAGCATA
        msa252409.2{85_1169NT}  AACTCCTTTT AGTAAGCAAA AAACAATAAC AGTTAGTGGA AATCAGCATA
                     Consensus  ********** ********** ********** ********** **********

                                401                                               450
      msa252409.2{85_090.con_}  CACCTGATGA TATTTTGATA GAaAAAACGA ATATTCAAAA AAACGATTAT
        msa252409.2{85_CJB110}  CACCTGATGA TATTTTGATA GAaAAAACGA ATATTCAAAA AAACGATTAT
          msa252409.2{85_COH1}  CACCTGATGA TATTTTGATA GAaAAAACGA ATATTCAAAA AAACGATTAT
          msa252409.2{85_M732}  CACCTGATGA TATTTTGATA GAaAAAACGA ATATTCAAAA AAACGATTAT
          msa252409.2{85_M781}  CACCTGATGA TATTTTGATA GAaAAAACGA ATATTCAAAA AAACGATTAT
        msa252409.2{85_18RS21}  CACCTGATGA TATTTTGATA GAgAAAACGA ATATTCAAAA AAACGATTAT
          msa252409.2{85_2603}  CACCTGATGA TATTTTGATA GAgAAAACGA ATATTCAAAA AAACGATTAT
          msa252409.2{85_A909}  CACCTGATGA TATTTTGATA GAgAAAACGA ATATTCAAAA AAACGATTAT
          msa252409.2{85_H36B}  CACCTGATGA TATTTTGATA GAgAAAACGA ATATTCAAAA AAACGATTAT
     msa252409.2{85_JM9130013}  CACCTGATGA TATTTTGATA GAgAAAACGA ATATTCAAAA AAACGATTAT
        msa252409.2{85_1169NT}  CACCTGATGA TATTTTGATA GAgAAAACGA ATATTCAAAA AAACGATTAT
                     Consensus  ********** ********** **-******* ********** **********

                                451                                               500
      msa252409.2{85_090.con_}  TTCTTTTCTT TAATTTTTAA ACATAAAGCT ATTGAACAAC GTTTAGCTGC
        msa252409.2{85_CJB110}  TTCTTTTCTT TAATTTTTAA ACATAAAGCT ATTGAACAAC GTTTAGCTGC
          msa252409.2{85_COH1}  TTCTTTTCTT TAATTTTTAA ACATAAAGCT ATTGAACAAC GTTTAGCTGC
```

Table 88: Comparative Sequences relating to SAG0477

```
      msa252409.2{85_M732}  TTCTTTTCTT TAATTTTTAA ACATAAAGCT ATTGAACAAC GTTTAGCTGC
      msa252409.2{85_M781}  TTCTTTTCTT TAATTTTTAA ACATAAAGCT ATTGAACAAC GTTTAGCTGC
    msa252409.2{85_18RS21}  TTCTTTTCTT TAATTTTTAA ACATAAAGCT ATTGAACAAC GTTTAGCTGC
      msa252409.2{85_2603}  TTCTTTTCTT TAATTTTTAA ACATAAAGCT ATTGAACAAC GTTTAGCTGC
      msa252409.2{85_A909}  TTCTTTTCTT TAATTTTTAA ACATAAAGCT ATTGAACAAC GTTTAGCTGC
      msa252409.2{85_H36B}  TTCTTTTCTT TAATTTTTAA ACATAAAGCT ATTGAACAAC GTTTAGCTGC
 msa252409.2{85_JM9130013}  TTCTTTTCTT TAATTTTTAA ACATAAAGCT ATTGAACAAC GTTTAGCTGC
   msa252409.2{85_1169NT}  TTCTTTTCTT TAATTTTTAA ACATAAAGCT ATTGAACAAC GTTTAGCTGC
                Consensus  ********** ********** ********** ********** **********

                           501                                                550
  msa252409.2{85_090.con_}  AGAAGATGTA TGGGTAAAAA CAGCTCAGAT GACTTATCAA TTTCCCAAtA
    msa252409.2{85_CJB110}  AGAAGATGTA TGGGTAAAAA CAGCTCAGAT GACTTATCAA TTTCCCAAtA
      msa252409.2{85_COH1}  AGAAGATGTA TGGGTAAAAA CAGCTCAGAT GACTTATCAA TTTCCCAAtA
      msa252409.2{85_M732}  AGAAGATGTA TGGGTAAAAA CAGCTCAGAT GACTTATCAA TTTCCCAAtA
      msa252409.2{85_M781}  AGAAGATGTA TGGGTAAAAA CAGCTCAGAT GACTTATCAA TTTCCCAAtA
    msa252409.2{85_18RS21}  AGAAGATGTA TGGGTAAAAA CAGCTCAGAT GACTTATCAA TTTCCCAAtA
      msa252409.2{85_2603}  AGAAGATGTA TGGGTAAAAA CAGCTCAGAT GACTTATCAA TTTCCCAAtA
      msa252409.2{85_A909}  AGAAGATGTA TGGGTAAAAA CAGCTCAGAT GACTTATCAA TTTCCCAAtA
      msa252409.2{85_H36B}  AGAAGATGTA TGGGTAAAAA CAGCTCAGAT GACTTATCAA TTTCCCAAtA
 msa252409.2{85_JM9130013}  AGAAGATGTA TGGGTAAAAA CAGCTCAGAT GACTTATCAA TTTCCCAAtA
    msa252409.2{85_1169NT}  AGAAGATGTA TGGGTAAAAA CAGCTCAGAT GACTTATCAA TTTCCCAAcA
                 Consensus  ********** ********** ********** ********** ********_*

                           551                                                600
  msa252409.2{85_090.con_}  AGTTTCATAT TCAAGTTCAA GAAAATAAGA TTATTGCATA TGCACATACA
    msa252409.2{85_CJB110}  AGTTTCATAT TCAAGTTCAA GAAAATAAGA TTATTGCATA TGCACATACA
      msa252409.2{85_COH1}  AGTTTCATAT TCAAGTTCAA GAAAATAAGA TTATTGCATA TGCACATACA
      msa252409.2{85_M732}  AGTTTCATAT TCAAGTTCAA GAAAATAAGA TTATTGCATA TGCACATACA
      msa252409.2{85_M781}  AGTTTCATAT TCAAGTTCAA GAAAATAAGA TTATTGCATA TGCACATACA
    msa252409.2{85_18RS21}  AGTTTCATAT TCAAGTTCAA GAAAATAAGA TTATTGCATA TGCACATACA
      msa252409.2{85_2603}  AGTTTCATAT TCAAGTTCAA GAAAATAAGA TTATTGCATA TGCACATACA
      msa252409.2{85_A909}  AGTTTCATAT TCAAGTTCAA GAAAATAAGA TTATTGCATA TGCACATACA
      msa252409.2{85_H36B}  AGTTTCATAT TCAAGTTCAA GAAAATAAGA TTATTGCATA TGCACATACA
 msa252409.2{85_JM9130013}  AGTTTCATAT TCAAGTTCAA GAAAATAAGA TTATTGCATA TGCACATACA
    msa252409.2{85_1169NT}  AGTTTCATAT TCAAGTTCAA GAAAATAAGA TTATTGCATA TGCACATACA
                 Consensus  ********** ********** ********** ********** **********

                           601                                                650
  msa252409.2{85_090.con_}  AAGCAAGGAT ATCAgCCTGT CTTGGAAACT GGAAAAAAGG CTGATCCTGT
    msa252409.2{85_CJB110}  AAGCAAGGAT ATCAgCCTGT CTTGGAAACT GGAAAAAAGG CTGATCCTGT
      msa252409.2{85_COH1}  AAGCAAGGAT ATCAgCCTGT CTTGGAAACT GGAAAAAAGG CTGATCCTGT
      msa252409.2{85_M732}  AAGCAAGGAT ATCAgCCTGT CTTGGAAACT GGAAAAAAGG CTGATCCTGT
      msa252409.2{85_M781}  AAGCAAGGAT ATCAgCCTGT CTTGGAAACT GGAAAAAAGG CTGATCCTGT
    msa252409.2{85_18RS21}  AAGCAAGGAT ATCAaCCTGT CTTGGAAACT GGAAAAAAGG CTGATCCTGT
      msa252409.2{85_2603}  AAGCAAGGAT ATCAaCCTGT CTTGGAAACT GGAAAAAAGG CTGATCCTGT
      msa252409.2{85_A909}  AAGCAAGGAT ATCAaCCTGT CTTGGAAACT GGAAAAAAGG CTGATCCTGT
      msa252409.2{85_H36B}  AAGCAAGGAT ATCAaCCTGT CTTGGAAACT GGAAAAAAGG CTGATCCTGT
 msa252409.2{85_JM9130013}  AAGCAAGGAT ATCAaCCTGT CTTGGAAACT GGAAAAAAGG CTGATCCTGT
    msa252409.2{85_1169NT}  AAGCAAGGAT ATCAgCCTGT CTTGGAAACT GGAAAAAAGG CTGATCCTGT
                 Consensus  ********** ****_***** ********** ********** **********

                           651                                                700
  msa252409.2{85_090.con_}  AAATAGTTCA GAGCTACCAA AGCACTTCTT AACAATTAAC CTTGATAAGG
    msa252409.2{85_CJB110}  AAATAGTTCA GAGCTACCAA AGCACTTCTT AACAATTAAC CTTGATAAGG
      msa252409.2{85_COH1}  AAATAGTTCA GAGCTACCAA AGCACTTCTT AACAATTAAC CTTGATAAGG
      msa252409.2{85_M732}  AAATAGTTCA GAGCTACCAA AGCACTTCTT AACAATTAAC CTTGATAAGG
      msa252409.2{85_M781}  AAATAGTTCA GAGCTACCAA AGCACTTCTT AACAATTAAC CTTGATAAGG
    msa252409.2{85_18RS21}  AAATAGTTCA GAGCTACCAA AGCACTTCTT AACAATTAAC CTTGATAAGG
      msa252409.2{85_2603}  AAATAGTTCA GAGCTACCAA AGCACTTCTT AACAATTAAC CTTGATAAGG
      msa252409.2{85_A909}  AAATAGTTCA GAGCTACCAA AGCACTTCTT AACAATTAAC CTTGATAAGG
      msa252409.2{85_H36B}  AAATAGTTCA GAGCTACCAA AGCACTTCTT AACAATTAAC CTTGATAAGG
 msa252409.2{85_JM9130013}  AAATAGTTCA GAGCTACCAA AGCACTTCTT AACAATTAAC CTTGATAAGG
    msa252409.2{85_1169NT}  AAATAGTTCA GAGCTACCAA AGCACTTCTT AACAATTAAC CTTGATAAGG
                 Consensus  ********** ********** ********** ********** **********

                           701                                                750
  msa252409.2{85_090.con_}  AAGATAGTAT TAAGCTATTA ATTAAAGATT TAAAGGCTTT AGACCCTGAT
    msa252409.2{85_CJB110}  AAGATAGTAT TAAGCTATTA ATTAAAGATT TAAAGGCTTT AGACCCTGAT
      msa252409.2{85_COH1}  AAGATAGTAT TAAGCTATTA ATTAAAGATT TAAAGGCTTT AGACCCTGAT
      msa252409.2{85_M732}  AAGATAGTAT TAAGCTATTA ATTAAAGATT TAAAGGCTTT AGACCCTGAT
      msa252409.2{85_M781}  AAGATAGTAT TAAGCTATTA ATTAAAGATT TAAAGGCTTT AGACCCTGAT
    msa252409.2{85_18RS21}  AAGATAGTAT TAAGCTATTA ATTAAAGATT TAAAGGCTTT AGACCCTGAT
      msa252409.2{85_2603}  AAGATAGTAT TAAGCTATTA ATTAAAGATT TAAAGGCTTT AGACCCTGAT
      msa252409.2{85_A909}  AAGATAGTAT TAAGCTATTA ATTAAAGATT TAAAGGCTTT AGACCCTGAT
      msa252409.2{85_H36B}  AAGATAGTAT TAAGCTATTA ATTAAAGATT TAAAGGCTTT AGACCCTGAT
 msa252409.2{85_JM9130013}  AAGATAGTAT TAAGCTATTA ATTAAAGATT TAAAGGCTTT AGACCCTGAT
    msa252409.2{85_1169NT}  AAGATAGTAT TAAGCTATTA ATTAAAGATT TAAAGGCTTT AGACCCTGAT
                 Consensus  ********** ********** ********** ********** **********

                           751                                                800
  msa252409.2{85_090.con_}  TTAATAAGTG AGATTCAGGT GATAAGTTTA GCTGATTCTA AAACGACACC
    msa252409.2{85_CJB110}  TTAATAAGTG AGATTCAGGT GATAAGTTTA GCTGATTCTA AAACGACACC
```

Table 88: Comparative Sequences relating to SAG0477

```
     msa252409.2{85_COH1}  TTAATAAGTG AGATTCAGGT GATAAGTTTA GCTGATTCTA AAACGACACC
     msa252409.2{85_M732}  TTAATAAGTG AGATTCAGGT GATAAGTTTA GCTGATTCTA AAACGACACC
     msa252409.2{85_M781}  TTAATAAGTG AGATTCAGGT GATAAGTTTA GCTGATTCTA AAACGACACC
   msa252409.2{85_18RS21}  TTAATAAGTG AGATTCAGGT GATAAGTTTA GCTGATTCTA AAACGACACC
     msa252409.2{85_2603}  TTAATAAGTG AGATTCAGGT GATAAGTTTA GCTGATTCTA AAACGACACC
     msa252409.2{85_A909}  TTAATAAGTG AGATTCAGGT GATAAGTTTA GCTGATTCTA AAACGACACC
     msa252409.2{85_H36B}  TTAATAAGTG AGATTCAGGT GATAAGTTTA GCTGATTCTA AAACGACACC
msa252409.2{85_JM9130013}  TTAATAAGTG AGATTCAGGT GATAAGTTTA GCTGATTCTA AAACGACACC
   msa252409.2{85_1169NT}  TTAATAAGTG AGATTCAGGT GATAAGTTTA GCTGATTCTA AAACGACACC
                Consensus  ********** ********** ********** ********** **********

                           801                                                 850
  msa252409.2{85_090.con_}  TGACCTCCTG CTGTTAGATA TGCAtGATGG AAATAGTATT AgAATACCAT
   msa252409.2{85_CJB110}  TGACCTCCTG CTGTTAGATA TGCAtGATGG AAATAGTATT AgAATACCAT
     msa252409.2{85_COH1}  TGACCTCCTG CTGTTAGATA TGCAtGATGG AAATAGTATT AgAATACCAT
     msa252409.2{85_M732}  TGACCTCCTG CTGTTAGATA TGCAtGATGG AAATAGTATT AgAATACCAT
     msa252409.2{85_M781}  TGACCTCCTG CTGTTAGATA TGCAtGATGG AAATAGTATT AgAATACCAT
   msa252409.2{85_18RS21}  TGACCTCCTG CTGTTAGATA TGCAcGATGG AAATAGTATT AgAATACCAT
     msa252409.2{85_2603}  TGACCTCCTG CTGTTAGATA TGCAcGATGG AAATAGTATT AgAATACCAT
     msa252409.2{85_A909}  TGACCTCCTG CTGTTAGATA TGCAcGATGG AAATAGTATT AsAATACCAT
     msa252409.2{85_H36B}  TGACCTCCTG CTGTTAGATA TGCAcGATGG AAATAGTATT AgAATACCAT
msa252409.2{85_JM9130013}  TGACCTCCTG CTGTTAGATA TGCAcGATGG AAATAGTATT AgAATACCAT
   msa252409.2{85_1169NT}  TGACCTCCTG CTGTTAGATA TGCAcGATGG AAATAGTATT AgAATACCAT
                Consensus  ********** ********** ****-***** ********** *-********

                           851                                                 900
  msa252409.2{85_090.con_}  TATCTAAATT TAAAGAAAGA CTTCCTTTTT ACAAACAAAT TAAGAAGAAC
   msa252409.2{85_CJB110}  TATCTAAATT TAAAGAAAGA CTTCCTTTTT ACAAACAAAT TAAGAAGAAC
     msa252409.2{85_COH1}  TATCTAAATT TAAAGAAAGA CTTCCTTTTT ACAAACAAAT TAAGAAGAAC
     msa252409.2{85_M732}  TATCTAAATT TAAAGAAAGA CTTCCTTTTT ACAAACAAAT TAAGAAGAAC
     msa252409.2{85_M781}  TATCTAAATT TAAAGAAAGA CTTCCTTTTT ACAAACAAAT TAAGAAGAAC
   msa252409.2{85_18RS21}  TATCTAAATT TAAAGAAAGA CTTCCTTTTT ACAAACAAAT TAAGAAGAAC
     msa252409.2{85_2603}  TATCTAAATT TAAAGAAAGA CTTCCTTTTT ACAAACAAAT TAAGAAGAAC
     msa252409.2{85_A909}  TATCTAAATT TAAAGAAAGA CTTCCTTTTT ACAAACAAAT TAAGAAGAAC
     msa252409.2{85_H36B}  TATCTAAATT TAAAGAAAGA CTTCCTTTTT ACAAACAAAT TAAGAAGAAC
msa252409.2{85_JM9130013}  TATCTAAATT TAAAGAAAGA CTTCCTTTTT ACAAACAAAT TAAGAAGAAC
   msa252409.2{85_1169NT}  TATCTAAATT TAAAGAAAGA CTTCCTTTTT ACAAACAAAT TAAGAAGAAC
                Consensus  ********** ********** ********** ********** **********

                           901                                                 950
  msa252409.2{85_090.con_}  CTTAAGGAAC CTTCTATTGT TGATATGGAA GTGGGAGTTT ACACAACAAC
   msa252409.2{85_CJB110}  CTTAAGGAAC CTTCTATTGT TGATATGGAA GTGGGAGTTT ACACAACAAC
     msa252409.2{85_COH1}  CTTAAGGAAC CTTCTATTGT TGATATGGAA GTGGGAGTTT ACACAACAAC
     msa252409.2{85_M732}  CTTAAGGAAC CTTCTATTGT TGATATGGAA GTGGGAGTTT ACACAACAAC
     msa252409.2{85_M781}  CTTAAGGAAC CTTCTATTGT TGATATGGAA GTGGGAGTTT ACACAACAAC
   msa252409.2{85_18RS21}  CTTAAGGAAC CTTCTATTGT TGATATGGAA GTGGGAGTTT ACACAACAAC
     msa252409.2{85_2603}  CTTAAGGAAC CTTCTATTGT TGATATGGAA GTGGGAGTTT ACACAACAAC
     msa252409.2{85_A909}  CTTAAGGAAC CTTCTATTGT TGATATGGAA GTGGGAGTTT ACACAACAAC
     msa252409.2{85_H36B}  CTTAAGGAAC CTTCTATTGT TGATATGGAA GTGGGAGTTT ACACAACAAC
msa252409.2{85_JM9130013}  CTTAAGGAAC CTTCTATTGT TGATATGGAA GTGGGAGTTT ACACAACAAC
   msa252409.2{85_1169NT}  CTTAAGGAAC CTTCTATTGT TGATATGGAA GTGGGAGTTT ACACAACAAC
                Consensus  ********** ********** ********** ********** **********

                           951                                                1000
  msa252409.2{85_090.con_}  AAgTACtATT GAATCAACCC CTGTgAAAGC gGAAGATACA AAAAATAAAT
   msa252409.2{85_CJB110}  AAgTACtATT GAATCAACCC CTGTgAAAGC gGAAGATACA AAAAATAAAT
     msa252409.2{85_COH1}  AAgTACtATT GAATCAACCC CTGTgAAAGC gGAAGATACA AAAAATAAAT
     msa252409.2{85_M732}  AAgTACtATT GAATCAACCC CTGTgAAAGC gGAAGATACA AAAAATAAAT
     msa252409.2{85_M781}  AAgTACtATT GAATCAACCC CTGTgAAAGC gGAAGATACA AAAAATAAAT
   msa252409.2{85_18RS21}  AAaTACcATT GAATCAACCC CTGTtAAAGC aGAAGATACA AAAAATAAAT
     msa252409.2{85_2603}  AAaTACcATT GAATCAACCC CTGTtAAAGC aGAAGATACA AAAAATAAAT
     msa252409.2{85_A909}  AAaTACcATT GAATCAACCC CTGTtAAAGC aGAAGATACA AAAAATAAAT
     msa252409.2{85_H36B}  AAaTACcATT GAATCAACCC CTGTtAAAGC aGAAGATACA AAAAATAAAT
msa252409.2{85_JM9130013}  AAaTACcATT GAATCAACCC CTGTtAAAGC aGAAGATACA AAAAATAAAT
   msa252409.2{85_1169NT}  AAgTACtATT GAATCAACCC CTGTgAAAGC gGAAGATACA AAAAATAAAT
                Consensus  **-***-*** ********** ****-***** -********* **********

                           1001                                               1050
  msa252409.2{85_090.con_}  CAACTGATAA AACACAAaCa CAAAATGGTC AGGTTGCGGA AAATAGTCAA
   msa252409.2{85_CJB110}  CAACTGATAA AACACAAaCa CAAAATGGTC AGGTTGCGGA AAATAGTCAA
     msa252409.2{85_COH1}  CAACTGATAA AACACAAaCa CAAAATGGTC AGGTTGCGGA AAATAGTCAA
     msa252409.2{85_M732}  CAACTGATAA AACACAAaCa CAAAATGGTC AGGTTGCGGA AAATAGTCAA
     msa252409.2{85_M781}  CAACTGATAA AACACAAaCa CAAAATGGTC AGGTTGCGGA AAATAGTCAA
   msa252409.2{85_18RS21}  CAACTGATAA AACACAAaCa CAAAATGGTC AGGTTGCGGA AAATAGTCAA
     msa252409.2{85_2603}  CAACTGATAA AACACAAaCa CAAAATGGTC AGGTTGCGGA AAATAGTCAA
     msa252409.2{85_A909}  CAACTGATAA AACACAAmCa CAAAATGGTC AGGTTGCGGA AAATAGTCAA
     msa252409.2{85_H36B}  CAACTGATAA AACACAAaCa CAAAATGGTC AGGTTGCGGA AAATAGTCAA
msa252409.2{85_JM9130013}  CAACTGATAA AACACAAaCa CAAAATGGTC AGGTTGCGGA AAATAGTCAA
   msa252409.2{85_1169NT}  CAACTGATAA AACACAAaCc CAAAATGGTC AGGTTGCGGA AAATAGTCAA
                Consensus  ********** *******-*- ********** ********** **********

                           1051                                               1100
  msa252409.2{85_090.con_}  GGACAAACAA ATAACTCAAA TACTAATCAA CAAGG...AC AACAGATAGC
```

Table 88: Comparative Sequences relating to SAG0477

```
    msa252409.2{85_CJB110}  GGACAAACAA ATAACTCAAA TACTAATCAA CAAGG...AC AACAGATAGC
      msa252409.2{85_COH1}  GGACAAACAA ATAACTCAAA TACTAATCAA CAAGG...AC AACAGATAGC
      msa252409.2{85_M732}  GGACAAACAA ATAACTCAAA TACTAATCAA CAAGG...AC AACAGATAGC
      msa252409.2{85_M781}  GGACAAACAA ATAACTCAAA TACTAATCAA CAAGG...AC AACAGATAGC
    msa252409.2{85_18RS21}  GGACAAACAA ATAACTCAAA TACTAATCAA CAAGG...AC AACAGATAGC
      msa252409.2{85_2603}  GGACAAACAA ATAACTCAAA TACTAATCAA CAAGG...AC AACAGATAGC
      msa252409.2{85_A909}  GGACAAACAA ATAACTCAAA TACTAATCAA CAAGG...AC AACAGATAGC
      msa252409.2{85_H36B}  GGACAAACAA ATAACTCAAA TACTAATCAA CAAGG...AC AACAGATAGC
 msa252409.2{85_JM9130013}  GGACAAACAA ATAACTCAAA TACTAATCAA CAAGG...AC AACAGATAGC
    msa252409.2{85_1169NT}  GGACAAACAA ATAACTCAAA TACTAATCAA CAAGGacaAC AACAGATAGC
                 Consensus  ********** ********** ********** *****---** **********

                            1101                             1134
  msa252409.2{85_090.con_}  AACaGAGCAG GCACCcAACC CTCAAAATGT TAAT
    msa252409.2{85_CJB110}  AACaGAGCAG GCACCcAACC CTCAAAATGT TAAT
      msa252409.2{85_COH1}  AACaGAGCAG GCACCcAACC CTCAAAATGT TAAT
      msa252409.2{85_M732}  AACaGAGCAG GCACCcAACC CTCAAAATGT TAAT
      msa252409.2{85_M781}  AACaGAGCAG GCACCcAACC CTCAAAATGT TAAT
    msa252409.2{85_18RS21}  AACaGAGCAG GCACCtAACC CTCAAAATGT TAAT
      msa252409.2{85_2603}  AACaGAGCAG GCACCtAACC CTCAAAATGT TAAT
      msa252409.2{85_A909}  AACaGAGCAG GCACCtAACC CTCAAAATGT TAAT
      msa252409.2{85_H36B}  AACaGAGCAG GCACCtAACC CTCAAAATGT TAAT
 msa252409.2{85_JM9130013}  AACaGAGCAG GCACCtAACC CTCAAAATGT TAAT
    msa252409.2{85_1169NT}  AACgGAGCAG GCACCcAACC CTCAAAATGT TAAT
                 Consensus  ***-****** *****-**** ********** ****
```

SEQ ID NO. 8812

STRAIN 2603 frame: 1

```
PKKKSDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
NTTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
LKEPSIVDMEVGVYTTTNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGQTNNSNTNQ
QGQQIATEQAPNPQNVN
```

SEQ ID NO. 8813

STRAIN H36B frame: 1

```
PKKKSDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
NTTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
LKEPSIVDMEVGVYTTTNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGQTNNSNTNQ
QGQQIATEQAPNPQNVN
```

SEQ ID NO. 8814

STRAIN 18RS21 frame: 1

```
PKKKSDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
NTTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
LKEPSIVDMEVGVYTTTNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGQTNNSNTNQ
QGQQIATEQAPNPQNVN
```

SEQ ID NO. 8815

STRAIN M732 frame: 1

```
PKKKSDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
NTTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
LKEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGQTNNSNTNQ
QGQQIATEQAPNPQNVN
```

SEQ ID NO. 8816

STRAIN COH1 frame: 1

```
PKKKSDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
NTTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
LKEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGQTNNSNTNQ
QGQQIATEQAPNPQNVN
```

SEQ ID NO. 8817

STRAIN M781 frame: 1

```
PKKKSDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
```

Table 88: Comparative Sequences relating to SAG0477

NTTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
LKEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGQTNNSNTNQ
QGQQIATEQAPNPQNVN

SEQ ID NO. 8818

STRAIN CJB110 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
NTTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
LKEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGQTNNSNTNQ
QGQQIATEQAPNPQNVN

SEQ ID NO. 8819

STRAIN 1169NT frame: 1

PKKKSDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
NTTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPIFIVAFLVILVSVFLLTPF
SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
LKEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGQTNNSNTNQ
QGQQQIATEQAPNPQNVN

SEQ ID NO. 8820

STRAIN JM9130013 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
NTTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
LKEPSIVDMEVGVYTTTNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGQTNNSNTNQ
QGQQIATEQAPNPQNVN

SEQ ID NO. 8821

STRAIN A909 frame: 1

PKKKSDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
NTTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
FPNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
IKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIXIPLSKFKERLPFYKQIKKN
LKEPSIVDMEVGVYTTTNTIESTPVKAEDTKNKSTDKTQXQNGQVAENSQGQTNNSNTNQ
QGQQIATEQAPNPQNVN

SEQ ID NO. 8822

STRAIN 090 frame: 2

KKKSDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQN
TTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPFS
KQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQF
PNKFHIQVQENKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLLI
KDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKNL
KEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGQTNNSNTNQQ
GQQIATEQAPNPQNVN

```
PRETTY of: /biotmp/msa252337.2{*}   January 31, 2003 03:32  ..

                           1                                                   50
      msa252337.2{85_090}  -KKKSDTPEK EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
   msa252337.2{85_18RS21}  PKKKSDTPEK EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
     msa252337.2{85_2603}  PKKKSDTPEK EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
     msa252337.2{85_A909}  PKKKSDTPEK EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
   msa252337.2{85_CJB110}  PKKKSDTPEK EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
     msa252337.2{85_COH1}  PKKKSDTPEK EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
     msa252337.2{85_H36B}  PKKKSDTPEK EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_JM9130013}  PKKKSDTPEK EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
     msa252337.2{85_M732}  PKKKSDTPEK EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
     msa252337.2{85_M781}  PKKKSDTPEK EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
   msa252337.2{85_1169NT}  PKKKSDTPEK EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
                Consensus  ********** ********** ********** ********** **********

                           51                                                 100
      msa252337.2{85_090}  LNISSPEEPQ NTTKIKKLHF PKISkPKIEK KQKKEKIVNS LAKTNRIRTA
   msa252337.2{85_18RS21}  LNISSPEEPQ NTTKIKKLHF PKISrPKIEK KQKKEKIVNS LAKTNRIRTA
     msa252337.2{85_2603}  LNISSPEEPQ NTTKIKKLHF PKISrPKIEK KQKKEKIVNS LAKTNRIRTA
     msa252337.2{85_A909}  LNISSPEEPQ NTTKIKKLHF PKISrPKIEK KQKKEKIVNS LAKTNRIRTA
   msa252337.2{85_CJB110}  LNISSPEEPQ NTTKIKKLHF PKISkPKIEK KQKKEKIVNS LAKTNRIRTA
```

Table 88: Comparative Sequences relating to SAG0477

```
     msa252337.2{85_COH1}  LNISSPEEPQ NTTKIKKLHF PKISkPKIEK KQKKEKIVNS LAKTNRIRTA
     msa252337.2{85_H36B}  LNISSPEEPQ NTTKIKKLHF PKISrPKIEK KQKKEKIVNS LAKTNRIRTA
msa252337.2{85_JM9130013}  LNISSPEEPQ NTTKIKKLHF PKISrPKIEK KQKKEKIVNS LAKTNRIRTA
     msa252337.2{85_M732}  LNISSPEEPQ NTTKIKKLHF PKISkPKIEK KQKKEKIVNS LAKTNRIRTA
     msa252337.2{85_M781}  LNISSPEEPQ NTTKIKKLHF PKISkPKIEK KQKKEKIVNS LAKTNRIRTA
   msa252337.2{85_1169NT}  LNISSPEEPQ NTTKIKKLHF PKISkPKIEK KQKKEKIVNS LAKTNRIRTA
                Consensus  ********** ********** ****_***** ********** **********

                           101                                                150
      msa252337.2{85_090}  PIFvVAFLVI LVSVFLLTPF SKQKTITVSG NQHTPDDILI EKTNIQKNDY
   msa252337.2{85_18RS21}  PIFvVAFLVI LVSVFLLTPF SKQKTITVSG NQHTPDDILI EKTNIQKNDY
     msa252337.2{85_2603}  PIFvVAFLVI LVSVFLLTPF SKQKTITVSG NQHTPDDILI EKTNIQKNDY
     msa252337.2{85_A909}  PIFvVAFLVI LVSVFLLTPF SKQKTITVSG NQHTPDDILI EKTNIQKNDY
   msa252337.2{85_CJB110}  PIFvVAFLVI LVSVFLLTPF SKQKTITVSG NQHTPDDILI EKTNIQKNDY
     msa252337.2{85_COH1}  PIFvVAFLVI LVSVFLLTPF SKQKTITVSG NQHTPDDILI EKTNIQKNDY
     msa252337.2{85_H36B}  PIFvVAFLVI LVSVFLLTPF SKQKTITVSG NQHTPDDILI EKTNIQKNDY
msa252337.2{85_JM9130013}  PIFvVAFLVI LVSVFLLTPF SKQKTITVSG NQHTPDDILI EKTNIQKNDY
     msa252337.2{85_M732}  PIFvVAFLVI LVSVFLLTPF SKQKTITVSG NQHTPDDILI EKTNIQKNDY
     msa252337.2{85_M781}  PIFvVAFLVI LVSVFLLTPF SKQKTITVSG NQHTPDDILI EKTNIQKNDY
   msa252337.2{85_1169NT}  PIFiVAFLVI LVSVFLLTPF SKQKTITVSG NQHTPDDILI EKTNIQKNDY
                Consensus  ***_****** ********** ********** ********** **********

                           151                                                200
      msa252337.2{85_090}  FFSLIFKHKA IEQRLAAEDV WVKTAQMTYQ FPNKFHIQVQ ENKIIAYAHT
   msa252337.2{85_18RS21}  FFSLIFKHKA IEQRLAAEDV WVKTAQMTYQ FPNKFHIQVQ ENKIIAYAHT
     msa252337.2{85_2603}  FFSLIFKHKA IEQRLAAEDV WVKTAQMTYQ FPNKFHIQVQ ENKIIAYAHT
     msa252337.2{85_A909}  FFSLIFKHKA IEQRLAAEDV WVKTAQMTYQ FPNKFHIQVQ ENKIIAYAHT
   msa252337.2{85_CJB110}  FFSLIFKHKA IEQRLAAEDV WVKTAQMTYQ FPNKFHIQVQ ENKIIAYAHT
     msa252337.2{85_COH1}  FFSLIFKHKA IEQRLAAEDV WVKTAQMTYQ FPNKFHIQVQ ENKIIAYAHT
     msa252337.2{85_H36B}  FFSLIFKHKA IEQRLAAEDV WVKTAQMTYQ FPNKFHIQVQ ENKIIAYAHT
msa252337.2{85_JM9130013}  FFSLIFKHKA IEQRLAAEDV WVKTAQMTYQ FPNKFHIQVQ ENKIIAYAHT
     msa252337.2{85_M732}  FFSLIFKHKA IEQRLAAEDV WVKTAQMTYQ FPNKFHIQVQ ENKIIAYAHT
     msa252337.2{85_M781}  FFSLIFKHKA IEQRLAAEDV WVKTAQMTYQ FPNKFHIQVQ ENKIIAYAHT
   msa252337.2{85_1169NT}  FFSLIFKHKA IEQRLAAEDV WVKTAQMTYQ FPNKFHIQVQ ENKIIAYAHT
                Consensus  ********** ********** ********** ********** **********

                           201                                                250
      msa252337.2{85_090}  KQGYQPVLET GKKADPVNSS ELPKHFLTIN LDKEDSIKLL IKDLKALDPD
   msa252337.2{85_18RS21}  KQGYQPVLET GKKADPVNSS ELPKHFLTIN LDKEDSIKLL IKDLKALDPD
     msa252337.2{85_2603}  KQGYQPVLET GKKADPVNSS ELPKHFLTIN LDKEDSIKLL IKDLKALDPD
     msa252337.2{85_A909}  KQGYQPVLET GKKADPVNSS ELPKHFLTIN LDKEDSIKLL IKDLKALDPD
   msa252337.2{85_CJB110}  KQGYQPVLET GKKADPVNSS ELPKHFLTIN LDKEDSIKLL IKDLKALDPD
     msa252337.2{85_COH1}  KQGYQPVLET GKKADPVNSS ELPKHFLTIN LDKEDSIKLL IKDLKALDPD
     msa252337.2{85_H36B}  KQGYQPVLET GKKADPVNSS ELPKHFLTIN LDKEDSIKLL IKDLKALDPD
msa252337.2{85_JM9130013}  KQGYQPVLET GKKADPVNSS ELPKHFLTIN LDKEDSIKLL IKDLKALDPD
     msa252337.2{85_M732}  KQGYQPVLET GKKADPVNSS ELPKHFLTIN LDKEDSIKLL IKDLKALDPD
     msa252337.2{85_M781}  KQGYQPVLET GKKADPVNSS ELPKHFLTIN LDKEDSIKLL IKDLKALDPD
   msa252337.2{85_1169NT}  KQGYQPVLET GKKADPVNSS ELPKHFLTIN LDKEDSIKLL IKDLKALDPD
                Consensus  ********** ********** ********** ********** **********

                           251                                                300
      msa252337.2{85_090}  LISEIQVISL ADSKTTPDLL LLDMHDGNSI rIPLSKFKER LPFYKQIKKN
   msa252337.2{85_18RS21}  LISEIQVISL ADSKTTPDLL LLDMHDGNSI rIPLSKFKER LPFYKQIKKN
     msa252337.2{85_2603}  LISEIQVISL ADSKTTPDLL LLDMHDGNSI rIPLSKFKER LPFYKQIKKN
     msa252337.2{85_A909}  LISEIQVISL ADSKTTPDLL LLDMHDGNSI xIPLSKFKER LPFYKQIKKN
   msa252337.2{85_CJB110}  LISEIQVISL ADSKTTPDLL LLDMHDGNSI rIPLSKFKER LPFYKQIKKN
     msa252337.2{85_COH1}  LISEIQVISL ADSKTTPDLL LLDMHDGNSI rIPLSKFKER LPFYKQIKKN
     msa252337.2{85_H36B}  LISEIQVISL ADSKTTPDLL LLDMHDGNSI rIPLSKFKER LPFYKQIKKN
msa252337.2{85_JM9130013}  LISEIQVISL ADSKTTPDLL LLDMHDGNSI rIPLSKFKER LPFYKQIKKN
     msa252337.2{85_M732}  LISEIQVISL ADSKTTPDLL LLDMHDGNSI rIPLSKFKER LPFYKQIKKN
     msa252337.2{85_M781}  LISEIQVISL ADSKTTPDLL LLDMHDGNSI rIPLSKFKER LPFYKQIKKN
   msa252337.2{85_1169NT}  LISEIQVISL ADSKTTPDLL LLDMHDGNSI rIPLSKFKER LPFYKQIKKN
                Consensus  ********** ********** ********** _********* **********

                           301                                                350
      msa252337.2{85_090}  LKEPSIVDME VGVYTTTsTI ESTPVKAEDT KNKSTDKTQt QNGQVAENSQ
   msa252337.2{85_18RS21}  LKEPSIVDME VGVYTTTnTI ESTPVKAEDT KNKSTDKTQt QNGQVAENSQ
     msa252337.2{85_2603}  LKEPSIVDME VGVYTTTnTI ESTPVKAEDT KNKSTDKTQt QNGQVAENSQ
     msa252337.2{85_A909}  LKEPSIVDME VGVYTTTnTI ESTPVKAEDT KNKSTDKTQx QNGQVAENSQ
   msa252337.2{85_CJB110}  LKEPSIVDME VGVYTTTsTI ESTPVKAEDT KNKSTDKTQt QNGQVAENSQ
     msa252337.2{85_COH1}  LKEPSIVDME VGVYTTTsTI ESTPVKAEDT KNKSTDKTQt QNGQVAENSQ
     msa252337.2{85_H36B}  LKEPSIVDME VGVYTTTnTI ESTPVKAEDT KNKSTDKTQt QNGQVAENSQ
msa252337.2{85_JM9130013}  LKEPSIVDME VGVYTTTnTI ESTPVKAEDT KNKSTDKTQt QNGQVAENSQ
     msa252337.2{85_M732}  LKEPSIVDME VGVYTTTsTI ESTPVKAEDT KNKSTDKTQt QNGQVAENSQ
     msa252337.2{85_M781}  LKEPSIVDME VGVYTTTsTI ESTPVKAEDT KNKSTDKTQt QNGQVAENSQ
   msa252337.2{85_1169NT}  LKEPSIVDME VGVYTTTsTI ESTPVKAEDT KNKSTDKTQt QNGQVAENSQ
                Consensus  ********** *******_** ********** *********_ **********

                           351                    378
      msa252337.2{85_090}  GQTNNSNTNQ QGQQiateqa pnpqnvn~
   msa252337.2{85_18RS21}  GQTNNSNTNQ QGQQiateqa pnpqnvn~
     msa252337.2{85_2603}  GQTNNSNTNQ QGQQiateqa pnpqnvn~
     msa252337.2{85_A909}  GQTNNSNTNQ QGQQiateqa pnpqnvn~
```

Table 88: Comparative Sequences relating to SAG0477

```
   msa252337.2{85_CJB110}  GQTNNSNTNQ QGQQiateqa pnpqnvn-
     msa252337.2{85_COH1}  GQTNNSNTNQ QGQQiateqa pnpqnvn-
     msa252337.2{85_H36B}  GQTNNSNTNQ QGQQiateqa pnpqnvn-
msa252337.2{85_JM9130013}  GQTNNSNTNQ QGQQiateqa pnpqnvn-
     msa252337.2{85_M732}  GQTNNSNTNQ QGQQiateqa pnpqnvn-
     msa252337.2{85_M781}  GQTNNSNTNQ QGQQiateqa pnpqnvn-
   msa252337.2{85_1169NT}  GQTNNSNTNQ QGQQqiateq apnpqnvn
                Consensus  ********** ****------ -------*
```

Table 89: Comparative Sequences relating to SAG1350

SEQ ID NO. 8901
STRAIN 2603
ATGAAAAAAGGACAAGTAAATGATACTAAGCAATCTTACTCTCTACGTAAA
TATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTCATAATGGTCACAAGTCCTGTT
TTTGCGGATCAAACTACATCGGTTCAAGTTAATAATCAGACAGGCACTAGTGTGGATGCT
AATAATTCTTCCAATGAGACAAGTGCGTCAAGTGTGATTACTTCCAATAATGATAGTGTT
CAAGCGTCTGATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCCT
TTAGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAGGGAATTATGTTTAT
AGCAAAGAAACCGAGGTGAAAAATACACCTTCAAAATCAGCCCCAGTAGCTTTCTATGCA
AAGAAAGGTGATAAAGTTTTCTATGACCAAGTATTTAATAAAGATAATGTGAAATGGATT
TCATATAAGTCTTTTTGTGGCGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCA
GGAGGTTCAGAGACTAAAGCACCTACTCCTGTAACAAATTCAGGAAGCAATAATCAAGAG
AAAATAGCAACGCAAGGAAATTATACATTTTCACATAAAGTAGAAGTAAAAAATGAAGCT
AAGGTAGCGAGTCCAACTCAATTTACATTGGACAAAGGAGACAGAATTTTTTACGACCAA
ATACTAACTATTGAAGGAAATCAGTGGTTATCTTATAAATCATTCAATGGTGTTCGTCGT
TTTGTTTTGCTAGGTAAAGCATCTTCAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCT
CCTCAACCACAAGCCCGTATTACTAAAACTGGTAGACTGACTATTTCTAACGAAACAACT
ACAGGTTTTGATATTTTAATTACGAATATTAAAGATGATAACGGTATCGCTGCTGTTAAG
GTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATTAAATGGTATACAGCTGTAACT
ACTGGGGATGGCAACTACAAAGTAGCTGTATCATTTGCTGACCATAAGAATGAGAAGGGT
CTTTATAATATTCATTTATACTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGA
ACTAAAGTGACAGTAGCTGGAACTAATTCTTCTCAAGAACCTATTGAAAATGGTTTAGCA
AAGACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAAATGAAGCTAAAATATCA
AGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAAATAAATTATGATCAAGTATTGACA
GCAGATGGTTACCAGTGGATTTCTTACAAATCTTATAGTGGTGTTCGTCGCTATATTCCT
GTGAAAAAGCTAACTACAAGTAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGT
TATCCCAACTTACCTAAAACAGGTACCTATACATTTACTAAAACTGTAGATGTGAAAAGT
CAACCTAAAGTATCAAGTCCAGTGGAATTTAATTTTCAAAAGGGTGAAAAAATACATTAT
GATCAAGTGTTAGTAGTAGATGGTCATCAGTGGATTTCATACAAGAGTTATTCCGGTATT
CGTCGCTATATTGAAATT

SEQ ID NO. 8902
STRAIN 090
AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACT
CTCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTC
ATAATGGTCACAAGTCCTGTTTTTGCGGATCAAACTACATCGGTTCAAGT
TAATAATCAGACAGGCACTAGTGTGGATGCTAATAATTCTTCCAATGAGA
CAAGTGCGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAAGCGTCT
GATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCC
TTTAGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAGGGA
ATTATGTTTATAGCAAAGAAACCGAGGTGAAAAATACACCTTCAAAATCA
GCCCCAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTTCTATGACCA
AGTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTTGTG
GCGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTCA
GAGACTAAAGCACCTACTCCTGTAACAAATTCAGGAAGCAATAATCAAGA
GAAAATAGCAACGCAAGGAAATTATACATTTTCACATAAAGTAGAAGTAA
AAAATGAAGcTAAGGTAGCGAGTCCAACTCAATTTACATTGGACAAAGGA
GACAGAATTTTTTACGACCAAATACTAACTATTGAAGGAAATCAGTGGTT
ATCTTATAAATCATTCAATGGTGTTCGTCGTTTTGTTtTGCTAGGTAAAG
CATCTTCAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCCTCAACCA
CAAGCCCGTATTACTAAAACTGGTAGACTGACTATTTCTAACGAAACAAC
TACAGGTTTTGATATTTTAATTACGAATATTAAAGATGATAACGGTATCG
CTGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATT
AAATGGTATACAGCTGTAACTACTGGGGATGGCAACTACAAAGTAGCTGT
ATCATTTGCTGACCATAAGAATGAGAAGGGTCTTTATAATATTCATTTAT
ACTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACTAAAGTG
ACAGTAGCTGGAACTAATTCTTCTCAAGAACCTATTGAAAATGGTTTAGC
AAAGACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAAATGAAG
CTAAAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAAATA
AATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTACAA
ATCTTATAGTGGTGTTCGTCGCTATATTCCTGTGAAAAAGCTAACTACAA
GTAGTGAAAAAGCGAAaGATGAGGCGACTAAACCGACTAGTTATCCCAAC
TTACCTAAAACAGGTACCTATACATTTACTAAAACTGTAGATGTGAAGAG
TCAACCTAAAGTATCAAGTCCAGTGGAATTTAATTTTCAAAAGGGTGAAA
AAATACATTATGATCAAGTGTTAGTAGTAGATGGTCATCAGTGGATTTCA
TACAAGAGTTATTCCGGTATTCGTCGCTATATTGAAATT

SEQ ID NO. 8903
STRAIN A909
AAAAAAGGACAAGTAAATGATACTAAGCAATCTTAC
TCTCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATT
CATAATGGTCACAAGTCCTGTTTTTGCGGATCAAACTACATCGGTTCAAG
TTAATAATCAGACAGGCACTAGTGTGGATGCTAATAATTCTTCCAATGAG
ACAAGTGCGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAAGCGTC
TGATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTC
CTTTAGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAGGG
AATTATGTTTATAGCAAAGAAACCGAGGTGAAAAATACACCTTCAAAATC
AGCCCCAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTTCTATGACC
AAGTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTTGT
GGCGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTC
AGAGACTAAAGCACCTACTCCTGTAACAAATTCAGGAAGCAATAATCAAG
AGAAAATAGCAACGCAAGGAAATTATACATTTTCACATAAAGTAGAAGTA
AAAAATGAAGCTAAGGTAGCGAGTCCAACTCAATTTACATTGGACAAAGG

Table 89: Comparative Sequences relating to SAG1350

AGACAGAATTTTTTACGACCAAATACTAACTATTGAAGGAAATCAGTGGT
TATCTTATAAATCATTCAATGGTGTTCGTCGTTTTGTTtTGCTAGGTAAA
GCATCTTCAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCCTCAACC
ACAAGCCCGTATTACTAAAACTGGTAGACTGACTATTTCTAACGAAACAA
CTACAGGTTTTGATATTTTAATTACGAATATTAAAGATGATAACGGTATC
GCTGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATAT
TAAATGGTATACAGCTGTAACTACTGGGGATGGCAACTACAAAGTAGCTG
TATCATTTGCTGACCATAAGAATGAGAAGGGTCTTTATAATATTCATTTA
TACTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACTAAAGT
GACAGTAGCTGGAACTAATTCTTCTCAAGAACCTATTGAAAATGGTTTAG
CAAAGACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAAATGAA
GCTAAAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAAAT
AAATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTACA
AATCTTATAGTGGTGTTCGTCGCTATATTCCTGTGAAAAAGCTAACTACA
AGTAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAA
CTTACCTAAAACAGGTACCTATACATTTACTAAAACTGTAGATGTGAAGA
GTCAACCTAAAGTATCAAGTCCAGTGGAATTTAATTTTCAAAAGGGTGAA
AAAATACATTATGATCAAGTGTTAGTAGTAGATGGTCATCAGTGGATTTC
ATACAAGAGTTATTCCGGTATTCGTCGCTATATTGAAATT

SEQ ID NO. 8904
STRAIN H36B
AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACT
CTCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTC
ATAATGGTCACAAGTCCTGTTTTTGCGGATCAAACTACATCGGTTCAAGT
TAATAATCAGACAGGCACTAGTGTGGATGATAATAATTCTTCCAATGAGA
CAAGTGCGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAAGCGTCT
GATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCC
TTTAGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAGGGA
ATTATGTTTATAGCAAAGAAACCGAGGTGAAAAATACACCTTCAAAATCA
GCCCCAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTTCTATGACCA
AGTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTTGTG
GCGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTCA
GAGACTAAAGCACCTACTCCTGTAACAAATTCAGGAAGCAATAATCAAGA
GAAAATAGCAACGCAAGGAAATTATACATTTTCACATAAAGTAGAAGTAA
AAAATGAAGCTAAGGTAGCGAGTCCAACTCAATTTACATTGGACAAAGGA
GACAGAATTTTTTACGACCAAATACTAACTATTGAAGGAAATCAGTGGTT
ATCTTATAAATCATTCAATGGTGTTCGTCGTTTTGTTtTGCTAGGTAAAG
CATCTTCAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCCTCAACCA
CAAGCCCGTATTACTAAAACTGGTAGACTGACTATTTCTAACGAAACAAC
TACAGGTTTTGATATTTTAATTACGAATATTAAAGATGATAACGGTATCG
CTGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATT
AAATGGTATACAGCTGTAACTACTGGGGATGGCAACTACAAAGTAGCTGT
ATCATTTGCTGACCATAAGAATGAGAAGGGTCTTTATAATATTCATTTAT
ACTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAgGAACTAAAGTG
ACAGTAGCTGGAACTAATTCTTCTCAAGAACCTATTGAAAATGGTTTAGC
AAAGACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAAATGAAG
CTAAAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAAATA
AATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTACAA
ATCTTATAGTGGTGTTCGTCGCTATATTCCTGTGAAAAAGCTAACTACAA
GTAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAAC
TTACCTAAAACAGGTACCTATACATTTACTAAAACTGTAGATGTGAAGAG
TCAACCTAAAGTATCAAGTCCAGTGGAATTTAATTTTCAAAAGGGTGAAA
AAATACATTATGATCAAGTGTTAGTAGTAGATGGTCATCAGTGGATTTCA
TACAAGAGTTATTCCGGTATTCGTCGCTATATTGAAATT

SEQ ID NO. 8905
STRAIN 18RS21
AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACTC
TCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTCA
TAATGGTCACAAGTCCTGTTTTTGCGGATCAAACTACATCGGTTCAAGTT
AATAATCAGACAGGCACTAGTGTGGATGCTAATAATTCTTCCAATGAGAC
AAGTGCGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAAGCGTCTG
ATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCCT
TTAGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAGGGAA
TTATGTTTATAGCAAAGAAACCGAGGTGAAAAATACACCTTCAAAATCAG
CCCCAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTTCTATGACCAA
GTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTTGTGG
CGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTCAG
AGACTAAAGCACCTACTCCTGTAACAAATTCAGGAAGCAATAATCAAGAG
AAAATAGCAACGCAAGGAAATTATACATTTTCACATAAAGTAGAAGTAAA
AAATGAAGcTAAGGTAGCGAGTCCAACTCAATTTACATTGGACAAAGGAG
ACAGAATTTTTTACGACCAAATACTAACTATTGAAGGAAATCAGTGGTTA
TCTTATAAATCATTCAATGGTGTTCGTCGTTTTGTTTTGCTAGGTAAAGC
ATCTTCAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCCTCAACCAC
AAGCCCGTATTACTAAAACTGGTAGACTGACTATTTCTAACGAAACAACT
ACAGGTTTTGATATTTTAATTACGAATATTAAAGATGATAACGGTATCGC
TGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATTA
AATGGTATACAGCTGTAACTACTGGGGATGGCAACTACAAAGTAGCTGTA
TCATTTGCTGACCATAAGAATGAGAAGGGTCTTTATAATATTCATTTATA
CTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACTAAAGTGA
CAGTAGCTGGAACTAATTCTTCTCAAGAACCTATTGAAAATGGTTTAGCA
AAGACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAAATGAAGC

Table 89: Comparative Sequences relating to SAG1350

TAAAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAAATAA
ATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTACAAA
TCTTATAGTGGTGTTCGTCGCTATATTCCTGTGAAAAAGCTAACTACAAG
TAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAACT
TACCTAAAACAGGTACCTATACATTTACTAAAACTGTAGATGTGAAAAGT
CAACCTAAAGTATCAAGTCCAGTGGAATTTAATTTTCAAAAGGGTGAAAA
AATACATTATGATCAAGTGTTAGTAGTAGATGGTCATCAGTGGATTTCAT
ACAAGAGTTATTCCGGTATTCGTCGCTATATTGAAATT

SEQ ID NO. 8906
STRAIN M732
CAAGTAAATGATaCTAAGCAATCTTACTCTCTACGTAAATATAAATTTGG
TTTAGCATCAGTAATTTTAGGGTCATTCATAATGGTCACAAGTCCTGTTT
TTGCGGATCAAAcTACATCGGTTCAAGTTAATAATCAGACAGGCACTAGT
GTGGATGCTAATAATTCTTCCAATGAGACAAGTGCGTCAAGTGTGATTAC
TTCCAATAATGATAGTGTTCAAGCGTCTGATAAAGTTGTAAATAGTCAAA
ATACGGCAACAAAGGACATTACTACTCCTTTAGTAGAGACAAAGCCAATG
GTGGAAAAAACATTACCTGAACAAGGGAATTATGTTTATAGCAAAGAAAC
CGAGGTGAAAAATACACCTTCAAAATCAGCCCCAGTAGCTTTCTATGCAA
AGAAAGGTGATAAAGTTTTCTATGACCAAGTATTTAATAAAGATAATGTG
AAATGGATTTCATATAAGTCTTTTGGTGGCGTACGTCGATACGCAGCTAT
TGAGTCACTAGATCCATCAGGAGGTTCAGAGACTAAAGCACCTACTCCTG
TAACAAATTCAGGAAGCAATAATCAAGAGAAAATAGCAACGCAAGGAAAT
TATACATTTTCACATAAAGTAGAAGTAAAAAATGAAGCTAAGGTAGCGAG
TCCAACTCAATTTACATTGGACAAAGGAGACAGAATTTTTTACGACCAAA
TACTAACTatTGAAGGAAATCAGTGGTTATCTTATAAATCATTCAATGGT
GTTCGTCGTTTTGtTttGcTAGGTAAAGCATCTTCAGTAGAAAAAACTGA
AGATAAAGAAAAAGTGTCTCCTCAACCACAAGCCCGTATTACTAAAACTG
GTAGACTGACTATTTCTAACGAAACAACTACAGGTTTTGATATTTTAATT
ACGAATATTAAAGATGATAACGGTATCGCTGCTGTTAAGGTACCGGTTTG
GACTGAACAAGGAGGGCAAGATGATATTAAATGGTATACAGCTGTAACTA
CTGGGGATGGCAACTACAAAGTAGCTGTATCATTTGCTGACCATAAGAAT
GAGAAGGGTCTTTATAATATTCATTTATACTACCAAGAAGCTAGTGGGAC
ACTTGTAGGTGTAACAGGAACTAAAGTGACAGTAGCTGGAACTAATTCTT
CTCAAGAACCTATTGAAAATGGTTTACCAAAGACTGGTGTTTATAATATT
ATCGGAAGTACTGAAGTAAAAAATGAAGCTAAAATATCAAGTCAGACCCA
ATTTACTTTAGAAAAAGGTGACAAAATAAATTATGATCAAGTATTGACAG
CAGATGGTTACCAGTGGATTTCTTACAAATCTTATAGTGGTGTTCGTCGC
TATATTCCTGTGAAAAAGCTAACTACAAGTAGTGAAAAAGCGAAAGATGA
GGCGACTAAACCGACTAGTTATCCCAACTTACCTAAAACAGGTACCTATA
CATTTACTAAAACTGTAGATGTGAAAAGTCAACCTAAAGTATCAAGTCCA
GTGGAATTTAATTTTCAAAAGGGTGAAAAAATACATTATGATCAAGTGTT
AGTAGTAGATGGTCATCAGTGGATTTCATACAAGAGTTATTCCGGTATTC
GTCGCTATATTGAAATT

SEQ ID NO. 8907
STRAIN COH1
AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACTCTCT
ACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTCATAA
TGGTCACAAGTCCTGTTTTTGCGGATCAAACTACATCGGTTCAAGTTAAT
AATCAGACAGGCACTAGTGTGGATGCTAATAATTCTTCCAATGAGACAAG
TGCGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAAGCGTCTGATA
AAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCCTTTA
GTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAGGGAATTA
TGTTTATAGCAAAGAAACCGAGGTGAAAAATACACCTTCAAAATCAGCCC
CAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTTCTATGACCAAGTA
TTTAATAAAGATAATGTTAAATGGATTTCATATAAGTCTTTTGGTGGCGT
ACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTCAGAGA
CTAAAGCACCTACTCCTGTAACAAATTCAGGAAGCAATAATCAAGAGAAA
ATAGCAACGCAAGGAAATTATACATTTTCACATAAAGTAGAAGTAaAAAA
TGAAGcTAAGGTAGCGAGTCCAACTCAATTTACATTGGACAAAGGAGACA
GAATTTTTTACGACCAAATACTAACTATTGAAGGAAATCAGTGGTTATCT
TATAAATCATTCAATGGTGTTCGTCGTTTTGTTtTGCTAGGTAAAGCATC
TTCAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCCTCAACCACAAG
CCCGTATTACTAAAACTGGTAGACTGACTATTTCTAACGAAACAACTACA
GGTTTTGATATTTTAATTACGAATATTAAAGATGATAACGGTATCGCTGC
TGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATTAAAT
GGTATACAGCTGTAACTACTGGGGATGGCAACTACAAAGTAGCTGTATCA
TTTGCTGACCATAAGAATGAGAAGGGTCTTTATAATATTCATTTATACTA
CCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACTAAAGTGACAG
TAGCTGGAACTAATTCTTCTCAAGAACCTATTGAAAATGGTTTACCAAAG
ACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAAATGAAGCTAA
AATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAAATAAATT
ATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTACAAATCT
TATAGTGGTGTTCGTCGCTATATTCCTGTGAAAAAGCTAACTACAAGTAG
TGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAACTTAC
CTAAAACAGGTACCTATACATTTACTAAAACTGTAGATGTGAAAAGTCAA
CCTAAAGTATCAAGTCCAGTGGAATTTAATTTTCAAAAGGGTGAAAAAAT
ACATTATGATCAAGTGTTAGTAGTAGATGGTCATCAGTGGATTTCATACA
AGAGTTATTCCGGTATTCGTCGCTATATTGAAATT

SEQ ID NO. 8908
STRAIN M781

Table 89: Comparative Sequences relating to SAG1350

AAAAAAGGACAAGTAAATGATACTAAGCAATCTT
ACTCTCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCA
TTCATAATGGTCACAAGTCCTGTTTTTGCGGATCAAACTACATCGGTTCA
AGTTAATAATCAGACAGGCACTAGTGTGGATGCTAATAATTCTTCCAATG
AGACAAGTGCGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAAGCG
TCTGATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTAC
TCCTTTAGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAG
GGAATTATGTTTATAGCAAAGAAACCGAGGTGAAAAATACACCTTCAAAA
TCAGCCCCAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTTCTATGA
CCAAGTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTG
GTGGCGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGT
TCAGAGACTAAAGCACCTACTCCTGTAACAAATTCAGGAAGCAATAATCA
AGAGAAAATAGCAACGCAAGGAAATTATACATTTTCACATAAAGTAGAAG
TAAAAAATGAAGCTAAGGTAGCGAGTCCAACTCAATTTACATTGGACAAA
GGAGACAGAATTTTTTACGACCAAATACTAACTATTGAAGGAAATCAGTG
GTTATCTTATAAATCATTCAATGGTGTTCGTCGTTTTGTTtTGCTAGGTA
AAGCATCTTCAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCCTCAA
CCACAAGCCCGTATTACTAAAACTGGTAGACTGACTATTTCTAACGAAAC
AACTACAGGTTTTGATATTTTAATTACGAATATTAAAGATGATAACGGTA
TCGCTGCTGTTAAggTACCGGTTTGGACTGAACAAGGAGGGCAAGATGAT
ATTAAATGGTATACAGCTGTAACTACTGGGGATGGCAACTACAAAGTAGC
TGTATCATTTGCTGACCATAAGAATGAGAAGGGTCTTTATAATATTCATT
TATACTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACTAAA
GTGACAGTAGCTGGAACTAATTCTTCTCAAGAACCTATTGAAAATGGTTT
ACCAAAGACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAAATG
AAGCTAAAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAA
ATAAATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTA
CAAATCTTATAGTGGTGTTCGTCGCTATATTCCTGTGAAAAAGCTAACTA
CAAGTAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCC
AACTTACCTAAAACAGGTACCTATACATTTACTAAAACTGTAGATGTGAA
AAGTCAACCTAAAGTATCAAGTCCAGTGGAATTTAATTTTCAAAAGGGTG
AAAAAATACATTATGATCAAGTGTTAGTAGTAGATGGTCATCAGTGGATT
TCATACAAGAGTTATTCCGGTATTCGTCGCTATATTGAAATT

SEQ ID NO. 8909
STRAIN CJB110
AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACTCTC
TACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTCATA
ATGGTCACAAGTCCTGTTTTTGCGGATCAAACTACATCGGTTCAAGTTAA
TAATCAGACAGGCACTAGTGTGGATGCTAATAATTCTTCCAATGAGACAA
GTGCGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAAGCGTCTGAT
AAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCCTTT
AGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAGGGAATT
ATGTTTATAGCAAAGAAACCGAGGTGAAAAATACACCTTCAAAATCAGCC
CCAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTTCTATGACCAAGT
ATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTTGTGGCG
TACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTCAGAG
ACTAAAGCACCTACTCCTGTAACAAATTCAGGAAGCAATAATCAAGAGAA
AATAGCAACGCAAGGAAATTATACATTTTCACATAAAGTAGAAGTAAAAA
ATGAAGCTAAGGTAGCGAGTCCAACTCAATTTACATTGGACAAAGGAGAC
AGAATTTTTTACGACCAAATACTAACTATTGAAGGAAATCAGTGGTTATC
TTATAAATCATTCAATGGTGTTCGTCGTTTTGTTTTGCTAGGTAAAGCAT
CTTCAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCCTCAACCACAA
GCCCGTATTACTAAAACTGGTAGACTGACTATTTCTAACGAAACAACTAC
AGGTTTTGATATTTTAATTACGAATATTAAAGATGATAACGGTATCGCTG
CTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATTAAA
TGGTATACAGCTGTAACTACTGGGGATGGCAACTACAAAGTAGCTGTATC
ATTTGCTGACCATAAGAATGAGAAGGGTCTTTATAATATTCATTTATACT
ACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACTAAAGTGACA
GTAGCTGGAACTAATTCTTCTCAAGAACCTATTGAAAATGGTTTAGCAAA
GACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAAATGAAGCTA
AAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAAATAAAT
TATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTACAAATC
TTATAGTGGTGTTCGTCGCTATATTCCTGTGAAAAAGCTAACTACAAGTA
GTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAACTTA
CCTAAAACAGGTACCTATACATTTACTAAAACTGTAGATGTGAAGAGTCA
ACCTAAAGTATCAAGTCCAGTGGAATTTAATTTTCAAAAGGGTGAAAAAA
TACATTATGATCAAGTGTTAGTAGTAGATGGTCATCAGTGGATTTCATAC
AAGAGTTATTCCGGTATTCGTCGCTATATTGAAATT

SEQ ID NO. 8910
STRAIN 1169NT
AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACTC
TCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTCA
TAATGGTCACAAGTCCTGTTTTTGCGGATCAAACTACATCGGTTCAAGTT
AATAATCAGACAGGCACTAGTGTGGATGCTAATAATTCTTCCAATGAGAC
AAGTGCGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAAGCGTCTG
ATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCCT
TTAGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAGGGAA
TTATGTTTATAGCAAAGAAACCGAGGTGAAAAATACACCTTCAAAATCAG
CCCCAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTTCTATGACCAA
GTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTGGTGG
CGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTCAG

Table 89: Comparative Sequences relating to SAG1350

AGACTAAAGCACCTACTCCTGTAACAAATTCAGGAAGCAATAATCAAGAG
AAAATAGCAACGCAAGGAAATTATACATTTTCACATAAAGTAGAAGTAAA
AAATGAAGCTAAGGTAGCGAGTCCAACTCAATTTACATTGGACAAAGGAG
ACAGAATTTTTTACGACCAAATACTAACTATTGAAGGAAATCAGTGGTTA
TCTTATAAATCATTCAATGGTGTTCGTCGTTTTGTTTTGCTAGGTAAAGC
ATCTTCAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCCTCAACCAC
AAGCCCGTATTACTAAAACTGGTAGACTGACTATTTCTAACGAAACAACT
ACAGGTTTTGATATTTTAATTACGAATATTAAAGATGATAACGGTATCGC
TGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATTA
AATGGTATACAGCTGTAACTACTGGGGATGGCAACTACAAAGTAGCTGTA
TCATTTGCTGACCATAAGAATGAGAAGGGTCTTTATAATATTCATTTATA
CTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACTAAAGTGA
CAGTAGCTGGAaCTAATTCTTCTCAAGAACCTATTGAAAATGGTTTAGCA
AAGACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAAATGAAGC
TAAAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAAATAA
ATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTACAAA
TCTTATAGTGGTGTTCGTCGCTATATTCCTGTGAAAAAGCTAACTACAAG
TAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAACT
TACCTAAAACAGGTACCTATACATTTACTAAAACTGTAGATGTGAAAAGT
CAACCTAAAGTATCAAGTCCAGTGGAATTTAATTTTCAAAAGGGTGAAAA
AATACATTATGATCAAGTGTTAGTAGTAGATGGTCATCAGTGGATTTCAT
ACAAGAGTTATTCCGGTATTCGTCGCTATATTGAAATT

SEQ ID NO. 8911
STRAIN JM9130013
AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACT
CTCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTC
ATAATGGTCACAAGTCCTGTTTTTGCGGATCAAACTACATCGGTTCAAGT
TAATAATCAGACAGGCACTAGTGTGGATGCTAATAATTCTTCCAATGAGA
CAAGTGCGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAAGCGTCT
GATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCC
TTTAGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAGGGA
ATTATGTTTATAGCAAAGAAACCGAGGTGAAAAATACACCTTCAAAATCA
GCCCCAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTTCTATGACCA
AGTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTTGTG
GCGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTCA
GAGACTAAAGCACCTACTCCTGTAACAAATTCAGGAAGCAATAATCAAGA
GAAAATAGCAACGCAAGGAAATTATACATTTTCACATAAAGTAGAAGTAA
AAAATGAAGCTAAGGTAGCGAGTCCAACTCAATTTACATTGGACAAAGGA
GACAGAATTTTTTACGACCAAATACTAACTATTGAAGGAAATCAGTGGTT
ATCTTATAAATCATTCAATGGTGTTCGTCGTTTTGTTTTGCTAGGTAAAG
CATCTTCAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCCTCAACCA
CAAGCCCGTATTACTAAAACTGGTAGACTGACTATTTATAACGAAACAAC
TACAGGTTTTGATATTTTAATTACGAATATTAAAGATGATAACGGTATCG
CTGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATT
AAATGGTATACAGCTGTAACTACTGGGGATGGCAACTACAAAGTAGCTGT
ATCATTTGCTGACCATAAGAATGAGAAGGGTCTTTATAATATTCATTTAT
ACTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACTAAAGTG
ACAGTAGCTGGAACTAATTCTTCTCAAGAACCTATTGAAAATGGTTTAGC
AAAGACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAAATGAAG
CTAAAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAAATA
AATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTACAA
ATCTTATAGTGGTGTTCGTCGCTATATTCCTGTGAAAAAGCTAACTACAA
GTAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAAC
TTACCTAAAACAGGTACCTATACATTTACTAAAACTGTAGATGTGAAGAG
TCAACCTAAAGTATCAAGTCCAGTGGAATTTAATTTTCAAAAGGGTGAAA
AAATACATTATGATCAAGTGTTAGTAGTAGATGGTCATCAGTGGATTTCA
TACAAGAGTTATTCCGGTATTCGTCGCTATATTGAAATT

```
PRETTY of: /biotmp/msa255059.2{*}   February 11, 2003 08:41  ..

                           1                                                    50
       msa255059.2{91_M732}   ---------- --CAAGTAAA TGATACTAAG CAATCTTACT CTCTACGTAA
       msa255059.2{91_M781}   ---AAAAAAG GACAAGTAAA TGATACTAAG CAATCTTACT CTCTACGTAA
       msa255059.2{91_COH1}   ---AAAAAAG GACAAGTAAA TGATACTAAG CAATCTTACT CTCTACGTAA
     msa255059.2{91_18RS21}   ---AAAAAAG GACAAGTAAA TGATACTAAG CAATCTTACT CTCTACGTAA
       msa255059.2{91_2603}   atgAAAAAAG GACAAGTAAA TGATACTAAG CAATCTTACT CTCTACGTAA
     msa255059.2{91_1169NT}   ---AAAAAAG GACAAGTAAA TGATACTAAG CAATCTTACT CTCTACGTAA
        msa255059.2{91_090}   ---AAAAAAG GACAAGTAAA TGATACTAAG CAATCTTACT CTCTACGTAA
       msa255059.2{91_A909}   ---AAAAAAG GACAAGTAAA TGATACTAAG CAATCTTACT CTCTACGTAA
     msa255059.2{91_CJB110}   ---AAAAAAG GACAAGTAAA TGATACTAAG CAATCTTACT CTCTACGTAA
       msa255059.2{91_H36B}   ---AAAAAAG GACAAGTAAA TGATACTAAG CAATCTTACT CTCTACGTAA
  msa255059.2{91_JM9130013}   ---AAAAAAG GACAAGTAAA TGATACTAAG CAATCTTACT CTCTACGTAA
                  Consensus   ********** ********** ********** ********** **********

                           51                                                  100
       msa255059.2{91_M732}   ATATAAATTT GGTTTAGCAT CAGTAATTTT AGGGTCATTC ATAATGGTCA
       msa255059.2{91_M781}   ATATAAATTT GGTTTAGCAT CAGTAATTTT AGGGTCATTC ATAATGGTCA
       msa255059.2{91_COH1}   ATATAAATTT GGTTTAGCAT CAGTAATTTT AGGGTCATTC ATAATGGTCA
     msa255059.2{91_18RS21}   ATATAAATTT GGTTTAGCAT CAGTAATTTT AGGGTCATTC ATAATGGTCA
       msa255059.2{91_2603}   ATATAAATTT GGTTTAGCAT CAGTAATTTT AGGGTCATTC ATAATGGTCA
     msa255059.2{91_1169NT}   ATATAAATTT GGTTTAGCAT CAGTAATTTT AGGGTCATTC ATAATGGTCA
```

Table 89: Comparative Sequences relating to SAG1350

```
     msa255059.2{91_090}  ATATAAATTT GGTTTAGCAT CAGTAATTTT AGGGTCATTC ATAATGGTCA
     msa255059.2{91_A909}  ATATAAATTT GGTTTAGCAT CAGTAATTTT AGGGTCATTC ATAATGGTCA
   msa255059.2{91_CJB110}  ATATAAATTT GGTTTAGCAT CAGTAATTTT AGGGTCATTC ATAATGGTCA
     msa255059.2{91_H36B}  ATATAAATTT GGTTTAGCAT CAGTAATTTT AGGGTCATTC ATAATGGTCA
msa255059.2{91_JM9130013}  ATATAAATTT GGTTTAGCAT CAGTAATTTT AGGGTCATTC ATAATGGTCA
                Consensus  ********** ********** ********** ********** **********

                           101                                              150
     msa255059.2{91_M732}  CAAGTCCTGT TTTTGCGGAT CAAACTACAT CGGTTCAAGT TAATAATCAG
     msa255059.2{91_M781}  CAAGTCCTGT TTTTGCGGAT CAAACTACAT CGGTTCAAGT TAATAATCAG
     msa255059.2{91_COH1}  CAAGTCCTGT TTTTGCGGAT CAAACTACAT CGGTTCAAGT TAATAATCAG
   msa255059.2{91_18RS21}  CAAGTCCTGT TTTTGCGGAT CAAACTACAT CGGTTCAAGT TAATAATCAG
     msa255059.2{91_2603}  CAAGTCCTGT TTTTGCGGAT CAAACTACAT CGGTTCAAGT TAATAATCAG
   msa255059.2{91_1169NT}  CAAGTCCTGT TTTTGCGGAT CAAACTACAT CGGTTCAAGT TAATAATCAG
      msa255059.2{91_090}  CAAGTCCTGT TTTTGCGGAT CAAACTACAT CGGTTCAAGT TAATAATCAG
     msa255059.2{91_A909}  CAAGTCCTGT TTTTGCGGAT CAAACTACAT CGGTTCAAGT TAATAATCAG
   msa255059.2{91_CJB110}  CAAGTCCTGT TTTTGCGGAT CAAACTACAT CGGTTCAAGT TAATAATCAG
     msa255059.2{91_H36B}  CAAGTCCTGT TTTTGCGGAT CAAACTACAT CGGTTCAAGT TAATAATCAG
msa255059.2{91_JM9130013}  CAAGTCCTGT TTTTGCGGAT CAAACTACAT CGGTTCAAGT TAATAATCAG
                Consensus  ********** ********** ********** ********** **********

                           151                                              200
     msa255059.2{91_M732}  ACAGGCACTA GTGTGGATGc TAATAATTCT TCCAATGAGA CAAGTGCGTC
     msa255059.2{91_M781}  ACAGGCACTA GTGTGGATGc TAATAATTCT TCCAATGAGA CAAGTGCGTC
     msa255059.2{91_COH1}  ACAGGCACTA GTGTGGATGc TAATAATTCT TCCAATGAGA CAAGTGCGTC
   msa255059.2{91_18RS21}  ACAGGCACTA GTGTGGATGc TAATAATTCT TCCAATGAGA CAAGTGCGTC
     msa255059.2{91_2603}  ACAGGCACTA GTGTGGATGc TAATAATTCT TCCAATGAGA CAAGTGCGTC
   msa255059.2{91_1169NT}  ACAGGCACTA GTGTGGATGc TAATAATTCT TCCAATGAGA CAAGTGCGTC
      msa255059.2{91_090}  ACAGGCACTA GTGTGGATGc TAATAATTCT TCCAATGAGA CAAGTGCGTC
     msa255059.2{91_A909}  ACAGGCACTA GTGTGGATGc TAATAATTCT TCCAATGAGA CAAGTGCGTC
   msa255059.2{91_CJB110}  ACAGGCACTA GTGTGGATGc TAATAATTCT TCCAATGAGA CAAGTGCGTC
     msa255059.2{91_H36B}  ACAGGCACTA GTGTGGATGa TAATAATTCT TCCAATGAGA CAAGTGCGTC
msa255059.2{91_JM9130013}  ACAGGCACTA GTGTGGATGc TAATAATTCT TCCAATGAGA CAAGTGCGTC
                Consensus  ********** *********. ********** ********** **********

                           201                                              250
     msa255059.2{91_M732}  AAGTGTGATT ACTTCCAATA ATGATAGTGT TCAAGCGTCT GATAAAGTTG
     msa255059.2{91_M781}  AAGTGTGATT ACTTCCAATA ATGATAGTGT TCAAGCGTCT GATAAAGTTG
     msa255059.2{91_COH1}  AAGTGTGATT ACTTCCAATA ATGATAGTGT TCAAGCGTCT GATAAAGTTG
   msa255059.2{91_18RS21}  AAGTGTGATT ACTTCCAATA ATGATAGTGT TCAAGCGTCT GATAAAGTTG
     msa255059.2{91_2603}  AAGTGTGATT ACTTCCAATA ATGATAGTGT TCAAGCGTCT GATAAAGTTG
   msa255059.2{91_1169NT}  AAGTGTGATT ACTTCCAATA ATGATAGTGT TCAAGCGTCT GATAAAGTTG
      msa255059.2{91_090}  AAGTGTGATT ACTTCCAATA ATGATAGTGT TCAAGCGTCT GATAAAGTTG
     msa255059.2{91_A909}  AAGTGTGATT ACTTCCAATA ATGATAGTGT TCAAGCGTCT GATAAAGTTG
   msa255059.2{91_CJB110}  AAGTGTGATT ACTTCCAATA ATGATAGTGT TCAAGCGTCT GATAAAGTTG
     msa255059.2{91_H36B}  AAGTGTGATT ACTTCCAATA ATGATAGTGT TCAAGCGTCT GATAAAGTTG
msa255059.2{91_JM9130013}  AAGTGTGATT ACTTCCAATA ATGATAGTGT TCAAGCGTCT GATAAAGTTG
                Consensus  ********** ********** ********** ********** **********

                           251                                              300
     msa255059.2{91_M732}  TAAATAGTCA AAATACGGCA ACAAAGGACA TTACTACTCC TTTAGTAGAG
     msa255059.2{91_M781}  TAAATAGTCA AAATACGGCA ACAAAGGACA TTACTACTCC TTTAGTAGAG
     msa255059.2{91_COH1}  TAAATAGTCA AAATACGGCA ACAAAGGACA TTACTACTCC TTTAGTAGAG
   msa255059.2{91_18RS21}  TAAATAGTCA AAATACGGCA ACAAAGGACA TTACTACTCC TTTAGTAGAG
     msa255059.2{91_2603}  TAAATAGTCA AAATACGGCA ACAAAGGACA TTACTACTCC TTTAGTAGAG
   msa255059.2{91_1169NT}  TAAATAGTCA AAATACGGCA ACAAAGGACA TTACTACTCC TTTAGTAGAG
      msa255059.2{91_090}  TAAATAGTCA AAATACGGCA ACAAAGGACA TTACTACTCC TTTAGTAGAG
     msa255059.2{91_A909}  TAAATAGTCA AAATACGGCA ACAAAGGACA TTACTACTCC TTTAGTAGAG
   msa255059.2{91_CJB110}  TAAATAGTCA AAATACGGCA ACAAAGGACA TTACTACTCC TTTAGTAGAG
     msa255059.2{91_H36B}  TAAATAGTCA AAATACGGCA ACAAAGGACA TTACTACTCC TTTAGTAGAG
msa255059.2{91_JM9130013}  TAAATAGTCA AAATACGGCA ACAAAGGACA TTACTACTCC TTTAGTAGAG
                Consensus  ********** ********** ********** ********** **********

                           301                                              350
     msa255059.2{91_M732}  ACAAAGCCAA TGGTGGAAAA AACATTACCT GAACAAGGGA ATTATGTTTA
     msa255059.2{91_M781}  ACAAAGCCAA TGGTGGAAAA AACATTACCT GAACAAGGGA ATTATGTTTA
     msa255059.2{91_COH1}  ACAAAGCCAA TGGTGGAAAA AACATTACCT GAACAAGGGA ATTATGTTTA
   msa255059.2{91_18RS21}  ACAAAGCCAA TGGTGGAAAA AACATTACCT GAACAAGGGA ATTATGTTTA
     msa255059.2{91_2603}  ACAAAGCCAA TGGTGGAAAA AACATTACCT GAACAAGGGA ATTATGTTTA
   msa255059.2{91_1169NT}  ACAAAGCCAA TGGTGGAAAA AACATTACCT GAACAAGGGA ATTATGTTTA
      msa255059.2{91_090}  ACAAAGCCAA TGGTGGAAAA AACATTACCT GAACAAGGGA ATTATGTTTA
     msa255059.2{91_A909}  ACAAAGCCAA TGGTGGAAAA AACATTACCT GAACAAGGGA ATTATGTTTA
   msa255059.2{91_CJB110}  ACAAAGCCAA TGGTGGAAAA AACATTACCT GAACAAGGGA ATTATGTTTA
     msa255059.2{91_H36B}  ACAAAGCCAA TGGTGGAAAA AACATTACCT GAACAAGGGA ATTATGTTTA
msa255059.2{91_JM9130013}  ACAAAGCCAA TGGTGGAAAA AACATTACCT GAACAAGGGA ATTATGTTTA
                Consensus  ********** ********** ********** ********** **********

                           351                                              400
     msa255059.2{91_M732}  TAGCAAAGAA ACCGAGGTGA AAAATACACC TTCAAAATCA GCCCCAGTAG
     msa255059.2{91_M781}  TAGCAAAGAA ACCGAGGTGA AAAATACACC TTCAAAATCA GCCCCAGTAG
     msa255059.2{91_COH1}  TAGCAAAGAA ACCGAGGTGA AAAATACACC TTCAAAATCA GCCCCAGTAG
   msa255059.2{91_18RS21}  TAGCAAAGAA ACCGAGGTGA AAAATACACC TTCAAAATCA GCCCCAGTAG
     msa255059.2{91_2603}  TAGCAAAGAA ACCGAGGTGA AAAATACACC TTCAAAATCA GCCCCAGTAG
```

Table 89: Comparative Sequences relating to SAG1350

```
  msa255059.2{91_1169NT}   TAGCAAAGAA ACCGAGGTGA AAAATACACC TTCAAAATCA GCCCCAGTAG
     msa255059.2{91_090}   TAGCAAAGAA ACCGAGGTGA AAAATACACC TTCAAAATCA GCCCCAGTAG
    msa255059.2{91_A909}   TAGCAAAGAA ACCGAGGTGA AAAATACACC TTCAAAATCA GCCCCAGTAG
  msa255059.2{91_CJB110}   TAGCAAAGAA ACCGAGGTGA AAAATACACC TTCAAAATCA GCCCCAGTAG
    msa255059.2{91_H36B}   TAGCAAAGAA ACCGAGGTGA AAAATACACC TTCAAAATCA GCCCCAGTAG
msa255059.2{91_JM9130013}  TAGCAAAGAA ACCGAGGTGA AAAATACACC TTCAAAATCA GCCCCAGTAG
               Consensus   ********** ********** ********** ********** **********

                           401                                                450
    msa255059.2{91_M732}   CTTTCTATGC AAAGAAAGGT GATAAAGTTT TCTATGACCA AGTATTTAAT
    msa255059.2{91_M781}   CTTTCTATGC AAAGAAAGGT GATAAAGTTT TCTATGACCA AGTATTTAAT
    msa255059.2{91_COH1}   CTTTCTATGC AAAGAAAGGT GATAAAGTTT TCTATGACCA AGTATTTAAT
  msa255059.2{91_18RS21}   CTTTCTATGC AAAGAAAGGT GATAAAGTTT TCTATGACCA AGTATTTAAT
    msa255059.2{91_2603}   CTTTCTATGC AAAGAAAGGT GATAAAGTTT TCTATGACCA AGTATTTAAT
  msa255059.2{91_1169NT}   CTTTCTATGC AAAGAAAGGT GATAAAGTTT TCTATGACCA AGTATTTAAT
     msa255059.2{91_090}   CTTTCTATGC AAAGAAAGGT GATAAAGTTT TCTATGACCA AGTATTTAAT
    msa255059.2{91_A909}   CTTTCTATGC AAAGAAAGGT GATAAAGTTT TCTATGACCA AGTATTTAAT
  msa255059.2{91_CJB110}   CTTTCTATGC AAAGAAAGGT GATAAAGTTT TCTATGACCA AGTATTTAAT
    msa255059.2{91_H36B}   CTTTCTATGC AAAGAAAGGT GATAAAGTTT TCTATGACCA AGTATTTAAT
msa255059.2{91_JM9130013}  CTTTCTATGC AAAGAAAGGT GATAAAGTTT TCTATGACCA AGTATTTAAT
               Consensus   ********** ********** ********** ********** **********

                           451                                                500
    msa255059.2{91_M732}   AAAGATAATG TgAAATGGAT TTCATATAAG TCTTTTgGTG GCGTACGTCG
    msa255059.2{91_M781}   AAAGATAATG TgAAATGGAT TTCATATAAG TCTTTTgGTG GCGTACGTCG
    msa255059.2{91_COH1}   AAAGATAATG TtAAATGGAT TTCATATAAG TCTTTTgGTG GCGTACGTCG
  msa255059.2{91_18RS21}   AAAGATAATG TgAAATGGAT TTCATATAAG TCTTTTtGTG GCGTACGTCG
    msa255059.2{91_2603}   AAAGATAATG TgAAATGGAT TTCATATAAG TCTTTTtGTG GCGTACGTCG
  msa255059.2{91_1169NT}   AAAGATAATG TgAAATGGAT TTCATATAAG TCTTTTgGTG GCGTACGTCG
     msa255059.2{91_090}   AAAGATAATG TgAAATGGAT TTCATATAAG TCTTTTtGTG GCGTACGTCG
    msa255059.2{91_A909}   AAAGATAATG TgAAATGGAT TTCATATAAG TCTTTTtGTG GCGTACGTCG
  msa255059.2{91_CJB110}   AAAGATAATG TgAAATGGAT TTCATATAAG TCTTTTtGTG GCGTACGTCG
    msa255059.2{91_H36B}   AAAGATAATG TgAAATGGAT TTCATATAAG TCTTTTtGTG GCGTACGTCG
msa255059.2{91_JM9130013}  AAAGATAATG TgAAATGGAT TTCATATAAG TCTTTTtGTG GCGTACGTCG
               Consensus   ********** *-******** ********** ******-*** **********

                           501                                                550
    msa255059.2{91_M732}   ATACGCAGCT ATTGAGTCAC TAGATCCATC AGGAGGTTCA GAGACTAAAG
    msa255059.2{91_M781}   ATACGCAGCT ATTGAGTCAC TAGATCCATC AGGAGGTTCA GAGACTAAAG
    msa255059.2{91_COH1}   ATACGCAGCT ATTGAGTCAC TAGATCCATC AGGAGGTTCA GAGACTAAAG
  msa255059.2{91_18RS21}   ATACGCAGCT ATTGAGTCAC TAGATCCATC AGGAGGTTCA GAGACTAAAG
    msa255059.2{91_2603}   ATACGCAGCT ATTGAGTCAC TAGATCCATC AGGAGGTTCA GAGACTAAAG
  msa255059.2{91_1169NT}   ATACGCAGCT ATTGAGTCAC TAGATCCATC AGGAGGTTCA GAGACTAAAG
     msa255059.2{91_090}   ATACGCAGCT ATTGAGTCAC TAGATCCATC AGGAGGTTCA GAGACTAAAG
    msa255059.2{91_A909}   ATACGCAGCT ATTGAGTCAC TAGATCCATC AGGAGGTTCA GAGACTAAAG
  msa255059.2{91_CJB110}   ATACGCAGCT ATTGAGTCAC TAGATCCATC AGGAGGTTCA GAGACTAAAG
    msa255059.2{91_H36B}   ATACGCAGCT ATTGAGTCAC TAGATCCATC AGGAGGTTCA GAGACTAAAG
msa255059.2{91_JM9130013}  ATACGCAGCT ATTGAGTCAC TAGATCCATC AGGAGGTTCA GAGACTAAAG
               Consensus   ********** ********** ********** ********** **********

                           551                                                600
    msa255059.2{91_M732}   CACCTACTCC TGTAACAAAT TCAGGAAGCA ATAATCAAGA GAAAATAGCA
    msa255059.2{91_M781}   CACCTACTCC TGTAACAAAT TCAGGAAGCA ATAATCAAGA GAAAATAGCA
    msa255059.2{91_COH1}   CACCTACTCC TGTAACAAAT TCAGGAAGCA ATAATCAAGA GAAAATAGCA
  msa255059.2{91_18RS21}   CACCTACTCC TGTAACAAAT TCAGGAAGCA ATAATCAAGA GAAAATAGCA
    msa255059.2{91_2603}   CACCTACTCC TGTAACAAAT TCAGGAAGCA ATAATCAAGA GAAAATAGCA
  msa255059.2{91_1169NT}   CACCTACTCC TGTAACAAAT TCAGGAAGCA ATAATCAAGA GAAAATAGCA
     msa255059.2{91_090}   CACCTACTCC TGTAACAAAT TCAGGAAGCA ATAATCAAGA GAAAATAGCA
    msa255059.2{91_A909}   CACCTACTCC TGTAACAAAT TCAGGAAGCA ATAATCAAGA GAAAATAGCA
  msa255059.2{91_CJB110}   CACCTACTCC TGTAACAAAT TCAGGAAGCA ATAATCAAGA GAAAATAGCA
    msa255059.2{91_H36B}   CACCTACTCC TGTAACAAAT TCAGGAAGCA ATAATCAAGA GAAAATAGCA
msa255059.2{91_JM9130013}  CACCTACTCC TGTAACAAAT TCAGGAAGCA ATAATCAAGA GAAAATAGCA
               Consensus   ********** ********** ********** ********** **********

                           601                                                650
    msa255059.2{91_M732}   ACGCAAGGAA ATTATACATT TTCACATAAA GTAGAAGTAA AAAATGAAGC
    msa255059.2{91_M781}   ACGCAAGGAA ATTATACATT TTCACATAAA GTAGAAGTAA AAAATGAAGC
    msa255059.2{91_COH1}   ACGCAAGGAA ATTATACATT TTCACATAAA GTAGAAGTAA AAAATGAAGC
  msa255059.2{91_18RS21}   ACGCAAGGAA ATTATACATT TTCACATAAA GTAGAAGTAA AAAATGAAGC
    msa255059.2{91_2603}   ACGCAAGGAA ATTATACATT TTCACATAAA GTAGAAGTAA AAAATGAAGC
  msa255059.2{91_1169NT}   ACGCAAGGAA ATTATACATT TTCACATAAA GTAGAAGTAA AAAATGAAGC
     msa255059.2{91_090}   ACGCAAGGAA ATTATACATT TTCACATAAA GTAGAAGTAA AAAATGAAGC
    msa255059.2{91_A909}   ACGCAAGGAA ATTATACATT TTCACATAAA GTAGAAGTAA AAAATGAAGC
  msa255059.2{91_CJB110}   ACGCAAGGAA ATTATACATT TTCACATAAA GTAGAAGTAA AAAATGAAGC
    msa255059.2{91_H36B}   ACGCAAGGAA ATTATACATT TTCACATAAA GTAGAAGTAA AAAATGAAGC
msa255059.2{91_JM9130013}  ACGCAAGGAA ATTATACATT TTCACATAAA GTAGAAGTAA AAAATGAAGC
               Consensus   ********** ********** ********** ********** **********

                           651                                                700
    msa255059.2{91_M732}   TAAGGTAGCG AGTCCAACTC AATTTACATT GGACAAAGGA GACAGAATTT
    msa255059.2{91_M781}   TAAGGTAGCG AGTCCAACTC AATTTACATT GGACAAAGGA GACAGAATTT
    msa255059.2{91_COH1}   TAAGGTAGCG AGTCCAACTC AATTTACATT GGACAAAGGA GACAGAATTT
  msa255059.2{91_18RS21}   TAAGGTAGCG AGTCCAACTC AATTTACATT GGACAAAGGA GACAGAATTT
```

Table 89: Comparative Sequences relating to SAG1350

```
    msa255059.2{91_2603}  TAAGGTAGCG AGTCCAACTC AATTTACATT GGACAAAGGA GACAGAATTT
  msa255059.2{91_1169NT}  TAAGGTAGCG AGTCCAACTC AATTTACATT GGACAAAGGA GACAGAATTT
     msa255059.2{91_090}  TAAGGTAGCG AGTCCAACTC AATTTACATT GGACAAAGGA GACAGAATTT
    msa255059.2{91_A909}  TAAGGTAGCG AGTCCAACTC AATTTACATT GGACAAAGGA GACAGAATTT
  msa255059.2{91_CJB110}  TAAGGTAGCG AGTCCAACTC AATTTACATT GGACAAAGGA GACAGAATTT
    msa255059.2{91_H36B}  TAAGGTAGCG AGTCCAACTC AATTTACATT GGACAAAGGA GACAGAATTT
msa255059.2{91_JM9130013}  TAAGGTAGCG AGTCCAACTC AATTTACATT GGACAAAGGA GACAGAATTT
               Consensus  ********** ********** ********** ********** **********

                          701                                                750
    msa255059.2{91_M732}  TTTACGACCA AATACTAACT ATTGAAGGAA ATCAGTGGTT ATCTTATAAA
    msa255059.2{91_M781}  TTTACGACCA AATACTAACT ATTGAAGGAA ATCAGTGGTT ATCTTATAAA
    msa255059.2{91_COH1}  TTTACGACCA AATACTAACT ATTGAAGGAA ATCAGTGGTT ATCTTATAAA
  msa255059.2{91_18RS21}  TTTACGACCA AATACTAACT ATTGAAGGAA ATCAGTGGTT ATCTTATAAA
    msa255059.2{91_2603}  TTTACGACCA AATACTAACT ATTGAAGGAA ATCAGTGGTT ATCTTATAAA
  msa255059.2{91_1169NT}  TTTACGACCA AATACTAACT ATTGAAGGAA ATCAGTGGTT ATCTTATAAA
     msa255059.2{91_090}  TTTACGACCA AATACTAACT ATTGAAGGAA ATCAGTGGTT ATCTTATAAA
    msa255059.2{91_A909}  TTTACGACCA AATACTAACT ATTGAAGGAA ATCAGTGGTT ATCTTATAAA
  msa255059.2{91_CJB110}  TTTACGACCA AATACTAACT ATTGAAGGAA ATCAGTGGTT ATCTTATAAA
    msa255059.2{91_H36B}  TTTACGACCA AATACTAACT ATTGAAGGAA ATCAGTGGTT ATCTTATAAA
msa255059.2{91_JM9130013}  TTTACGACCA AATACTAACT ATTGAAGGAA ATCAGTGGTT ATCTTATAAA
               Consensus  ********** ********** ********** ********** **********

                          751                                                800
    msa255059.2{91_M732}  TCATTCAATG GTGTTCGTCG TTTTGTTTTG CTAGGTAAAG CATCTTCAGT
    msa255059.2{91_M781}  TCATTCAATG GTGTTCGTCG TTTTGTTTTG CTAGGTAAAG CATCTTCAGT
    msa255059.2{91_COH1}  TCATTCAATG GTGTTCGTCG TTTTGTTTTG CTAGGTAAAG CATCTTCAGT
  msa255059.2{91_18RS21}  TCATTCAATG GTGTTCGTCG TTTTGTTTTG CTAGGTAAAG CATCTTCAGT
    msa255059.2{91_2603}  TCATTCAATG GTGTTCGTCG TTTTGTTTTG CTAGGTAAAG CATCTTCAGT
  msa255059.2{91_1169NT}  TCATTCAATG GTGTTCGTCG TTTTGTTTTG CTAGGTAAAG CATCTTCAGT
     msa255059.2{91_090}  TCATTCAATG GTGTTCGTCG TTTTGTTTTG CTAGGTAAAG CATCTTCAGT
    msa255059.2{91_A909}  TCATTCAATG GTGTTCGTCG TTTTGTTTTG CTAGGTAAAG CATCTTCAGT
  msa255059.2{91_CJB110}  TCATTCAATG GTGTTCGTCG TTTTGTTTTG CTAGGTAAAG CATCTTCAGT
    msa255059.2{91_H36B}  TCATTCAATG GTGTTCGTCG TTTTGTTTTG CTAGGTAAAG CATCTTCAGT
msa255059.2{91_JM9130013}  TCATTCAATG GTGTTCGTCG TTTTGTTTTG CTAGGTAAAG CATCTTCAGT
               Consensus  ********** ********** ********** ********** **********

                          801                                                850
    msa255059.2{91_M732}  AGAAAAAACT GAAGATAAAG AAAAAGTGTC TCCTCAACCA CAAGCCCGTA
    msa255059.2{91_M781}  AGAAAAAACT GAAGATAAAG AAAAAGTGTC TCCTCAACCA CAAGCCCGTA
    msa255059.2{91_COH1}  AGAAAAAACT GAAGATAAAG AAAAAGTGTC TCCTCAACCA CAAGCCCGTA
  msa255059.2{91_18RS21}  AGAAAAAACT GAAGATAAAG AAAAAGTGTC TCCTCAACCA CAAGCCCGTA
    msa255059.2{91_2603}  AGAAAAAACT GAAGATAAAG AAAAAGTGTC TCCTCAACCA CAAGCCCGTA
  msa255059.2{91_1169NT}  AGAAAAAACT GAAGATAAAG AAAAAGTGTC TCCTCAACCA CAAGCCCGTA
     msa255059.2{91_090}  AGAAAAAACT GAAGATAAAG AAAAAGTGTC TCCTCAACCA CAAGCCCGTA
    msa255059.2{91_A909}  AGAAAAAACT GAAGATAAAG AAAAAGTGTC TCCTCAACCA CAAGCCCGTA
  msa255059.2{91_CJB110}  AGAAAAAACT GAAGATAAAG AAAAAGTGTC TCCTCAACCA CAAGCCCGTA
    msa255059.2{91_H36B}  AGAAAAAACT GAAGATAAAG AAAAAGTGTC TCCTCAACCA CAAGCCCGTA
msa255059.2{91_JM9130013}  AGAAAAAACT GAAGATAAAG AAAAAGTGTC TCCTCAACCA CAAGCCCGTA
               Consensus  ********** ********** ********** ********** **********

                          851                                                900
    msa255059.2{91_M732}  TTACTAAAAC TGGTAGACTG ACTATTTcTA ACGAAACAAC TACAGGTTTT
    msa255059.2{91_M781}  TTACTAAAAC TGGTAGACTG ACTATTTcTA ACGAAACAAC TACAGGTTTT
    msa255059.2{91_COH1}  TTACTAAAAC TGGTAGACTG ACTATTTcTA ACGAAACAAC TACAGGTTTT
  msa255059.2{91_18RS21}  TTACTAAAAC TGGTAGACTG ACTATTTcTA ACGAAACAAC TACAGGTTTT
    msa255059.2{91_2603}  TTACTAAAAC TGGTAGACTG ACTATTTcTA ACGAAACAAC TACAGGTTTT
  msa255059.2{91_1169NT}  TTACTAAAAC TGGTAGACTG ACTATTTcTA ACGAAACAAC TACAGGTTTT
     msa255059.2{91_090}  TTACTAAAAC TGGTAGACTG ACTATTTcTA ACGAAACAAC TACAGGTTTT
    msa255059.2{91_A909}  TTACTAAAAC TGGTAGACTG ACTATTTcTA ACGAAACAAC TACAGGTTTT
  msa255059.2{91_CJB110}  TTACTAAAAC TGGTAGACTG ACTATTTcTA ACGAAACAAC TACAGGTTTT
    msa255059.2{91_H36B}  TTACTAAAAC TGGTAGACTG ACTATTTcTA ACGAAACAAC TACAGGTTTT
msa255059.2{91_JM9130013}  TTACTAAAAC TGGTAGACTG ACTATTTaTA ACGAAACAAC TACAGGTTTT
               Consensus  ********** ********** *******-** ********** **********

                          901                                                950
    msa255059.2{91_M732}  GATATTTTAA TTACGAATAT TAAAGATGAT AACGGTATCG CTGCTGTTAA
    msa255059.2{91_M781}  GATATTTTAA TTACGAATAT TAAAGATGAT AACGGTATCG CTGCTGTTAA
    msa255059.2{91_COH1}  GATATTTTAA TTACGAATAT TAAAGATGAT AACGGTATCG CTGCTGTTAA
  msa255059.2{91_18RS21}  GATATTTTAA TTACGAATAT TAAAGATGAT AACGGTATCG CTGCTGTTAA
    msa255059.2{91_2603}  GATATTTTAA TTACGAATAT TAAAGATGAT AACGGTATCG CTGCTGTTAA
  msa255059.2{91_1169NT}  GATATTTTAA TTACGAATAT TAAAGATGAT AACGGTATCG CTGCTGTTAA
     msa255059.2{91_090}  GATATTTTAA TTACGAATAT TAAAGATGAT AACGGTATCG CTGCTGTTAA
    msa255059.2{91_A909}  GATATTTTAA TTACGAATAT TAAAGATGAT AACGGTATCG CTGCTGTTAA
  msa255059.2{91_CJB110}  GATATTTTAA TTACGAATAT TAAAGATGAT AACGGTATCG CTGCTGTTAA
    msa255059.2{91_H36B}  GATATTTTAA TTACGAATAT TAAAGATGAT AACGGTATCG CTGCTGTTAA
msa255059.2{91_JM9130013}  GATATTTTAA TTACGAATAT TAAAGATGAT AACGGTATCG CTGCTGTTAA
               Consensus  ********** ********** ********** ********** **********

                          951                                               1000
    msa255059.2{91_M732}  GGTACCGGTT TGGACTGAAC AAGGAGGGCA AGATGATATT AAATGGTATA
    msa255059.2{91_M781}  GGTACCGGTT TGGACTGAAC AAGGAGGGCA AGATGATATT AAATGGTATA
    msa255059.2{91_COH1}  GGTACCGGTT TGGACTGAAC AAGGAGGGCA AGATGATATT AAATGGTATA
```

Table 89: Comparative Sequences relating to SAG1350

```
     msa255059.2{91_18RS21}  GGTACCGGTT TGGACTGAAC AAGGAGGGCA AGATGATATT AAATGGTATA
       msa255059.2{91_2603}  GGTACCGGTT TGGACTGAAC AAGGAGGGCA AGATGATATT AAATGGTATA
     msa255059.2{91_1169NT}  GGTACCGGTT TGGACTGAAC AAGGAGGGCA AGATGATATT AAATGGTATA
        msa255059.2{91_090}  GGTACCGGTT TGGACTGAAC AAGGAGGGCA AGATGATATT AAATGGTATA
       msa255059.2{91_A909}  GGTACCGGTT TGGACTGAAC AAGGAGGGCA AGATGATATT AAATGGTATA
     msa255059.2{91_CJB110}  GGTACCGGTT TGGACTGAAC AAGGAGGGCA AGATGATATT AAATGGTATA
       msa255059.2{91_H36B}  GGTACCGGTT TGGACTGAAC AAGGAGGGCA AGATGATATT AAATGGTATA
 msa255059.2{91_JM9130013}  GGTACCGGTT TGGACTGAAC AAGGAGGGCA AGATGATATT AAATGGTATA
                  Consensus  ********** ********** ********** ********** **********

                             1001                                            1050
       msa255059.2{91_M732}  CAGCTGTAAC TACTGGGGAT GGCAACTACA AAGTAGCTGT ATCATTTGCT
       msa255059.2{91_M781}  CAGCTGTAAC TACTGGGGAT GGCAACTACA AAGTAGCTGT ATCATTTGCT
       msa255059.2{91_COH1}  CAGCTGTAAC TACTGGGGAT GGCAACTACA AAGTAGCTGT ATCATTTGCT
     msa255059.2{91_18RS21}  CAGCTGTAAC TACTGGGGAT GGCAACTACA AAGTAGCTGT ATCATTTGCT
       msa255059.2{91_2603}  CAGCTGTAAC TACTGGGGAT GGCAACTACA AAGTAGCTGT ATCATTTGCT
     msa255059.2{91_1169NT}  CAGCTGTAAC TACTGGGGAT GGCAACTACA AAGTAGCTGT ATCATTTGCT
        msa255059.2{91_090}  CAGCTGTAAC TACTGGGGAT GGCAACTACA AAGTAGCTGT ATCATTTGCT
       msa255059.2{91_A909}  CAGCTGTAAC TACTGGGGAT GGCAACTACA AAGTAGCTGT ATCATTTGCT
     msa255059.2{91_CJB110}  CAGCTGTAAC TACTGGGGAT GGCAACTACA AAGTAGCTGT ATCATTTGCT
       msa255059.2{91_H36B}  CAGCTGTAAC TACTGGGGAT GGCAACTACA AAGTAGCTGT ATCATTTGCT
  msa255059.2{91_JM9130013}  CAGCTGTAAC TACTGGGGAT GGCAACTACA AAGTAGCTGT ATCATTTGCT
                  Consensus  ********** ********** ********** ********** **********

                             1051                                            1100
       msa255059.2{91_M732}  GACCATAAGA ATGAGAAGGG TCTTTATAAT ATTCATTTAT ACTACCAAGA
       msa255059.2{91_M781}  GACCATAAGA ATGAGAAGGG TCTTTATAAT ATTCATTTAT ACTACCAAGA
       msa255059.2{91_COH1}  GACCATAAGA ATGAGAAGGG TCTTTATAAT ATTCATTTAT ACTACCAAGA
     msa255059.2{91_18RS21}  GACCATAAGA ATGAGAAGGG TCTTTATAAT ATTCATTTAT ACTACCAAGA
       msa255059.2{91_2603}  GACCATAAGA ATGAGAAGGG TCTTTATAAT ATTCATTTAT ACTACCAAGA
     msa255059.2{91_1169NT}  GACCATAAGA ATGAGAAGGG TCTTTATAAT ATTCATTTAT ACTACCAAGA
        msa255059.2{91_090}  GACCATAAGA ATGAGAAGGG TCTTTATAAT ATTCATTTAT ACTACCAAGA
       msa255059.2{91_A909}  GACCATAAGA ATGAGAAGGG TCTTTATAAT ATTCATTTAT ACTACCAAGA
     msa255059.2{91_CJB110}  GACCATAAGA ATGAGAAGGG TCTTTATAAT ATTCATTTAT ACTACCAAGA
       msa255059.2{91_H36B}  GACCATAAGA ATGAGAAGGG TCTTTATAAT ATTCATTTAT ACTACCAAGA
  msa255059.2{91_JM9130013}  GACCATAAGA ATGAGAAGGG TCTTTATAAT ATTCATTTAT ACTACCAAGA
                  Consensus  ********** ********** ********** ********** **********

                             1101                                            1150
       msa255059.2{91_M732}  AGCTAGTGGG ACACTTGTAG GTGTAACAGG AACTAAAGTG ACAGTAGCTG
       msa255059.2{91_M781}  AGCTAGTGGG ACACTTGTAG GTGTAACAGG AACTAAAGTG ACAGTAGCTG
       msa255059.2{91_COH1}  AGCTAGTGGG ACACTTGTAG GTGTAACAGG AACTAAAGTG ACAGTAGCTG
     msa255059.2{91_18RS21}  AGCTAGTGGG ACACTTGTAG GTGTAACAGG AACTAAAGTG ACAGTAGCTG
       msa255059.2{91_2603}  AGCTAGTGGG ACACTTGTAG GTGTAACAGG AACTAAAGTG ACAGTAGCTG
     msa255059.2{91_1169NT}  AGCTAGTGGG ACACTTGTAG GTGTAACAGG AACTAAAGTG ACAGTAGCTG
        msa255059.2{91_090}  AGCTAGTGGG ACACTTGTAG GTGTAACAGG AACTAAAGTG ACAGTAGCTG
       msa255059.2{91_A909}  AGCTAGTGGG ACACTTGTAG GTGTAACAGG AACTAAAGTG ACAGTAGCTG
     msa255059.2{91_CJB110}  AGCTAGTGGG ACACTTGTAG GTGTAACAGG AACTAAAGTG ACAGTAGCTG
       msa255059.2{91_H36B}  AGCTAGTGGG ACACTTGTAG GTGTAACAGG AACTAAAGTG ACAGTAGCTG
  msa255059.2{91_JM9130013}  AGCTAGTGGG ACACTTGTAG GTGTAACAGG AACTAAAGTG ACAGTAGCTG
                  Consensus  ********** ********** ********** ********** **********

                             1151                                            1200
       msa255059.2{91_M732}  GAACTAATTC TTCTCAAGAA CCTATTGAAA ATGGTTTAcC AAAGACTGGT
       msa255059.2{91_M781}  GAACTAATTC TTCTCAAGAA CCTATTGAAA ATGGTTTAcC AAAGACTGGT
       msa255059.2{91_COH1}  GAACTAATTC TTCTCAAGAA CCTATTGAAA ATGGTTTAcC AAAGACTGGT
     msa255059.2{91_18RS21}  GAACTAATTC TTCTCAAGAA CCTATTGAAA ATGGTTTAgC AAAGACTGGT
       msa255059.2{91_2603}  GAACTAATTC TTCTCAAGAA CCTATTGAAA ATGGTTTAgC AAAGACTGGT
     msa255059.2{91_1169NT}  GAACTAATTC TTCTCAAGAA CCTATTGAAA ATGGTTTAgC AAAGACTGGT
        msa255059.2{91_090}  GAACTAATTC TTCTCAAGAA CCTATTGAAA ATGGTTTAgC AAAGACTGGT
       msa255059.2{91_A909}  GAACTAATTC TTCTCAAGAA CCTATTGAAA ATGGTTTAgC AAAGACTGGT
     msa255059.2{91_CJB110}  GAACTAATTC TTCTCAAGAA CCTATTGAAA ATGGTTTAgC AAAGACTGGT
       msa255059.2{91_H36B}  GAACTAATTC TTCTCAAGAA CCTATTGAAA ATGGTTTAgC AAAGACTGGT
  msa255059.2{91_JM9130013}  GAACTAATTC TTCTCAAGAA CCTATTGAAA ATGGTTTAgC AAAGACTGGT
                  Consensus  ********** ********** ********** ********_* **********

                             1201                                            1250
       msa255059.2{91_M732}  GTTTATAATA TTATCGGAAG TACTGAAGTA AAAAATGAAG CTAAAATATC
       msa255059.2{91_M781}  GTTTATAATA TTATCGGAAG TACTGAAGTA AAAAATGAAG CTAAAATATC
       msa255059.2{91_COH1}  GTTTATAATA TTATCGGAAG TACTGAAGTA AAAAATGAAG CTAAAATATC
     msa255059.2{91_18RS21}  GTTTATAATA TTATCGGAAG TACTGAAGTA AAAAATGAAG CTAAAATATC
       msa255059.2{91_2603}  GTTTATAATA TTATCGGAAG TACTGAAGTA AAAAATGAAG CTAAAATATC
     msa255059.2{91_1169NT}  GTTTATAATA TTATCGGAAG TACTGAAGTA AAAAATGAAG CTAAAATATC
        msa255059.2{91_090}  GTTTATAATA TTATCGGAAG TACTGAAGTA AAAAATGAAG CTAAAATATC
       msa255059.2{91_A909}  GTTTATAATA TTATCGGAAG TACTGAAGTA AAAAATGAAG CTAAAATATC
     msa255059.2{91_CJB110}  GTTTATAATA TTATCGGAAG TACTGAAGTA AAAAATGAAG CTAAAATATC
       msa255059.2{91_H36B}  GTTTATAATA TTATCGGAAG TACTGAAGTA AAAAATGAAG CTAAAATATC
  msa255059.2{91_JM9130013}  GTTTATAATA TTATCGGAAG TACTGAAGTA AAAAATGAAG CTAAAATATC
                  Consensus  ********** ********** ********** ********** **********

                             1251                                            1300
       msa255059.2{91_M732}  AAGTCAGACC CAATTTACTT TAGAAAAAGG TGACAAAATA AATTATGATC
       msa255059.2{91_M781}  AAGTCAGACC CAATTTACTT TAGAAAAAGG TGACAAAATA AATTATGATC
```

Table 89: Comparative Sequences relating to SAG1350

```
     msa255059.2{91_COH1}  AAGTCAGACC CAATTTACTT TAGAAAAAGG TGACAAAATA AATTATGATC
   msa255059.2{91_18RS21}  AAGTCAGACC CAATTTACTT TAGAAAAAGG TGACAAAATA AATTATGATC
     msa255059.2{91_2603}  AAGTCAGACC CAATTTACTT TAGAAAAAGG TGACAAAATA AATTATGATC
   msa255059.2{91_1169NT}  AAGTCAGACC CAATTTACTT TAGAAAAAGG TGACAAAATA AATTATGATC
      msa255059.2{91_090}  AAGTCAGACC CAATTTACTT TAGAAAAAGG TGACAAAATA AATTATGATC
     msa255059.2{91_A909}  AAGTCAGACC CAATTTACTT TAGAAAAAGG TGACAAAATA AATTATGATC
   msa255059.2{91_CJB110}  AAGTCAGACC CAATTTACTT TAGAAAAAGG TGACAAAATA AATTATGATC
     msa255059.2{91_H36B}  AAGTCAGACC CAATTTACTT TAGAAAAAGG TGACAAAATA AATTATGATC
msa255059.2{91_JM9130013}  AAGTCAGACC CAATTTACTT TAGAAAAAGG TGACAAAATA AATTATGATC
                Consensus  ********** ********** ********** ********** **********

                           1301                                              1350
     msa255059.2{91_M732}  AAGTATTGAC AGCAGATGGT TACCAGTGGA TTTCTTACAA ATCTTATAGT
     msa255059.2{91_M781}  AAGTATTGAC AGCAGATGGT TACCAGTGGA TTTCTTACAA ATCTTATAGT
     msa255059.2{91_COH1}  AAGTATTGAC AGCAGATGGT TACCAGTGGA TTTCTTACAA ATCTTATAGT
   msa255059.2{91_18RS21}  AAGTATTGAC AGCAGATGGT TACCAGTGGA TTTCTTACAA ATCTTATAGT
     msa255059.2{91_2603}  AAGTATTGAC AGCAGATGGT TACCAGTGGA TTTCTTACAA ATCTTATAGT
   msa255059.2{91_1169NT}  AAGTATTGAC AGCAGATGGT TACCAGTGGA TTTCTTACAA ATCTTATAGT
      msa255059.2{91_090}  AAGTATTGAC AGCAGATGGT TACCAGTGGA TTTCTTACAA ATCTTATAGT
     msa255059.2{91_A909}  AAGTATTGAC AGCAGATGGT TACCAGTGGA TTTCTTACAA ATCTTATAGT
   msa255059.2{91_CJB110}  AAGTATTGAC AGCAGATGGT TACCAGTGGA TTTCTTACAA ATCTTATAGT
     msa255059.2{91_H36B}  AAGTATTGAC AGCAGATGGT TACCAGTGGA TTTCTTACAA ATCTTATAGT
msa255059.2{91_JM9130013}  AAGTATTGAC AGCAGATGGT TACCAGTGGA TTTCTTACAA ATCTTATAGT
                Consensus  ********** ********** ********** ********** **********

                           1351                                              1400
     msa255059.2{91_M732}  GGTGTTCGTC GCTATATTCC TGTGAAAAAG CTAACTACAA GTAGTGAAAA
     msa255059.2{91_M781}  GGTGTTCGTC GCTATATTCC TGTGAAAAAG CTAACTACAA GTAGTGAAAA
     msa255059.2{91_COH1}  GGTGTTCGTC GCTATATTCC TGTGAAAAAG CTAACTACAA GTAGTGAAAA
   msa255059.2{91_18RS21}  GGTGTTCGTC GCTATATTCC TGTGAAAAAG CTAACTACAA GTAGTGAAAA
     msa255059.2{91_2603}  GGTGTTCGTC GCTATATTCC TGTGAAAAAG CTAACTACAA GTAGTGAAAA
   msa255059.2{91_1169NT}  GGTGTTCGTC GCTATATTCC TGTGAAAAAG CTAACTACAA GTAGTGAAAA
      msa255059.2{91_090}  GGTGTTCGTC GCTATATTCC TGTGAAAAAG CTAACTACAA GTAGTGAAAA
     msa255059.2{91_A909}  GGTGTTCGTC GCTATATTCC TGTGAAAAAG CTAACTACAA GTAGTGAAAA
   msa255059.2{91_CJB110}  GGTGTTCGTC GCTATATTCC TGTGAAAAAG CTAACTACAA GTAGTGAAAA
     msa255059.2{91_H36B}  GGTGTTCGTC GCTATATTCC TGTGAAAAAG CTAACTACAA GTAGTGAAAA
msa255059.2{91_JM9130013}  GGTGTTCGTC GCTATATTCC TGTGAAAAAG CTAACTACAA GTAGTGAAAA
                Consensus  ********** ********** ********** ********** **********

                           1401                                              1450
     msa255059.2{91_M732}  AGCGAAAGAT GAGGCGACTA AACCGACTAG TTATCCCAAC TTACCTAAAA
     msa255059.2{91_M781}  AGCGAAAGAT GAGGCGACTA AACCGACTAG TTATCCCAAC TTACCTAAAA
     msa255059.2{91_COH1}  AGCGAAAGAT GAGGCGACTA AACCGACTAG TTATCCCAAC TTACCTAAAA
   msa255059.2{91_18RS21}  AGCGAAAGAT GAGGCGACTA AACCGACTAG TTATCCCAAC TTACCTAAAA
     msa255059.2{91_2603}  AGCGAAAGAT GAGGCGACTA AACCGACTAG TTATCCCAAC TTACCTAAAA
   msa255059.2{91_1169NT}  AGCGAAAGAT GAGGCGACTA AACCGACTAG TTATCCCAAC TTACCTAAAA
      msa255059.2{91_090}  AGCGAAAGAT GAGGCGACTA AACCGACTAG TTATCCCAAC TTACCTAAAA
     msa255059.2{91_A909}  AGCGAAAGAT GAGGCGACTA AACCGACTAG TTATCCCAAC TTACCTAAAA
   msa255059.2{91_CJB110}  AGCGAAAGAT GAGGCGACTA AACCGACTAG TTATCCCAAC TTACCTAAAA
     msa255059.2{91_H36B}  AGCGAAAGAT GAGGCGACTA AACCGACTAG TTATCCCAAC TTACCTAAAA
msa255059.2{91_JM9130013}  AGCGAAAGAT GAGGCGACTA AACCGACTAG TTATCCCAAC TTACCTAAAA
                Consensus  ********** ********** ********** ********** **********

                           1451                                              1500
     msa255059.2{91_M732}  CAGGTACCTA TACATTTACT AAAACTGTAG ATGTGAAaAG TCAACCTAAA
     msa255059.2{91_M781}  CAGGTACCTA TACATTTACT AAAACTGTAG ATGTGAAaAG TCAACCTAAA
     msa255059.2{91_COH1}  CAGGTACCTA TACATTTACT AAAACTGTAG ATGTGAAaAG TCAACCTAAA
   msa255059.2{91_18RS21}  CAGGTACCTA TACATTTACT AAAACTGTAG ATGTGAAaAG TCAACCTAAA
     msa255059.2{91_2603}  CAGGTACCTA TACATTTACT AAAACTGTAG ATGTGAAaAG TCAACCTAAA
   msa255059.2{91_1169NT}  CAGGTACCTA TACATTTACT AAAACTGTAG ATGTGAAaAG TCAACCTAAA
      msa255059.2{91_090}  CAGGTACCTA TACATTTACT AAAACTGTAG ATGTGAAgAG TCAACCTAAA
     msa255059.2{91_A909}  CAGGTACCTA TACATTTACT AAAACTGTAG ATGTGAAgAG TCAACCTAAA
   msa255059.2{91_CJB110}  CAGGTACCTA TACATTTACT AAAACTGTAG ATGTGAAgAG TCAACCTAAA
     msa255059.2{91_H36B}  CAGGTACCTA TACATTTACT AAAACTGTAG ATGTGAAgAG TCAACCTAAA
msa255059.2{91_JM9130013}  CAGGTACCTA TACATTTACT AAAACTGTAG ATGTGAAgAG TCAACCTAAA
                Consensus  ********** ********** ********** *******_** **********

                           1501                                              1550
     msa255059.2{91_M732}  GTATCAAGTC CAGTGGAATT TAATTTTCAA AAGGGTGAAA AAATACATTA
     msa255059.2{91_M781}  GTATCAAGTC CAGTGGAATT TAATTTTCAA AAGGGTGAAA AAATACATTA
     msa255059.2{91_COH1}  GTATCAAGTC CAGTGGAATT TAATTTTCAA AAGGGTGAAA AAATACATTA
   msa255059.2{91_18RS21}  GTATCAAGTC CAGTGGAATT TAATTTTCAA AAGGGTGAAA AAATACATTA
     msa255059.2{91_2603}  GTATCAAGTC CAGTGGAATT TAATTTTCAA AAGGGTGAAA AAATACATTA
   msa255059.2{91_1169NT}  GTATCAAGTC CAGTGGAATT TAATTTTCAA AAGGGTGAAA AAATACATTA
      msa255059.2{91_090}  GTATCAAGTC CAGTGGAATT TAATTTTCAA AAGGGTGAAA AAATACATTA
     msa255059.2{91_A909}  GTATCAAGTC CAGTGGAATT TAATTTTCAA AAGGGTGAAA AAATACATTA
   msa255059.2{91_CJB110}  GTATCAAGTC CAGTGGAATT TAATTTTCAA AAGGGTGAAA AAATACATTA
     msa255059.2{91_H36B}  GTATCAAGTC CAGTGGAATT TAATTTTCAA AAGGGTGAAA AAATACATTA
msa255059.2{91_JM9130013}  GTATCAAGTC CAGTGGAATT TAATTTTCAA AAGGGTGAAA AAATACATTA
                Consensus  ********** ********** ********** ********** **********

                           1551                                              1600
     msa255059.2{91_M732}  TGATCAAGTG TTAGTAGTAG ATGGTCATCA GTGGATTTCA TACAAGAGTT
```

Table 89: Comparative Sequences relating to SAG1350

```
    msa255059.2{91_M781}  TGATCAAGTG TTAGTAGTAG ATGGTCATCA GTGGATTTCA TACAAGAGTT
    msa255059.2{91_COH1}  TGATCAAGTG TTAGTAGTAG ATGGTCATCA GTGGATTTCA TACAAGAGTT
  msa255059.2{91_18RS21}  TGATCAAGTG TTAGTAGTAG ATGGTCATCA GTGGATTTCA TACAAGAGTT
    msa255059.2{91_2603}  TGATCAAGTG TTAGTAGTAG ATGGTCATCA GTGGATTTCA TACAAGAGTT
  msa255059.2{91_1169NT}  TGATCAAGTG TTAGTAGTAG ATGGTCATCA GTGGATTTCA TACAAGAGTT
     msa255059.2{91_090}  TGATCAAGTG TTAGTAGTAG ATGGTCATCA GTGGATTTCA TACAAGAGTT
    msa255059.2{91_A909}  TGATCAAGTG TTAGTAGTAG ATGGTCATCA GTGGATTTCA TACAAGAGTT
  msa255059.2{91_CJB110}  TGATCAAGTG TTAGTAGTAG ATGGTCATCA GTGGATTTCA TACAAGAGTT
    msa255059.2{91_H36B}  TGATCAAGTG TTAGTAGTAG ATGGTCATCA GTGGATTTCA TACAAGAGTT
msa255059.2{91_JM9130013}  TGATCAAGTG TTAGTAGTAG ATGGTCATCA GTGGATTTCA TACAAGAGTT
               Consensus  ********** ********** ********** ********** **********

                          1601                        1629
    msa255059.2{91_M732}  ATTCCGGTAT TCGTCGCTAT ATTGAAATT
    msa255059.2{91_M781}  ATTCCGGTAT TCGTCGCTAT ATTGAAATT
    msa255059.2{91_COH1}  ATTCCGGTAT TCGTCGCTAT ATTGAAATT
  msa255059.2{91_18RS21}  ATTCCGGTAT TCGTCGCTAT ATTGAAATT
    msa255059.2{91_2603}  ATTCCGGTAT TCGTCGCTAT ATTGAAATT
  msa255059.2{91_1169NT}  ATTCCGGTAT TCGTCGCTAT ATTGAAATT
     msa255059.2{91_090}  ATTCCGGTAT TCGTCGCTAT ATTGAAATT
    msa255059.2{91_A909}  ATTCCGGTAT TCGTCGCTAT ATTGAAATT
  msa255059.2{91_CJB110}. ATTCCGGTAT TCGTCGCTAT ATTGAAATT
    msa255059.2{91_H36B}  ATTCCGGTAT TCGTCGCTAT ATTGAAATT
msa255059.2{91_JM9130013}  ATTCCGGTAT TCGTCGCTAT ATTGAAATT
               Consensus  ********** ********** *********
```

SEQ ID NO. 8912
STRAIN 2603 frame: 1

```
MKKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNS
SNETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNYVYSKE
TEVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFCGVRRYAAIESLDPSGGS
ETKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILT
IEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGF
DILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAVSFADHKNEKGLYN
IHLYYQEASGTLVGVTGTKVTVAGTNSSQEPIENGLAKTGVYNIIGSTEVKNEAKISSQT
QFTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPN
LPKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRY
IEI
```

SEQ ID NO. 8913
STRAIN 090 frame: 1

```
KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNYVYSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFCGVRRYAAIESLDPSGGSE
TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGTKVTVAGTNSSQEPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI
```

SEQ ID NO. 8914
STRAIN A909 frame: 1

```
KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNYVYSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFCGVRRYAAIESLDPSGGSE
TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGTKVTVAGTNSSQEPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI
```

SEQ ID NO. 8915
STRAIN H36B frame: 1

```
KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDDNNSS
NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNYVYSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFCGVRRYAAIESLDPSGGSE
TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGTKVTVAGTNSSQEPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI
```

SEQ ID NO. 8916
STRAIN 18RS21 frame: 1

```
KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNYVYSKET
```

Table 89: Comparative Sequences relating to SAG1350

EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFCGVRRYAAIESLDPSGGSE
TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGTKVTVAGTNSSQEPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8917
STRAIN M732 frame: 1
QVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSSNET
SASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNYVYSKETEVK
NTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFGGVRRYAAIESLDPSGGSETKA
PTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTIEGN
QWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFDILI
TNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAVSFADHKNEKGLYNIHLY
YQEASGTLVGVTGTKVTVAGTNSSQEPIENGLPKTGVYNIIGSTEVKNEAKISSQTQFTL
EKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNLPKT
GTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYIEI

SEQ ID NO. 8918
STRAIN COH1 frame: 1
KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNYVYSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFGGVRRYAAIESLDPSGGSE
TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGTKVTVAGTNSSQEPIENGLPKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8919
STRAIN M781 frame: 1
KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNYVYSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFGGVRRYAAIESLDPSGGSE
TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGTKVTVAGTNSSQEPIENGLPKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8920
STRAIN CJB110 frame: 1
KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNYVYSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFCGVRRYAAIESLDPSGGSE
TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGTKVTVAGTNSSQEPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8921
STRAIN 1169NT frame: 1
KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNYVYSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFGGVRRYAAIESLDPSGGSE
TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGTKVTVAGTNSSQEPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8922
STRAIN JM9130013 frame: 1
KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNYVYSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFCGVRRYAAIESLDPSGGSE
TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTIYNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVTGTKVTVAGTNSSQEPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ

Table 89: Comparative Sequences relating to SAG1350

```
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI


PRETTY of: /biotmp/msa255178.2{*}   February 11, 2003 08:51  ..

                           1                                                 50
       msa255178.2{91_090}  ~kkgQVNDTK QSYSLRKYKF GLASVILGSF IMVTSPVFAD QTTSVQVNNQ
     msa255178.2{91_18RS21}  ~kkgQVNDTK QSYSLRKYKF GLASVILGSF IMVTSPVFAD QTTSVQVNNQ
      msa255178.2{91_2603}  mkkgQVNDTK QSYSLRKYKF GLASVILGSF IMVTSPVFAD QTTSVQVNNQ
      msa255178.2{91_A909}  ~kkgQVNDTK QSYSLRKYKF GLASVILGSF IMVTSPVFAD QTTSVQVNNQ
     msa255178.2{91_CJB110}  ~kkgQVNDTK QSYSLRKYKF GLASVILGSF IMVTSPVFAD QTTSVQVNNQ
      msa255178.2{91_H36B}  ~kkgQVNDTK QSYSLRKYKF GLASVILGSF IMVTSPVFAD QTTSVQVNNQ
  msa255178.2{91_JM9130013}  ~kkgQVNDTK QSYSLRKYKF GLASVILGSF IMVTSPVFAD QTTSVQVNNQ
      msa255178.2{91_COH1}  ~kkgQVNDTK QSYSLRKYKF GLASVILGSF IMVTSPVFAD QTTSVQVNNQ
      msa255178.2{91_M781}  ~kkgQVNDTK QSYSLRKYKF GLASVILGSF IMVTSPVFAD QTTSVQVNNQ
      msa255178.2{91_M732}  ~~~~QVNDTK QSYSLRKYKF GLASVILGSF IMVTSPVFAD QTTSVQVNNQ
     msa255178.2{91_1169NT}  ~kkgQVNDTK QSYSLRKYKF GLASVILGSF IMVTSPVFAD QTTSVQVNNQ
                 Consensus  *---****** ********** ********** ********** **********

                           51                                               100
       msa255178.2{91_090}  TGTSVDaNNS SNETSASSVI TSNNDSVQAS DKVVNSQNTA TKDITTPLVE
     msa255178.2{91_18RS21}  TGTSVDaNNS SNETSASSVI TSNNDSVQAS DKVVNSQNTA TKDITTPLVE
      msa255178.2{91_2603}  TGTSVDaNNS SNETSASSVI TSNNDSVQAS DKVVNSQNTA TKDITTPLVE
      msa255178.2{91_A909}  TGTSVDaNNS SNETSASSVI TSNNDSVQAS DKVVNSQNTA TKDITTPLVE
     msa255178.2{91_CJB110}  TGTSVDaNNS SNETSASSVI TSNNDSVQAS DKVVNSQNTA TKDITTPLVE
      msa255178.2{91_H36B}  TGTSVDdNNS SNETSASSVI TSNNDSVQAS DKVVNSQNTA TKDITTPLVE
  msa255178.2{91_JM9130013}  TGTSVDaNNS SNETSASSVI TSNNDSVQAS DKVVNSQNTA TKDITTPLVE
      msa255178.2{91_COH1}  TGTSVDaNNS SNETSASSVI TSNNDSVQAS DKVVNSQNTA TKDITTPLVE
      msa255178.2{91_M781}  TGTSVDaNNS SNETSASSVI TSNNDSVQAS DKVVNSQNTA TKDITTPLVE
      msa255178.2{91_M732}  TGTSVDaNNS SNETSASSVI TSNNDSVQAS DKVVNSQNTA TKDITTPLVE
     msa255178.2{91_1169NT}  TGTSVDaNNS SNETSASSVI TSNNDSVQAS DKVVNSQNTA TKDITTPLVE
                 Consensus  ******-*** ********** ********** ********** **********

                           101                                              150
       msa255178.2{91_090}  TKPMVEKTLP EQGNYVYSKE TEVKNTPSKS APVAFYAKKG DKVFYDQVFN
     msa255178.2{91_18RS21}  TKPMVEKTLP EQGNYVYSKE TEVKNTPSKS APVAFYAKKG DKVFYDQVFN
      msa255178.2{91_2603}  TKPMVEKTLP EQGNYVYSKE TEVKNTPSKS APVAFYAKKG DKVFYDQVFN
      msa255178.2{91_A909}  TKPMVEKTLP EQGNYVYSKE TEVKNTPSKS APVAFYAKKG DKVFYDQVFN
     msa255178.2{91_CJB110}  TKPMVEKTLP EQGNYVYSKE TEVKNTPSKS APVAFYAKKG DKVFYDQVFN
      msa255178.2{91_H36B}  TKPMVEKTLP EQGNYVYSKE TEVKNTPSKS APVAFYAKKG DKVFYDQVFN
  msa255178.2{91_JM9130013}  TKPMVEKTLP EQGNYVYSKE TEVKNTPSKS APVAFYAKKG DKVFYDQVFN
      msa255178.2{91_COH1}  TKPMVEKTLP EQGNYVYSKE TEVKNTPSKS APVAFYAKKG DKVFYDQVFN
      msa255178.2{91_M781}  TKPMVEKTLP EQGNYVYSKE TEVKNTPSKS APVAFYAKKG DKVFYDQVFN
      msa255178.2{91_M732}  TKPMVEKTLP EQGNYVYSKE TEVKNTPSKS APVAFYAKKG DKVFYDQVFN
     msa255178.2{91_1169NT}  TKPMVEKTLP EQGNYVYSKE TEVKNTPSKS APVAFYAKKG DKVFYDQVFN
                 Consensus  ********** ********** ********** ********** **********

                           151                                              200
       msa255178.2{91_090}  KDNVKWISYK SFcGVRRYAA IESLDPSGGS ETKAPTPVTN SGSNNQEKIA
     msa255178.2{91_18RS21}  KDNVKWISYK SFcGVRRYAA IESLDPSGGS ETKAPTPVTN SGSNNQEKIA
      msa255178.2{91_2603}  KDNVKWISYK SFcGVRRYAA IESLDPSGGS ETKAPTPVTN SGSNNQEKIA
      msa255178.2{91_A909}  KDNVKWISYK SFcGVRRYAA IESLDPSGGS ETKAPTPVTN SGSNNQEKIA
     msa255178.2{91_CJB110}  KDNVKWISYK SFcGVRRYAA IESLDPSGGS ETKAPTPVTN SGSNNQEKIA
      msa255178.2{91_H36B}  KDNVKWISYK SFcGVRRYAA IESLDPSGGS ETKAPTPVTN SGSNNQEKIA
  msa255178.2{91_JM9130013}  KDNVKWISYK SFcGVRRYAA IESLDPSGGS ETKAPTPVTN SGSNNQEKIA
      msa255178.2{91_COH1}  KDNVKWISYK SFgGVRRYAA IESLDPSGGS ETKAPTPVTN SGSNNQEKIA
      msa255178.2{91_M781}  KDNVKWISYK SFgGVRRYAA IESLDPSGGS ETKAPTPVTN SGSNNQEKIA
      msa255178.2{91_M732}  KDNVKWISYK SFgGVRRYAA IESLDPSGGS ETKAPTPVTN SGSNNQEKIA
     msa255178.2{91_1169NT}  KDNVKWISYK SFgGVRRYAA IESLDPSGGS ETKAPTPVTN SGSNNQEKIA
                 Consensus  ********** **-******* ********** ********** **********

                           201                                              250
       msa255178.2{91_090}  TQGNYTFSHK VEVKNEAKVA SPTQFTLDKG DRIFYDQILT IEGNQWLSYK
     msa255178.2{91_18RS21}  TQGNYTFSHK VEVKNEAKVA SPTQFTLDKG DRIFYDQILT IEGNQWLSYK
      msa255178.2{91_2603}  TQGNYTFSHK VEVKNEAKVA SPTQFTLDKG DRIFYDQILT IEGNQWLSYK
      msa255178.2{91_A909}  TQGNYTFSHK VEVKNEAKVA SPTQFTLDKG DRIFYDQILT IEGNQWLSYK
     msa255178.2{91_CJB110}  TQGNYTFSHK VEVKNEAKVA SPTQFTLDKG DRIFYDQILT IEGNQWLSYK
      msa255178.2{91_H36B}  TQGNYTFSHK VEVKNEAKVA SPTQFTLDKG DRIFYDQILT IEGNQWLSYK
  msa255178.2{91_JM9130013}  TQGNYTFSHK VEVKNEAKVA SPTQFTLDKG DRIFYDQILT IEGNQWLSYK
      msa255178.2{91_COH1}  TQGNYTFSHK VEVKNEAKVA SPTQFTLDKG DRIFYDQILT IEGNQWLSYK
      msa255178.2{91_M781}  TQGNYTFSHK VEVKNEAKVA SPTQFTLDKG DRIFYDQILT IEGNQWLSYK
      msa255178.2{91_M732}  TQGNYTFSHK VEVKNEAKVA SPTQFTLDKG DRIFYDQILT IEGNQWLSYK
     msa255178.2{91_1169NT}  TQGNYTFSHK VEVKNEAKVA SPTQFTLDKG DRIFYDQILT IEGNQWLSYK
                 Consensus  ********** ********** ********** ********** **********

                           251                                              300
       msa255178.2{91_090}  SFNGVRRFVL LGKASSVEKT EDKEKVSPQP QARITKTGRL TIsNETTTGF
     msa255178.2{91_18RS21}  SFNGVRRFVL LGKASSVEKT EDKEKVSPQP QARITKTGRL TIsNETTTGF
      msa255178.2{91_2603}  SFNGVRRFVL LGKASSVEKT EDKEKVSPQP QARITKTGRL TIsNETTTGF
      msa255178.2{91_A909}  SFNGVRRFVL LGKASSVEKT EDKEKVSPQP QARITKTGRL TIsNETTTGF
     msa255178.2{91_CJB110}  SFNGVRRFVL LGKASSVEKT EDKEKVSPQP QARITKTGRL TIsNETTTGF
```

Table 89: Comparative Sequences relating to SAG1350

```
      msa255178.2{91_H36B}  SFNGVRRFVL LGKASSVEKT EDKEKVSPQP QARITKTGRL TIsNETTTGF
  msa255178.2{91_JM9130013}  SFNGVRRFVL LGKASSVEKT EDKEKVSPQP QARITKTGRL TIyNETTTGF
      msa255178.2{91_COH1}  SFNGVRRFVL LGKASSVEKT EDKEKVSPQP QARITKTGRL TIsNETTTGF
      msa255178.2{91_M781}  SFNGVRRFVL LGKASSVEKT EDKEKVSPQP QARITKTGRL TIsNETTTGF
      msa255178.2{91_M732}  SFNGVRRFVL LGKASSVEKT EDKEKVSPQP QARITKTGRL TIsNETTTGF
    msa255178.2{91_1169NT}  SFNGVRRFVL LGKASSVEKT EDKEKVSPQP QARITKTGRL TIsNETTTGF
                 Consensus  ********** ********** ********** ********** **_*******

                            301                                              350
       msa255178.2{91_090}  DILITNIKDD NGIAAVKVPV WTEQGGQDDI KWYTAVTTGD GNYKVAVSFA
     msa255178.2{91_18RS21}  DILITNIKDD NGIAAVKVPV WTEQGGQDDI KWYTAVTTGD GNYKVAVSFA
      msa255178.2{91_2603}  DILITNIKDD NGIAAVKVPV WTEQGGQDDI KWYTAVTTGD GNYKVAVSFA
      msa255178.2{91_A909}  DILITNIKDD NGIAAVKVPV WTEQGGQDDI KWYTAVTTGD GNYKVAVSFA
    msa255178.2{91_CJB110}  DILITNIKDD NGIAAVKVPV WTEQGGQDDI KWYTAVTTGD GNYKVAVSFA
      msa255178.2{91_H36B}  DILITNIKDD NGIAAVKVPV WTEQGGQDDI KWYTAVTTGD GNYKVAVSFA
  msa255178.2{91_JM9130013}  DILITNIKDD NGIAAVKVPV WTEQGGQDDI KWYTAVTTGD GNYKVAVSFA
      msa255178.2{91_COH1}  DILITNIKDD NGIAAVKVPV WTEQGGQDDI KWYTAVTTGD GNYKVAVSFA
      msa255178.2{91_M781}  DILITNIKDD NGIAAVKVPV WTEQGGQDDI KWYTAVTTGD GNYKVAVSFA
      msa255178.2{91_M732}  DILITNIKDD NGIAAVKVPV WTEQGGQDDI KWYTAVTTGD GNYKVAVSFA
    msa255178.2{91_1169NT}  DILITNIKDD NGIAAVKVPV WTEQGGQDDI KWYTAVTTGD GNYKVAVSFA
                 Consensus  ********** ********** ********** ********** **********

                            351                                              400
       msa255178.2{91_090}  DHKNEKGLYN IHLYYQEASG TLVGVTGTKV TVAGTNSSQE PIENGLaKTG
     msa255178.2{91_18RS21}  DHKNEKGLYN IHLYYQEASG TLVGVTGTKV TVAGTNSSQE PIENGLaKTG
      msa255178.2{91_2603}  DHKNEKGLYN IHLYYQEASG TLVGVTGTKV TVAGTNSSQE PIENGLaKTG
      msa255178.2{91_A909}  DHKNEKGLYN IHLYYQEASG TLVGVTGTKV TVAGTNSSQE PIENGLaKTG
    msa255178.2{91_CJB110}  DHKNEKGLYN IHLYYQEASG TLVGVTGTKV TVAGTNSSQE PIENGLaKTG
      msa255178.2{91_H36B}  DHKNEKGLYN IHLYYQEASG TLVGVTGTKV TVAGTNSSQE PIENGLaKTG
  msa255178.2{91_JM9130013}  DHKNEKGLYN IHLYYQEASG TLVGVTGTKV TVAGTNSSQE PIENGLaKTG
      msa255178.2{91_COH1}  DHKNEKGLYN IHLYYQEASG TLVGVTGTKV TVAGTNSSQE PIENGLpKTG
      msa255178.2{91_M781}  DHKNEKGLYN IHLYYQEASG TLVGVTGTKV TVAGTNSSQE PIENGLpKTG
      msa255178.2{91_M732}  DHKNEKGLYN IHLYYQEASG TLVGVTGTKV TVAGTNSSQE PIENGLpKTG
    msa255178.2{91_1169NT}  DHKNEKGLYN IHLYYQEASG TLVGVTGTKV TVAGTNSSQE PIENGLaKTG
                 Consensus  ********** ********** ********** ********** ******_***

                            401                                              450
       msa255178.2{91_090}  VYNIIGSTEV KNEAKISSQT QFTLEKGDKI NYDQVLTADG YQWISYKSYS
     msa255178.2{91_18RS21}  VYNIIGSTEV KNEAKISSQT QFTLEKGDKI NYDQVLTADG YQWISYKSYS
      msa255178.2{91_2603}  VYNIIGSTEV KNEAKISSQT QFTLEKGDKI NYDQVLTADG YQWISYKSYS
      msa255178.2{91_A909}  VYNIIGSTEV KNEAKISSQT QFTLEKGDKI NYDQVLTADG YQWISYKSYS
    msa255178.2{91_CJB110}  VYNIIGSTEV KNEAKISSQT QFTLEKGDKI NYDQVLTADG YQWISYKSYS
      msa255178.2{91_H36B}  VYNIIGSTEV KNEAKISSQT QFTLEKGDKI NYDQVLTADG YQWISYKSYS
  msa255178.2{91_JM9130013}  VYNIIGSTEV KNEAKISSQT QFTLEKGDKI NYDQVLTADG YQWISYKSYS
      msa255178.2{91_COH1}  VYNIIGSTEV KNEAKISSQT QFTLEKGDKI NYDQVLTADG YQWISYKSYS
      msa255178.2{91_M781}  VYNIIGSTEV KNEAKISSQT QFTLEKGDKI NYDQVLTADG YQWISYKSYS
      msa255178.2{91_M732}  VYNIIGSTEV KNEAKISSQT QFTLEKGDKI NYDQVLTADG YQWISYKSYS
    msa255178.2{91_1169NT}  VYNIIGSTEV KNEAKISSQT QFTLEKGDKI NYDQVLTADG YQWISYKSYS
                 Consensus  ********** ********** ********** ********** **********

                            451                                              500
       msa255178.2{91_090}  GVRRYIPVKK LTTSSEKAKD EATKPTSYPN LPKTGTYTFT KTVDVKSQPK
     msa255178.2{91_18RS21}  GVRRYIPVKK LTTSSEKAKD EATKPTSYPN LPKTGTYTFT KTVDVKSQPK
      msa255178.2{91_2603}  GVRRYIPVKK LTTSSEKAKD EATKPTSYPN LPKTGTYTFT KTVDVKSQPK
      msa255178.2{91_A909}  GVRRYIPVKK LTTSSEKAKD EATKPTSYPN LPKTGTYTFT KTVDVKSQPK
    msa255178.2{91_CJB110}  GVRRYIPVKK LTTSSEKAKD EATKPTSYPN LPKTGTYTFT KTVDVKSQPK
      msa255178.2{91_H36B}  GVRRYIPVKK LTTSSEKAKD EATKPTSYPN LPKTGTYTFT KTVDVKSQPK
  msa255178.2{91_JM9130013}  GVRRYIPVKK LTTSSEKAKD EATKPTSYPN LPKTGTYTFT KTVDVKSQPK
      msa255178.2{91_COH1}  GVRRYIPVKK LTTSSEKAKD EATKPTSYPN LPKTGTYTFT KTVDVKSQPK
      msa255178.2{91_M781}  GVRRYIPVKK LTTSSEKAKD EATKPTSYPN LPKTGTYTFT KTVDVKSQPK
      msa255178.2{91_M732}  GVRRYIPVKK LTTSSEKAKD EATKPTSYPN LPKTGTYTFT KTVDVKSQPK
    msa255178.2{91_1169NT}  GVRRYIPVKK LTTSSEKAKD EATKPTSYPN LPKTGTYTFT KTVDVKSQPK
                 Consensus  ********** ********** ********** ********** **********

                            501                                   543
       msa255178.2{91_090}  VSSPVEFNFQ KGEKIHYDQV LVVDGHQWIS YKSYSGIRRY IEI
     msa255178.2{91_18RS21}  VSSPVEFNFQ KGEKIHYDQV LVVDGHQWIS YKSYSGIRRY IEI
      msa255178.2{91_2603}  VSSPVEFNFQ KGEKIHYDQV LVVDGHQWIS YKSYSGIRRY IEI
      msa255178.2{91_A909}  VSSPVEFNFQ KGEKIHYDQV LVVDGHQWIS YKSYSGIRRY IEI
    msa255178.2{91_CJB110}  VSSPVEFNFQ KGEKIHYDQV LVVDGHQWIS YKSYSGIRRY IEI
      msa255178.2{91_H36B}  VSSPVEFNFQ KGEKIHYDQV LVVDGHQWIS YKSYSGIRRY IEI
  msa255178.2{91_JM9130013}  VSSPVEFNFQ KGEKIHYDQV LVVDGHQWIS YKSYSGIRRY IEI
      msa255178.2{91_COH1}  VSSPVEFNFQ KGEKIHYDQV LVVDGHQWIS YKSYSGIRRY IEI
      msa255178.2{91_M781}  VSSPVEFNFQ KGEKIHYDQV LVVDGHQWIS YKSYSGIRRY IEI
      msa255178.2{91_M732}  VSSPVEFNFQ KGEKIHYDQV LVVDGHQWIS YKSYSGIRRY IEI
    msa255178.2{91_1169NT}  VSSPVEFNFQ KGEKIHYDQV LVVDGHQWIS YKSYSGIRRY IEI
                 Consensus  ********** ********** ********** ********** ***
```

CLAIMS:

1. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS polynucleotide sequence which is homologous to a polynucleotide sequence of both GAS and *Streptococcus pneumoniae*.

2. The immunogenic composition of claim 1, wherein said GBS polypeptides are encoded by GBS polynucleotide sequences selected from GBS Subset 1.

3. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS polynucleotide sequence which is homologous to a polynucleotide sequence of GAS.

4. The immunogenic composition of claim 3, wherein said GBS polypeptides are encoded by GBS polynucleotide sequences selected from GBS Subset 2.

5. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS polynucleotide sequence which is homologous to a polynucleotide sequence of *Streptococcus pneumoniae*.

6. The immunogenic composition of claim 5, wherein said GBS polypeptides are encoded by GBS polynucleotide sequences selected from GBS Subset 3.

7. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS serotype polynucleotide sequence which is homologous to at least one other GBS serotype.

8. The immunogenic composition of claim 2, 4 or 6, wherein one or more of the GBS polypeptides are encoded by GBS serotype polynucleotide sequences which are homologous to at least one other GBS serotype.

9. An immunogenic composition comprising a fusion protein, wherein said fusion protein comprises a first polypeptide sequence which is encoded by a GBS serotype polynucleotide which is conserved across one or more GBS serotypes.

10. A polynucleotide sequence, or a fragment comprising at least 10 contiguous polynucleotides, selected from the sequences set forth on Tables 13 – 31 and 40 – 89.

11. The polynucleotide fragment of claim 10, wherein said fragment is derived from a GBS serotype polynucleotide sequence and is homologous to at least one additional GBS serotype polynucleotide sequence.

Figure 1

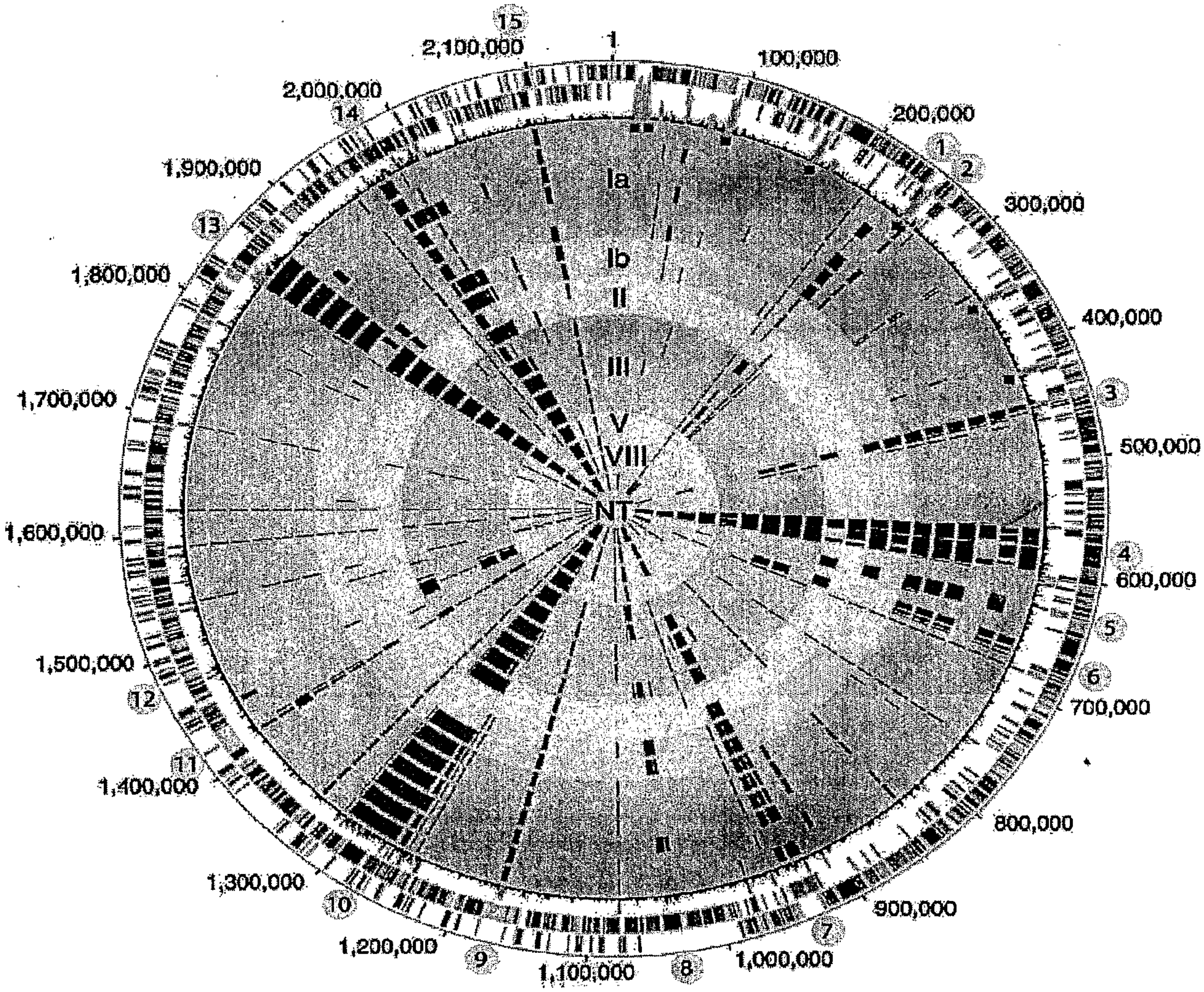

1
100,000
200,000
300,000
400,000
500,000
600,000
700,000
800,000
900,000
1,000,000
1,100,000
1,200,000
1,300,000
1,400,000
1,500,000
1,600,000
1,700,000
1,800,000
1,900,000
2,000,000
2,100,000
①
②
③
④
⑤
⑥
⑦
⑧
⑨
⑩
⑪
⑫
⑬
⑭
⑮
Ia
Ib
II
III
V
VIII
NT

Figure 2

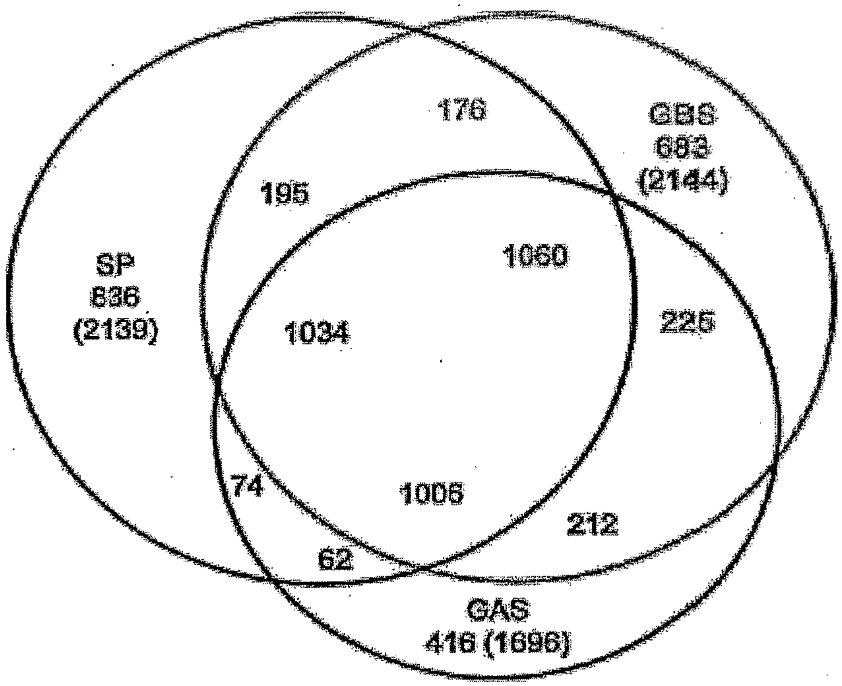
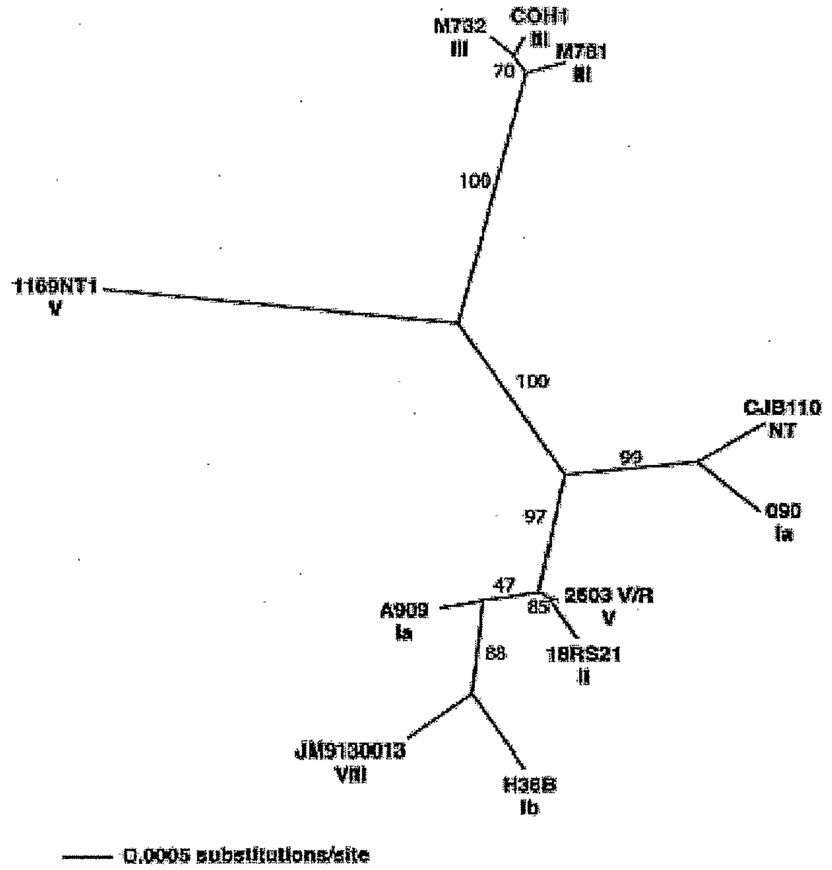

176
GBS
683
(2144)
195
1060
SP
836
(2139)
1034
225
74
1006
212
62
GAS
416 (1696)

Figure 3


M732
III
COH1
III
M781
III
70
100
1169NT1
V
100
CJB110
NT
99
090
Ia
97
47
2603 V/R
V
85
A909
Ia
88
18RS21
II
JM9130013
VIII
H36B
Ib
0.0005 substitutions/site

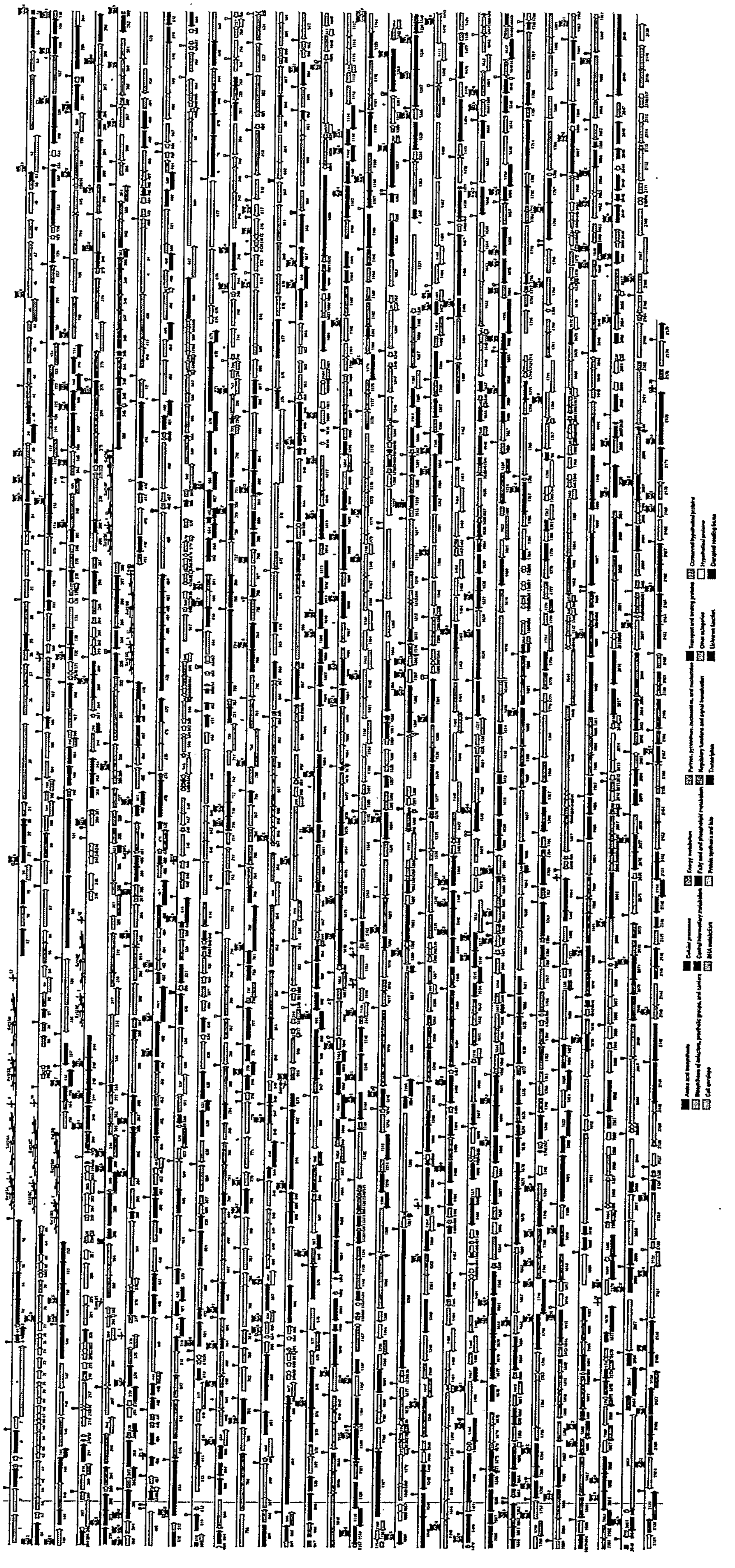

Amino acid biosynthesis
Biosynthesis of cofactors, prosthetic groups, and carriers
Cell envelope
Cellular processes
Central intermediary metabolism
DNA metabolism
Energy metabolism
Fatty acid and phospholipid metabolism
Protein synthesis and fate
Purines, pyrimidines, nucleosides, and nucleotides
Regulatory functions and signal transduction
Transcription
Transport and binding proteins
Other categories
Unknown function
Conserved hypothetical proteins
Hypothetical proteins
Disrupted reading frame

FIGURE 4

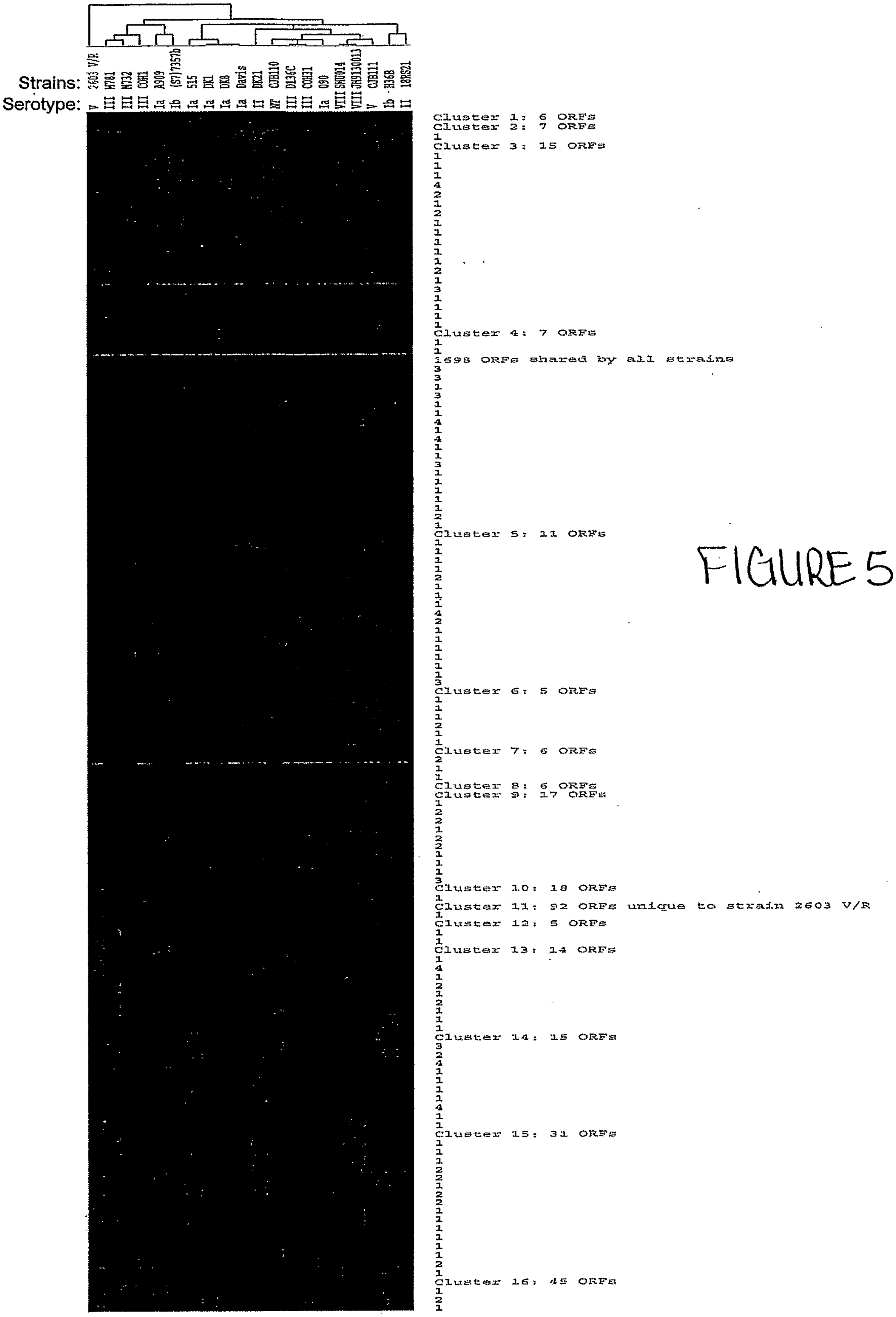

Strains:
2603 V/R
M781
M732
COH1
A909
(S7)7357b
515
DK1
DK8
Davis
DK21
CJB110
D136C
COH31
090
SMU014
JM9130013
CJB111
H36B
18RS21
Serotype:
V
III
III
III
Ia
Ib
Ia
Ia
Ia
Ia
II
NT
III
III
Ia
VIII
VIII
V
Ib
II
Cluster 1: 6 ORFs
Cluster 2: 7 ORFs
1
Cluster 3: 15 ORFs
1
1
1
4
2
1
2
1
1
1
1
1
2
1
3
1
1
1
1
Cluster 4: 7 ORFs
1
1
1698 ORFs shared by all strains
3
3
1
3
1
1
4
1
4
1
1
3
1
1
1
1
1
2
1
Cluster 5: 11 ORFs
1
1
1
1
2
1
1
1
4
2
1
1
1
1
1
1
3
Cluster 6: 5 ORFs
1
1
1
2
1
1
Cluster 7: 6 ORFs
2
1
1
Cluster 8: 6 ORFs
Cluster 9: 17 ORFs
1
2
2
1
2
2
1
1
1
3
Cluster 10: 18 ORFs
1
Cluster 11: 92 ORFs unique to strain 2603 V/R
1
Cluster 12: 5 ORFs
1
1
Cluster 13: 14 ORFs
1
4
1
2
1
2
1
1
1
Cluster 14: 15 ORFs
3
2
4
1
1
1
1
4
1
1
Cluster 15: 31 ORFs
1
1
1
2
2
1
2
2
1
1
1
1
1
2
1
Cluster 16: 45 ORFs
1
2
1

FIGURE 5